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Protein kinase C- $\eta$  (PKC $\eta$ ) is involved in cell proliferation, differentiation and plays an anti-apoptotic role in various cancer models. The purpose of this dissertation is to understand the regulation of PKC $\eta$  in cell death signaling in breast cancer cells.

Tumor promoting phorbol esters are potent activators of PKC and prolonged treatment with these activators leads to downregulation and desensitization of PKC signaling. PKC $\eta$  resists phorbol ester-induced downregulation and upregulated in response to prolonged treatment. We have found that phosphorylation of PKC $\eta$  at conserved serine/threonine sites is increased by phorbol ester treatment. Single mutations that prevent phosphorylation at these conserved sites resulted in downregulation of PKC $\eta$ . These results suggest that phosphorylation of PKC $\eta$  at conserved sites prevents its downregulation.

We have found that PKC $\eta$  can be significantly downregulated by inhibition of two pathways: PKC and phosphoinositide 3-kinase (PI3K) using pharmacological inhibitors. Inhibitors of PKC and PI3K induce dephosphorylation of PKC $\eta$  by a calyculin A-specific phosphatase. These inhibitors differ in their ability to degrade PKC $\eta$  via the proteasome-mediated pathway. Downregulation of PKC $\eta$  by PKC inhibitor is not mediated by the proteasome degradation pathway, whereas downregulation by PI3K inhibitor is dependent on the proteasome. These results demonstrate that dephosphorylation is important for PKC $\eta$  downregulation and this occurs through two distinct mechanisms.

A comparison of PKC protein levels in a series of isogenic cell lines representing a breast cancer progression model revealed that PKC $\eta$  protein levels increased from the normal, benign

stage to the pre-malignant and metastatic stages. These results indicate that PKC $\eta$  plays a potential role in breast cancer progression. Further analysis indicated that overexpression of PKC $\eta$  in the MCF-7 breast adenocarcinoma cell line conferred resistance to tumor necrosis factor-alpha-related apoptosis-inducing ligand (TRAIL)-induced cell death. Therefore, PKC $\eta$  protects breast cancer cells from TRAIL-induced apoptosis. Depletion of PKC $\eta$  by small interfering RNA (siRNA) resulted in increased dimerization of pro-apoptotic Bax and decreased induction of anti-apoptotic Mcl-1 by TRAIL. These results indicate that PKC $\eta$  may exert its anti-apoptotic effect by targeting Bcl-2 proteins, Bax and Mcl-1.

**REGULATION OF PROTEIN KINASE C  $\epsilon$  IN BREAST CANCER CELLS**

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## LIST OF ABBREVIATIONS

A	Alanine
A-loop	activation loop
Bak	Bcl-2 antagonist/killer
Bax	Bcl-2-associated X protein
BH	Bcl-2 homology
BHK	baby hamster kidney cells
BID	BH3-interacting domain death agonist
Bok	Bcl-2-related ovarian killer
Cal A	calyculin A
cIAP-2	cytoplasmic inhibitor of apoptosis protein-2
DAG	diacylglycerol
DcR	decoy receptor
DD	death domain

DGK	diacylglycerol kinase
DISC	death-inducing signaling complex
DR	death receptor
E	glutamate
ERK	extracellular signal-related kinase
FADD	Fas-associated death domain
FRET	fluorescent resonance energy transfer
GAPDH	glyceraldehydes-3-phosphate dehydrogenase
HEK 293	human embryonic kidney 293 cells
HM	hydrophobic motif
I $\kappa$ B	inhibitor of $\kappa$ B
IKK $\alpha$	I $\kappa$ B kinase $\alpha$
IKK $\beta$	I $\kappa$ B kinase $\beta$
ILV	indolactam V
IP3	inositol-1,4,5-trisphosphate

JNK	c-Jun NH(2)-terminal kinase
MAPK	mitogen-activated protein kinase
Mcl-1	myeloid cell leukemia sequence-1
mTOR	mammalian target of rapamycin
mTORC2	mammalian target of rapamycin complex 2
NF- $\kappa$ B	nuclear factor kappa-B
OA	okadaic acid
p70S6K	p70 ribosomal S6 kinase
PARP	poly(ADP)ribose polymerase
PDBu	phorbol 12, 13-dibutyrate
PKD1	phosphoinositide-dependent kinase-1
PHLPP	PH domain and leucin rich repeat protein phosphatase
PI3K	phosphoinositide 3-kinase
PIP <sub>2</sub>	phosphatidylinositol bisphosphate

PIP <sub>3</sub>	phosphatidylinositol (3,4,5)-trisphosphate
PKC	Protein kinase C
PLC	phospholipase C
PMA	phorbol 12-myristate 13-acetate
PP1	protein phosphatase 1
PP2A	protein phosphatase 2A
PP2B	protein phosphatase 2B
PS	phosphatidylserine
PTEN	phosphatase and tensin homologue deleted from chromosome-10
RACK	receptors for activated C kinase
S	serine
siRNA	small interfering RNA
T	threonine
TM	transmembrane domain



TM	turn motif
TNF	Tumor necrosis factor- $\alpha$
TPA	12- <i>O</i> -tetradecanoyl-phorbol-13-acetate
TRAIL	TNF-related apoptosis-inducing ligand
WT	wild-type

## CHAPTER I

### INTRODUCTION

#### **Breast Cancer**

Breast cancer is the most common type of cancer among American women, with the exception of skin cancer. It is estimated that 1 in 8 women (12%) will develop invasive breast cancer at some point in their lives. The American Cancer Society reported an expected diagnosis of 192,370 new invasive breast cancer cases and 40,610 breast cancer-related deaths among women in the United States in 2009 ([www.cancer.org](http://www.cancer.org)). Since deregulation of cellular processes such as cell proliferation and cell death can contribute to the cancer, it is critical to identify and characterize proteins involved in regulating these cellular processes to improve drug therapy and patient outcome. Members of the protein kinase C (PKC) family play critical roles in regulating cell proliferation, cell survival and tumor progression. Consequently they are attractive targets for cancer therapy [1].

#### **Protein Kinase C (PKC)**

##### **a. Molecular heterogeneity and structure**

PKC was first identified by Nishizuka and colleagues as calcium-activated, phospholipid-dependent serine/threonine kinases [2, 3]. It is now established that PKC is a multigene family consisting of 10 isozymes differing in their structural characteristics and biochemical properties

[4-6]. All PKC family members share a common structural backbone mainly consisting of a C-terminal catalytic domain and an N-terminal regulatory domain (Figure 1) [7]. The catalytic domain contains motifs involved in ATP-binding, substrate binding and catalysis [8]. The regulatory domain maintains PKCs in an inactive conformation by interacting with the catalytic domain through an autoinhibitory pseudosubstrate sequence (resembling a PKC substrate but contains an alanine in the phospho-acceptor position) [9]. This interaction prevents substrate access to the catalytic site [10]. The catalytic and regulatory domains are connected by a hinge region (V3) which also serves as a site of proteolysis. PKC isozymes are divided into three subclasses based on their cofactor requirements and structural characteristics [11]. Conventional PKCs (cPKC $\alpha$ , - $\beta$ I,  $\beta$ II,  $\gamma$ ) contain the four conserved regions (C1-C4) and variable regions (V1-V5) and are dependent on both Ca<sup>2+</sup> and diacylglycerol (DAG) for activation. Novel PKCs (nPKC $\delta$ , - $\epsilon$ , - $\eta$ , - $\theta$ ) differ from conventional PKCs because their C2 domain (Ca<sup>2+</sup>-binding domain) is replaced by a C2-like domain that does not depend on Ca<sup>2+</sup> for activation. The C1 domain contains the two cysteine-rich zinc finger structures (C1A and C1B) involved in membrane targeting and binding to DAG [12]. Phorbol esters are pharmacological activators of PKCs that mimic DAG and bind to the C1A and C1B domains [13]. Atypical PKCs (aPKC $\iota/\lambda$ , - $\zeta$ ) lack the calcium-sensitive C2 domain and contain an atypical C1 domain with only one cysteine-rich zinc finger structure that binds to PIP<sub>3</sub> and ceramide, but not DAG or phorbol esters. These distinct structural and biochemical properties of PKC isozymes provide a basis for their diverse functional roles as key signal transducers in a wide range of cellular processes

including proliferation, differentiation and cell death [14]. The activity and function of PKCs are controlled by three major mechanisms: 1) phosphorylation, 2) co-factor binding and membrane translocation and 3) desensitization mechanisms resulting in degradation of the enzyme and signal termination [15]. These mechanisms will be described in detail in the following sections.

### **b. Regulation by phosphorylation**

It is generally accepted that PKCs are phosphorylated at three conserved phosphorylation sites which influence their maturation, activity and stability [16]. The three conserved sites of phosphorylation are located in the *activation loop* (near the active site), *turn motif* (at a turn in the structure) and *hydrophobic motif* (in the hydrophobic pocket of the kinase). Phosphoinositide-dependent kinase-1 (PDK1) has been shown to phosphorylate the activation loop of many proteins including PKC isozymes [17-21], Akt/PKB [22] and p70S6K [23]. The sequence of phosphorylation events has been well documented for conventional PKC isozymes; however, controversy remains regarding the phosphorylation events for novel and atypical PKCs. Newly synthesized PKCs are loosely tethered to the membrane in “open” conformation with the substrate binding and activation loop sites exposed [24]. PDK1 can phosphorylate the exposed activation loop site which triggers autophosphorylation events at the turn motif site and the hydrophobic site [25]. These phosphorylations stabilize the mature kinase in a conformation that is optimal for activity, not only for PKCs, but for many growth-factor activated AGC kinases [16, 26]. In addition to serine/threonine phosphorylation, conventional, novel and atypical PKCs can be phosphorylated at tyrosine sites [27]; however, most studies have been

centered on regulation of PKC $\delta$  by tyrosine phosphorylation [28–30]. The regulation of PKC $\eta$  by phosphorylation is not well established and this will be addressed in the second and third chapters.

### **c. Regulation by co-factors, activators and inhibitors**

PKCs are dependent on interaction with acidic phospholipids, such as phosphatidylserine (PS) at the plasma membrane for activity [31]. PKCs are generally inactive in the cytosol in a closed, auto-inhibited conformation that is resistant to proteolysis [24]. In response to activation by extracellular stimuli, PKCs are translocated from the cytosol to the membrane by interaction with receptors for activated C kinase (RACKS) [32]. Specific RACK binding sites on each PKC isozyme have been identified allowing for isozyme- specific localization and cellular responses [33, 34]. Once PKCs are in close proximity to the membrane, they bind with high affinity to co-factors such as DAG through their C1 and C2 domains [35]. This interaction provides the energy necessary to induce an open conformational change in the kinase that exposes the substrate-binding site leading to phosphorylation of downstream substrates [36] (Figure 2).

Another mode of activation involves proteolytic dissociation of the regulatory domain from the catalytic domain following membrane translocation. For cPKCs and nPKCs, proteolysis is achieved by Ca<sup>2+</sup> activated proteases, calpains [37] which leads to downregulation via the proteasome-mediated pathway [38]. In response to apoptotic stimuli, PKCs undergo limited proteolysis by caspases, a family of cysteine proteases that cleave proteins after aspartate

residues [39-41]. The catalytic fragment generated can activate downstream signaling events in the absence of activators or cofactors.

Two classes of PKC activators have been identified: tumor-promoting and non-tumor-promoting. The tumor-promoting activators include phorbol esters [42], ingenols [43], teleocidins [44] and octylindolactam V [45]. Non-tumor-promoting activators include bryostatins and DAG derivatives to name a few [46]. Conventional and novel PKCs are intracellular receptors for phorbol esters that activate PKCs in a manner similar to DAG because they share a common binding site [47-50]. Bryostatins antagonize the effects of phorbol esters and have been exploited for anti-cancer therapy [6]. Because of the differential actions of PKC activators, they have become useful tools in studying the function of PKC isozymes in tumor-promotion. Chapter 2 will focus on the regulation of PKC $\eta$  phosphorylation by tumor-promoting phorbol ester, phorbol 12, 13-dibutyrate (PDBu).

PKC inhibitors are classified based on their sites of action: catalytic site inhibitors and regulatory site inhibitors [6]. Catalytic site inhibitors such as bisindolymaleimides and derivatives act as competitive inhibitors for the ATP-binding site of PKCs [51, 52]. Regulatory domain inhibitors such as calphostin C act on the phorbol ester/DAG binding site of PKCs and is highly specific to PKC, but inhibits all isozymes to the same extent [53]. Another class of PKC inhibitors called cofactor inhibitors include molecules such as tamoxifen and spingosine which contain lipophilic regions that can interfere with PKC binding to phospholipids and DAG [54, 55]. Recently, isozyme-specific inhibitors have been identified based on their unique RACK

binding sequence [56, 57]. These peptide inhibitors act as competitive inhibitors that bind to RACKs and prevent them from binding and activating PKCs [56]. The IC<sub>50</sub> values for PKC inhibitors used in this study are described in Table 1.

#### **d. Inactivation and termination of PKC signaling**

Since localization to the membrane is important for PKC activation, termination of PKC signaling can be achieved by reversal of membrane translocation. PKCs are disengaged from the membrane by desensitization of G-protein coupled receptors and by their own autophosphorylation [58, 59]. PKC reporter assay studies indicate that the levels of active PKC correlate with the levels of Ca<sup>2+</sup> and DAG [60]. Therefore, depletion of these second messengers can result in inactivation of PKCs. DAGs are metabolized by diacylglycerol kinases (DGKs) that phosphorylate DAG to convert it to phosphatidic acid [61]. Thus, DGKs decrease the levels of DAG and thus inhibit activation of PKC.

Prolonged activation by phorbol esters leads to subsequent inactivation and degradation of PKCs [62]. This process is known as activation-induced downregulation. Downregulation occurs through an increased rate of degradation of PKCs rather than a decrease in protein synthesis [63]. However, there are controversies surrounding the mechanism of phorbol ester-induced downregulation of PKCs. It was first hypothesized that activation of PKCs results in a change in conformation that is more susceptible to proteolytic cleavage by proteases such as calpains [64]. It was later discovered that mutants lacking calpain cleavage sites or treatment with calpain inhibitors did not block downregulation of PKCs by phorbol esters indicating

calpains were not involved in this process [65-67]. The requirement of kinase activity of PKCs for downregulation by phorbol esters was also a subject of controversy. A mutation in the ATP-binding site rendered the PKC “catalytically inactive” and these mutants resisted downregulation by phorbol esters [68]. Other studies indicated that the catalytically inactive mutant could be downregulated in response to phorbol esters through the activity of other PKCs [69-71]. Furthermore, studies with specific PKC isozymes indicated kinase activity was required for PKC $\delta$  downregulation, but PKC $\epsilon$  downregulation required the activity of another endogenous PKC [63]. Therefore differences exist among PKC isozymes with regards to their downregulation mechanisms.

The active conformation of PKC is not only susceptible to cleavage by proteases, but also to dephosphorylation by phosphatases. As explained in the previous section, phosphorylation at three conserved sites is important to maintain PKC in a mature and active form. For conventional PKCs, it is generally known that dephosphorylation of these sites precedes degradation [72]. However, this mechanism is not well established for novel PKC isozymes, since it was shown that PKC $\delta$  requires phosphorylation at the activation loop site for phorbol ester-induced downregulation [73]. Furthermore, a recent report indicated that unphosphorylated kinase-inactive mutants of PKC $\epsilon$  and PKC $\alpha$  resisted PMA-induced downregulation and kinase-inactive mutants that retained priming phosphorylation were susceptible to PMA-induced downregulation [74]. Therefore, conflicts exist in the literature with regards to the link between phosphorylation state of PKCs and downregulation by phorbol esters.



Several downregulation mechanisms have been described for PKCs. The first was via the ubiquitin/proteasome pathway, a process by which proteins are “tagged” with ubiquitin for degradation via the proteasome machinery [75]. Ubiquitination and degradation of PKC- $\alpha$ , - $\delta$  and - $\epsilon$  were shown to be physiological responses to activation by several activators such as TPA, PMA, bryostatin and DAG [38, 76]. Dephosphorylation of PKC $\epsilon$  and PKC $\alpha$  seems to predispose them to ubiquitinylation [76]. A second PKC desensitization pathway bears similarity to receptor desensitization via internalization and endosome targeting. Several reports indicate that upon phorbol ester treatment, PKCs are targeted to endosomes for degradation [77-79]. Conventional PKCs (PKC $\alpha$  and PKC $\beta$ II) accumulate in the juxtannuclear/perinuclear region upon phorbol ester stimulation [78, 80] which is associated with dephosphorylation [72] and trafficking to endosomal compartments via caveolae (in the case PKC $\alpha$ ) [79]. The sequence of events for vesicle-mediated downregulation of novel PKC isozymes have not been fully elucidated, although there is evidence that novel PKCs are targeted to endosomes [77]. Interestingly, phorbol ester-induced accumulation of PKCs in the perinuclear region not only targets PKCs for degradation, but it also allows PKCs to perform their function to regulate internalization and membrane trafficking of receptors and other membrane-bound proteins [81]. The focus of chapter 3 is to elucidate the mechanisms of PKC $\eta$  downregulation in breast cancer cells.

Since PKCs were first identified as signaling molecules involved in the tumor promoting effects of phorbol esters [48], they have become therapeutic targets for the treatment of cancer [82]. PKC isozymes are commonly deregulated in various cancer types including prostate,

breast, colon, pancreatic, liver and kidney [82]. PKC isozymes also have variable roles in tumor biology depending on the cell type, tissue specificity and subcellular localization. Because of these differential effects of PKC isozymes, several PKC inhibitors such as staurosporine, bryostatin 1, curcumin and resveratrol have not gained much success in clinical trials [82]. Therefore, further research must be conducted to elucidate isozyme-specific regulation of PKCs to improve the current anti-cancer therapies. PKCs can function as “molecular sensors” to promote cell survival or execute cell death, thereby playing an important role in regulating apoptosis [83].

## **Apoptosis**

Activation of cell death pathways is a major mechanism by which anti-cancer drugs exert their cytotoxic effect. Apoptosis or programmed cell death is a physiological process by which an organism can maintain tissue homeostasis and development to promote cellular functions [84]. A deregulation in apoptosis can lead to disease states, such as Alzheimer’s, Huntington’s, glaucoma, autoimmune disorders and cancer. A defect in apoptotic signaling can also contribute to resistance to chemotherapeutic agents by tumors. Identifying and targeting key players that cause deregulation of apoptosis is an important strategy in developing effective therapeutics for these disease states.

The biochemical events leading to apoptosis can be characterized into two phases, the initial “commitment” phase and the execution phase. Caspases, a family of aspartate-specific cysteine

proteases, play a vital role in both the initiation and execution phases of apoptosis. Initiator caspase-8, -9, and -10 can activate executioner caspase-3, -6 and -7 to cleave intracellular substrates such as poly(ADP)ribose polymerase (PARP), lamins, PKC $\delta$  and other structural and regulatory proteins contributing to the apoptotic cascade [85]. Two major pathways involving the activation of caspases are the extrinsic (receptor-mediated) and intrinsic (mitochondrial) apoptotic pathways which will be described in the following sections (Figure 3).

### **TRAIL/TNF Signaling**

The extrinsic pathway is mediated by death receptors which belong to the tumor necrosis factor- $\alpha$  (TNF) superfamily, including Fas ligand, TNF and TRAIL [86-88]. TRAIL signaling is mediated by interaction with two types of receptors: death receptors which trigger apoptosis or decoy receptors which prevent apoptosis (Figure 4). There are five human TRAIL receptors identified to date; DR4/TRAIL-R1 [89], DR5/TRAIL-R2/KILLER [90-93], TRID/DcR1/TRAIL-R3 [90, 91, 94], TRAIL-R4/DcR2 [95, 96] and soluble receptor osteoprotegerin [97]. The apoptotic machinery is activated by oligomerization of the death receptors (DR4, DR5) upon ligand binding which leads to recruitment of the Fas-associated death domain (FADD) and initiator caspase-8 or -10 to form the death-inducing signaling complex (DISC) [98-100]. FADD is not recruited upon binding of TRAIL with decoy receptors (DcR1, DcR2) and apoptosis is prevented. Caspase-8 or -10 is activated by proteolysis in the

DISC complex and further activates caspase-3 which cleaves downstream death substrates (Figure 3).

Different PKC isozymes may have pro- or anti-apoptotic functions in TRAIL-mediated cell death [101-107]. Our lab has previously shown that PKC $\epsilon$  confers a protective role against TNF- or TRAIL-induced cell death in MCF-7 breast cancer cells [103, 108]. Additionally, phorbol-ester mediated down-modulation of PKC $\epsilon$  can sensitize acute myeloid leukaemia (AML) cells to TRAIL [102]. Conversely, activation of PKC $\delta$  by phorbol esters induced apoptosis in androgen-dependent prostate cancer cells by releasing death receptor ligands such as TNF and TRAIL [109]. The levels of PKC isozymes can influence TRAIL sensitivity or resistance. Pretreatment of melanoma cells containing low levels of PKC $\epsilon$  with phorbol 12-myristate 13-acetate (PMA) reversed sensitization of cells to TRAIL-induced apoptosis [101]. Introduction of PKC $\epsilon$  into the cells containing low PKC $\epsilon$  reversed the sensitization to TRAIL. Furthermore, introduction of dominant-negative PKC $\epsilon$  sensitized cells to TRAIL-induced cell death [101]. Thus, the status of PKC is important in determining the outcome of TRAIL treatment in cancer.

### **Bcl-2 Family and regulation of apoptosis**

The mitochondrial membrane integrity is regulated by Bcl-2 family members [110]. Bcl-2 family includes both pro- and anti-apoptotic members which share conserved Bcl-2 homology (BH) 3 domains (Figure 4). The anti-apoptotic or Bcl-2-like members contain three to four BH domains essential for their anti-apoptotic function [111]. These members include Bcl-2, Bcl-X<sub>L</sub>,

Bcl-w, A1/Bfl-1 and Mcl-1[111]. Pro-apoptotic members include: Bax, Bak and BH3-only members: BIM, BID, PUMA, NOXA, BAD, BMF, HRK and BIK [112]. Activation of proapoptotic Bax and Bak leads to depolarization of the mitochondrial membrane and release of cytochrome c into the cytosol [113-115], whereas antiapoptotic members such as Bcl-2 and Bcl-X<sub>L</sub> antagonizes the action of Bax and Bak [116]. The released cytochrome c binds to Apaf-1 to form the apoptosome to activate caspase-9 and downstream caspase -3, and -7 [117]. Cancer cells may act to inhibit the intrinsic mitochondrial pathway by increasing antiapoptotic or decreasing proapoptotic proteins, including those of the Bcl-2 family to prevent cell death [118]. Recently, another antiapoptotic member of the Bcl-2 family, Mcl-1 was shown to play an important role in mediating TRAIL resistance in cancer cells. TRAIL appears to be a promising cancer therapeutic agent since it can induce cytotoxicity in cancer cells without harming normal cells [119, 120]. TRAIL can also induce a synergistic effect with conventional radiotherapy or chemotherapy to potentiate cancer cell death [121-125]. Mcl-1 and antiapoptotic protein cIAP-2 were induced by TRAIL treatment in TRAIL-resistant cells and downregulation of Mcl-1 and cIAP-2 greatly sensitized cells to TRAIL-induced cell death [126-128]. Similarly, downregulation of antiapoptotic PKC $\epsilon$  [104] and PKC $\eta$  [106] sensitized cancer cells to cell death by TRAIL. Therefore, targeting specific antiapoptotic proteins of the PKC and Bcl2 family may be an effective strategy to combat TRAIL resistance in cancer cells.

## PKC $\eta$

### a. Structure, phosphorylation and activation

PKC $\eta$  is a member of the novel PKC family. It is structurally distinct from other PKCs and displays the most homology with PKC $\epsilon$  [129, 130]. PKC $\eta$  contains three conserved phosphorylation sites at the activation loop (Thr513), turn motif (Thr655) and hydrophobic motif (Ser674) (Figure 5). Similar to other PKCs, PKC $\eta$  is known to be phosphorylated by PDK1 at the activation loop *in vitro* [131]. Recently, it was reported that PKC $\lambda$  phosphorylates PKC $\eta$  at the Ser674 hydrophobic motif site, which allows PDK1 to dock and subsequently phosphorylate PKC $\eta$  at its activation loop in A9 mouse fibroblasts in response to parvovirus infection. The Thr655 turn motif site of PKC $\eta$  was autophosphorylated as a result of Thr513 and Ser674 phosphorylations [132]. Cholesterol sulfates and sulfatides can specifically activate PKC $\eta$  [133, 134]. In the presence of cholesterol-3-sulfate, casein kinase I (CK-I) was shown to phosphorylate PKC $\eta$  at threonine residues *in vitro* [135]. In response to chronic activation by tumor promoting phorbol esters, we and others have shown that in MCF-7 breast carcinoma cells [136], EL4 mouse thymoma cells [137], and glioblastoma cells [138], PKC $\eta$  levels were upregulated whereas other PKCs were downregulated. This suggests that PKC $\eta$  may play a role in tumor promotion in these cells.

## **b. Role in tumor promotion**

PKC $\eta$  has limited tissue distribution compared to other PKCs wherein it is specifically expressed in epithelial cells, predominantly in the skin, lung and heart [129, 130]. Depending on the cell type, PKC $\eta$  plays different roles in regulating proliferation and differentiation which contributes to its function in tumor promotion. Several lines of evidence support the function of PKC $\eta$  as a tumor promoter in breast cancer cells. First, PKC $\eta$  plays a role in enhancing G1/S phase cell-cycle progression in MCF-7 cells [139]. Second, PKC $\eta$  plays a positive role in mammary gland development and signaling and its expression is upregulated in response to estradiol in MCF-7 cells [140] and during branching in pregnancy [141]. Third, PKC $\eta$  expression was increased in locally invasive breast tumors and were strongly associated with lymph node metastases in human breast tissue samples [142]. Therefore, PKC $\eta$  can be a potential target for therapeutic intervention in breast cancer.

PKC $\eta$  has been identified as a potential therapeutic target in glioblastoma multiform [143]. Overexpression of PKC $\eta$  promoted proliferation and resistance to irradiation-induced cell death in glioblastoma cells [144]. Glioblastoma cell proliferation is regulated by PKC $\eta$  via extracellular signal-related kinase (ERK) and its downstream transcription factor target Elk-1 [145]. In response to phorbol ester activation, PKC $\eta$  regulates glioblastoma cell proliferation by targeting the Akt and mammalian target of rapamycin (mTOR) pathways [146]. Furthermore, PKC $\eta$  overexpressing glioblastoma cells exhibited a decrease in sensitivity to rapamycin and in

response to phorbol esters through the interaction of PKC $\eta$  and p70S6K, a downstream target of mTOR to regulate cell proliferation [147].

In contrast, PKC $\eta$  negatively regulates proliferation in keratinocytes. PKC $\eta$  induces differentiation of keratinocytes to a squamous cell phenotype that is concomitant with growth arrest [148]. This growth arrest was only detected in normal human and mouse keratinocytes, but not in human or mouse fibroblasts [148]. Using a skin tumor mouse model, pretreatment with the PKC $\eta$  activator, cholesterol sulfate was found to inhibit skin tumor formation induced by tumor promoters [134]. Moreover, PKC $\eta$  null mice displayed an increased susceptibility to tumor formation in a two-stage skin carcinogenesis model using 7,12-dimethylbenz(a)anthracene (DMBA) for tumor initiation and TPA for tumor promotion [149]. Interestingly, in renal cell carcinoma, a 3-fold increase in PKC $\eta$  levels was detected in grade 3 and 4 versus grade 1 and 2 tumors, whereas other PKC isozymes showed a modest difference [150]. Therefore, the negative role of PKC $\eta$  in tumorigenesis is specific only to skin carcinoma, whereas PKC $\eta$  promotes tumorigenesis in breast and renal carcinomas and glioblastomas.

### **c. Anti-apoptotic role of PKC $\eta$ in response to chemotherapeutic agents**

PKC $\eta$  contributes to resistance to chemotherapeutics in various cancer types. We have reported that overexpression of PKC $\eta$  in MCF-7 cells delayed the onset of TNF-induced cell death via attenuation of caspase activation [151]. Lung carcinoma cells were sensitized to vincristine and paclitaxel treatment through downregulation of PKC $\eta$  by antisense



oligonucleotides [152]. In addition, prostate cancer cells were sensitized to TRAIL-induced cell death by PKC $\eta$  downregulation [106]. Furthermore, downregulation of PKC $\eta$  by small interfering RNA (siRNA) sensitized Hodgkin's Lymphoma cells to doxorubicin- and camptothecin-induced apoptosis. Based on these reports, targeting PKC $\eta$  downregulation can improve the efficacy of chemotherapeutic agents.

## **Project Hypothesis and Specific Aims**

Improving the effectiveness of anti-cancer drugs has been a challenge to scientists and researchers world-wide due to the development of resistance by the cancer cells to the therapy. Research focused on identifying possible targets involved in the pro-survival mechanisms of cancer cells can greatly improve the outcome of cancer therapy. PKC $\eta$  is one potential target that plays a major role in cell proliferation and cell cycle control [139]. PKC $\eta$  levels are upregulated in many cancers, especially breast cancer [140-142]. PKC $\eta$  is associated with tumor progression in renal cells [150], glioblastoma [143, 144, 146] and breast cancer cells [139]. PKC $\eta$  is also associated with resistance to apoptosis in a variety of cancer cell types including Hodgkin's lymphoma [153], human lung carcinoma [152] and prostate cancer [106]. Our laboratory has shown that PKC $\eta$  functions as an anti-apoptotic protein because overexpression of PKC $\eta$  prevents apoptosis induced by tumor necrosis factor- $\alpha$  (TNF) [151]. Furthermore, PKC $\eta$  resists downregulation by persistent treatment with tumor-promoting phorbol esters, suggesting that PKC $\eta$  plays a role in tumorigenesis [137]. Therefore, targeting PKC $\eta$  downregulation in breast cancer may provide an important strategy in cancer therapy. Since the phosphorylation status of a protein can regulate its state of activation as well as stability, **we hypothesize that the downregulation and function of PKC $\eta$  is regulated by phosphorylation.** We will test this hypothesis through the following specific aims:

**Specific Aim 1:** To determine if phosphorylation of PKC $\eta$  is important for downregulation

**Specific Aim 2:** To determine the mechanism of PKC $\eta$  downregulation

**Specific Aim 3:** To determine the functional significance of PKC $\eta$  downregulation on cell death.

The hypothetical model for the project is illustrated in Figure 6.

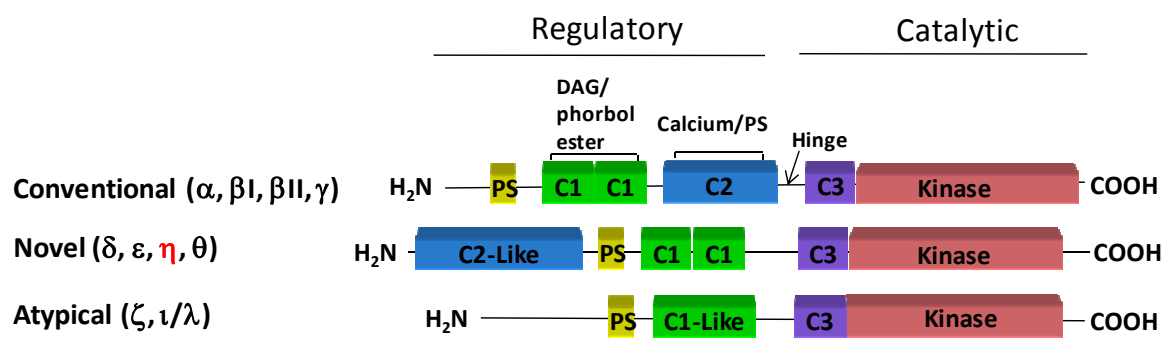
#### **Notes on Materials used in the Dissertation**

Chapter II represents submitted manuscript (Persaud, S., Pal, D. and Basu, A, Biochemistry, 2009)

### **Figure 1. PKC structure and isozymes**

The PKC family consists of 10 members that are classified into three groups based on their structure and biochemical properties. All PKCs have a regulatory domain at the N-terminus and a catalytic domain at the C-terminus separated by a hinge region. The regulatory domain contains a pseudosubstrate sequence that interacts with the substrate-binding site in the catalytic domain in an auto-inhibitory manner. The conventional PKCs are dependent on both DAG and  $\text{Ca}^{2+}$  for activity. Novel PKCs are  $\text{Ca}^{2+}$ -independent but DAG/phorbol ester dependent. Atypical PKCs depend only on phospholipids for activity. Modified from Parker, P.J. and Murray-Rust, J. PKC at a glance. 2004. Journal of Cell Science. 117:131-132.

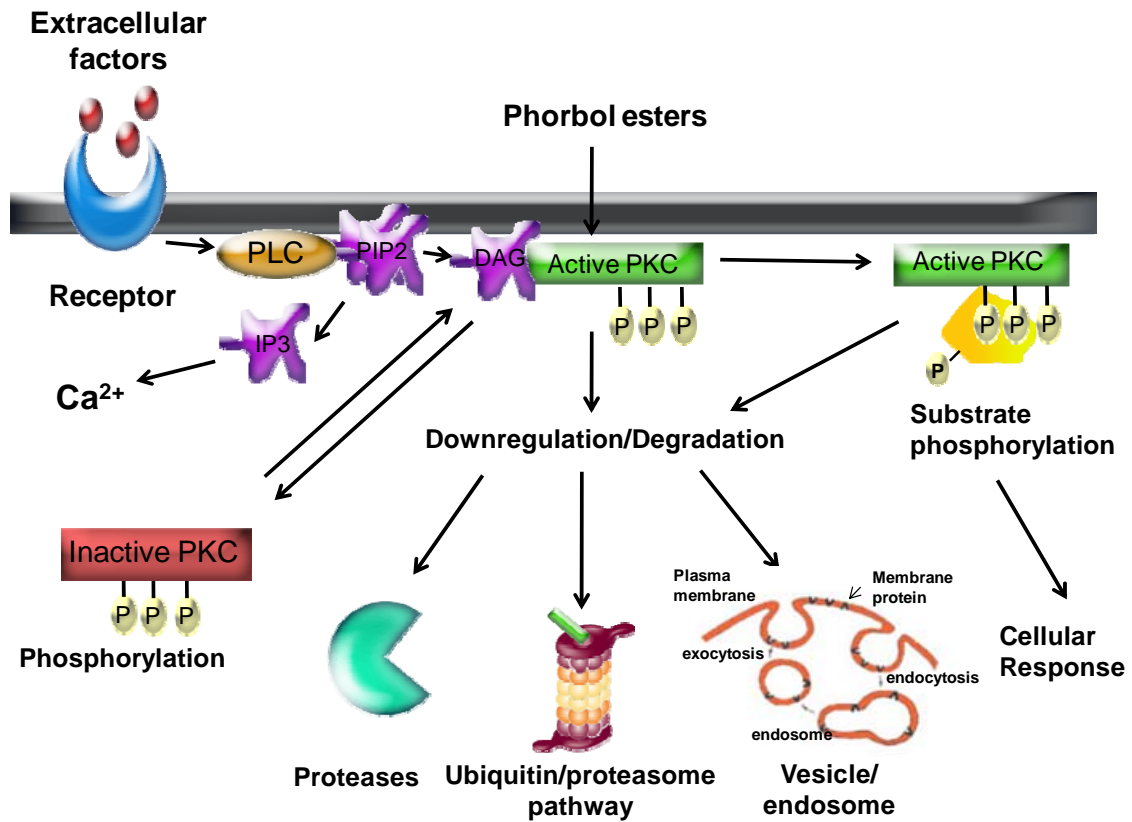
**Figure 1**



## **Figure 2. Regulation of PKCs**

PKCs are inactive in the cytosol and are phosphorylated at three conserved sites in the activation loop, turn motif and hydrophobic motif which are important for the maturation, catalytic competence and stability of the kinase. Upon binding of extracellular factors to receptors on the plasma membrane, phospholipase C is activated to generate second messengers DAG (and IP3). IP3 acts to release  $\text{Ca}^{2+}$  from the endoplasmic reticulum.  $\text{Ca}^{2+}$  and DAG are physiological cofactors for PKC activation. PKCs are fully activated upon translocation to the plasma membrane which releases pseudosubstrate inhibition and allows PKCs to bind to downstream substrates to elicit a cellular response. Prolonged activation by pharmacological activators, such as phorbol esters triggers PKCs downregulation by protease-mediated, ubiquitin/proteasome-mediated or vesicle-mediated degradation, thereby terminating PKC signaling.

**Figure 2**



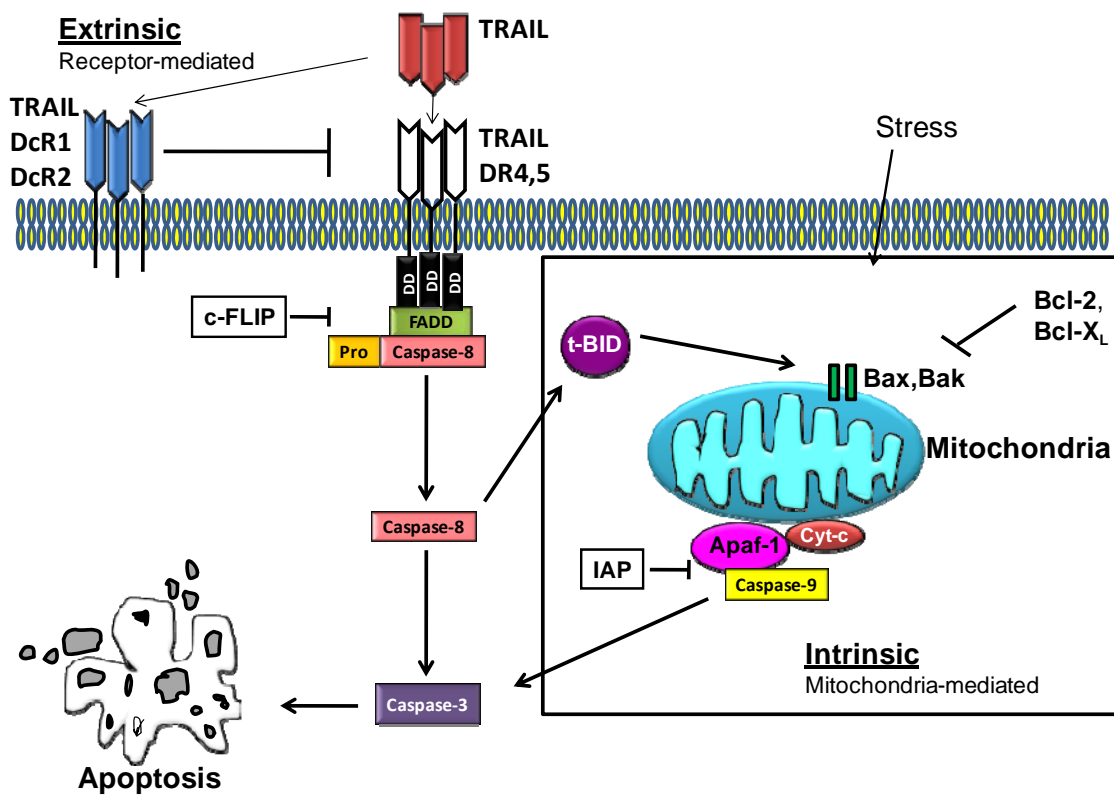
Adapted from Nature Reviews | Cancer

### **Figure 3: Apoptosis: Extrinsic and Intrinsic pathways**

The hallmark of apoptosis or programmed cell death is the activation of caspases. Caspases can be either initiators (caspase-8, -9, -10) or executioners (caspase-3, -6, -7). Two major apoptotic pathways involving the activation of caspases are the extrinsic (receptor-mediated) and intrinsic (mitochondrial) pathways. The extrinsic pathway can be initiated by ligands such as TRAIL which bind to their receptors (DR4, DR5) containing death domains (DD) which trigger the recruitment of adaptor proteins such as FADD and caspase 8 forming the death-inducing signaling complex (DISC). Initiator procaspase 8 is processed into active caspase 8 which can activate executioner caspase 3 to trigger apoptosis. TRAIL can also bind to decoy receptors which do not have a functional death domain. The intrinsic pathway involves the Bcl-2 family of proteins which regulate the integrity of the mitochondrial membrane. Active caspase-8 can process the pro-apoptotic Bcl-2 family member Bid to form truncated Bid (t-Bid) that activates two other pro-apoptotic members Bax and Bak. Bax and Bak dimerize and bind to the mitochondrial membrane which depolarizes and destabilizes the membrane. Cytochrome C is released from the mitochondria and binds to Apaf1 forming the apoptosome which binds and activates initiator caspase-9. Active caspase-9 can activate caspase 3 and trigger apoptosis. Anti-apoptotic members such as Bcl-2 and Bcl-X<sub>L</sub> antagonize Bax and Bak to prevent apoptosis. Modified from MacFarlane, M. TRAIL-induced signaling and apoptosis. *Toxicology Letters* 2003. 139: 89-97. [154]



**Figure 3**



#### **Figure 4: Bcl-2 protein family**

The Bcl-2 family consists of anti-apoptotic and pro-apoptotic members. The multidomain members share four Bcl-2 homology (BH) domains which are important for their three-dimensional folding. BH3-interacting domain death agonist (BID) is the exception, since it displays similar folding as the multidomain members, but possesses only the BH3 domain. The transmembrane domain (TM) is important for interaction with the mitochondrial membrane. Bcl-2 antagonist/killer (Bak) and Bcl-2-associated X protein (Bax) are pro-apoptotic members that function to permeabilize the mitochondrial outer membrane. Bcl-2-related ovarian killer (Bok) is another pro-apoptotic membrane that is not well characterized. Anti-apoptotic members Bcl-2, Bcl-X<sub>L</sub>, Bcl-w, Mcl-1 and A1 antagonize the activity of Bax and Bak in part by directly binding to them. The BH3 only domain members antagonize the activity of the anti-apoptotic members by inserting in their binding domain via the BH3 domain. Modified from Lessene, G. et. al. BCL-2 family antagonists for cancer therapy. *Nature Reviews Drug Discovery* 2008; 7: 989-1000

**Figure 4.**

**Anti-apoptotic**

Bcl-2, Bcl-X<sub>L</sub>, Bcl-w  
Mcl-1, A1



**Pro-apoptotic**

Bax, Bak



**BH3 only Pro-apoptotic**

Bim, HRK, BMF, BIK



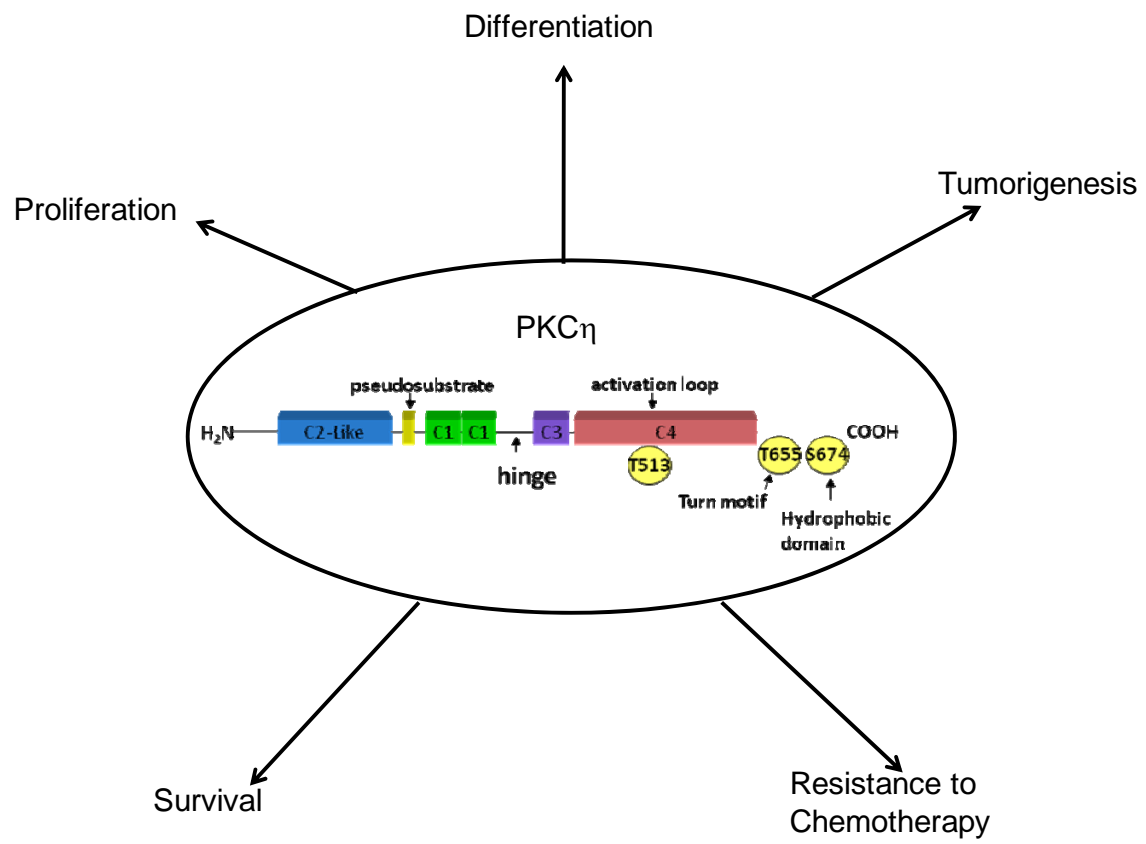
BID, PUMA, BAD, Noxa



**Figure 5: PKC $\eta$  structure, phosphorylation, function**

PKC $\eta$  is a member of the novel group of PKCs. It is activated by DAG/phorbol ester binding through the C1 domain and its C2-like domain renders it insensitive to Ca<sup>2+</sup>. PKC $\eta$ , like other PKCs, contains three conserved sites of phosphorylation: activation loop (Thr513), turn motif (Thr655) and hydrophobic motif (Ser674); however, the regulation of PKC $\eta$  by phosphorylation at these sites is not well understood. PKC $\eta$  regulates several cellular functions, including, cell proliferation, differentiation and tumorigenesis. PKC $\eta$  also functions as an anti-apoptotic protein and its overexpression can lead to resistance to apoptosis by chemotherapeutic agents. Depending on the cell-type, PKC $\eta$  may have opposing effects in regulating proliferation and tumorigenesis.

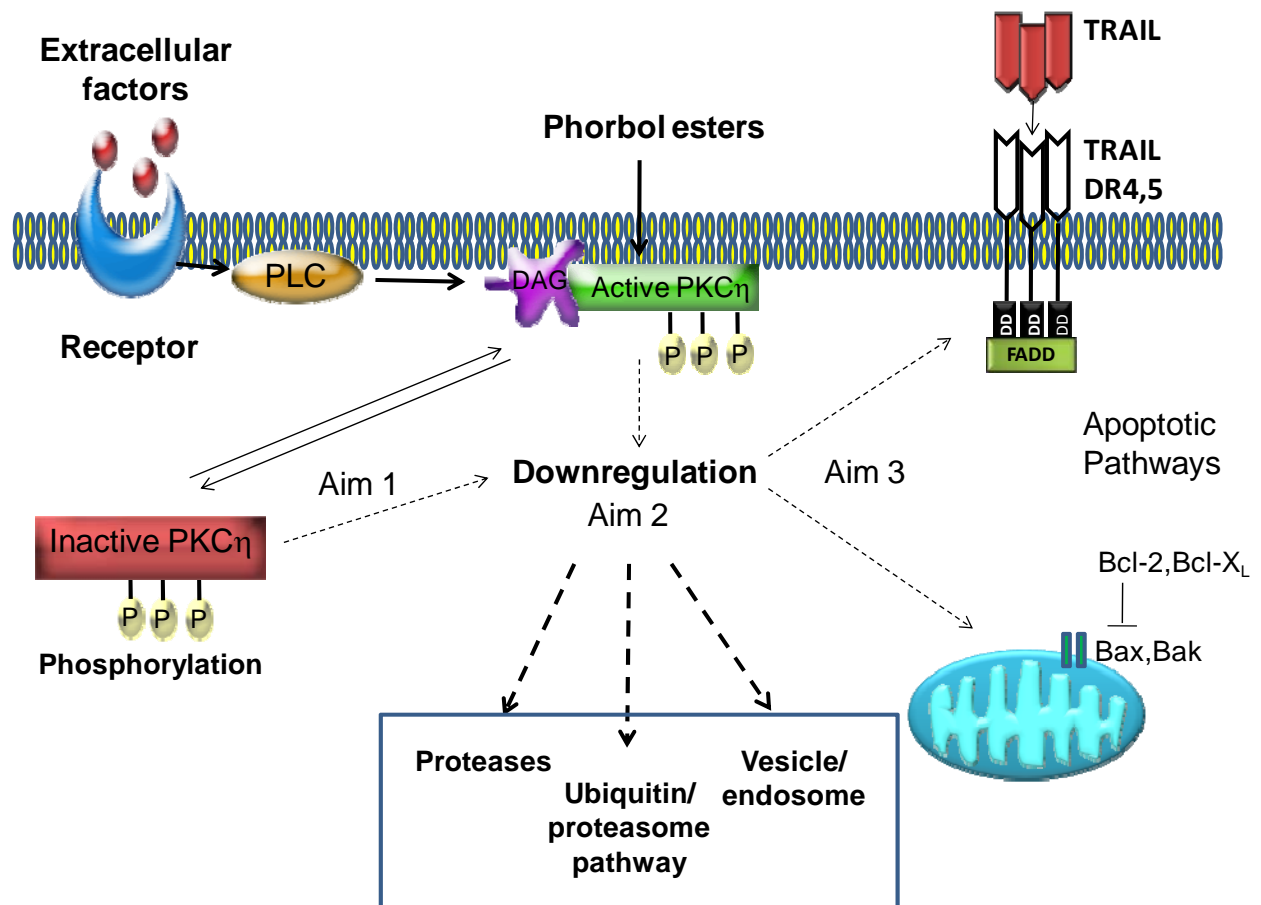
**Figure 5:**



**Figure 6. Hypothetical model of the project**

Since PKC $\eta$  plays a major role in regulating signaling events leading to survival and proliferation, it is worthwhile to study the mechanisms of PKC $\eta$  downregulation so that it can be exploited for therapeutic intervention. In this study, we will use a breast cancer model to investigate how PKC $\eta$  is regulated by phosphorylation and if mutations at the conserved phosphorylation sites can alter its expression (Aim 1). The second aim focuses on elucidating the mechanism(s) of PKC $\eta$  downregulation. The third aim will evaluate the functional significance of PKC $\eta$  downregulation on cell death via the extrinsic pathway through TRAIL-mediated apoptosis or the intrinsic pathway by regulating members of the Bcl-2 family. We hypothesize that the downregulation and function of PKC $\eta$  is regulated by phosphorylation.

Figure 6.



**Table 1. PKC inhibitors used in this study**

<b>Inhibitors</b>				
<b>Bisindolylmaleimide 1 GF-109203X</b>	Catalytic ATP-binding	cPKC	8-20	Toullec, D., <i>et al.</i> 1991
		nPKC	200-700	
		aPKC	5800	
<b>Gö 6983</b>	Catalytic ATP-binding	cPKC	6-7	Gschwendt, M., <i>et al.</i> 1996.
		nPKC	10	
		aPKC	60	
<b>Gö 6976</b>	Catalytic ATP-binding	cPKC	2-6 (rat brain)	Martiny-Baron, G., <i>et al.</i> 1993
		nPKC	No inhibition	
		aPKCs	No inhibition	



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## CHAPTER II

### PHOSPHORYLATION OF PROTEIN KINASE C $\eta$ AT CONSERVED SITES PREVENTS ITS DOWNREGULATION

#### SUMMARY

Tumor promoting phorbol esters are potent activators of conventional and novel PKCs, but persistent treatment with phorbol esters leads to downregulation of these PKCs. Interestingly, PKC $\eta$ , a novel PKC isozyme, resists downregulation by tumor-promoting phorbol esters. In the present study, we have investigated if the phosphorylation status of PKC $\eta$  regulates its stability. Prolonged treatment with several PKC activators, including phorbol 12, 13-dibutyrate, 12-*O*-tetradecanoylphorbol-13-acetate and indolactam V caused upregulation of PKC $\eta$  whereas the general PKC inhibitor Gö 6983 led to the downregulation of PKC $\eta$  in MCF-7 cells. The conventional PKC inhibitor Gö 6976 had little effect on PKC $\eta$  downregulation. Treatment of MCF-7 cells with the protein phosphatase inhibitor calyculin A prevented PKC $\eta$  downregulation by the PKC inhibitor Gö 6983. Mutation of PKC $\eta$  at the activation loop (Thr513), turn-motif (Thr655) or hydrophobic motif (Ser674) to Ala but not Glu decreased PKC $\eta$  level compared to wild-type PKC $\eta$ . Gö 6983 had no additional effect on the downregulation of PKC $\eta$  in these Ala mutants. Thus, phosphorylation of PKC $\eta$  at the conserved serine/threonine sites is important for its stability.



## INTRODUCTION

Protein kinase C (PKC) is a family of phospholipid-dependent serine/threonine kinases involved in regulating various cellular processes including cell proliferation, differentiation and cell death [1, 2]. To date, there are at least ten PKC isozymes identified which differ in their structure, function and biochemical properties [3-7]. Conventional PKC $\alpha$ , - $\beta$ I, - $\beta$ II and - $\gamma$  require both calcium and diacylglycerol (DAG) for activation. Novel PKC $\delta$ , - $\epsilon$ , - $\eta$  and - $\theta$  are calcium-independent but DAG-dependent whereas atypical PKC $\iota$ / $\lambda$  and - $\zeta$  require neither calcium nor DAG for their activity. PKCs are receptors for tumor promoting phorbol esters which are potent activators of conventional and novel PKCs and can substitute for DAG [8, 9]. Interaction of PKC with DAG is transient, whereas phorbol esters bind to PKC with higher affinity leading to persistent activation [10]. Prolonged treatment with tumor promoting phorbol esters leads to the degradation or downregulation of phorbol-ester sensitive PKCs.

In addition to cofactors, PKCs are also regulated by phosphorylation at three conserved sites: the activation loop (A-loop), turn motif (TM) and hydrophobic motif (HM) [11]. Phosphorylation of PKCs at these sites primes them for activation and maintains them in a closed protease/phosphatase resistant form [11, 12]. While the A-loop phosphorylation of PKCs and other AGC kinases has been shown to regulate their activity [11], the phosphorylation at HM has been implicated in regulating stability and phosphatase resistance [13-16]. The phosphorylation at TM site has been reported to regulate both kinase activity and stability [14, 15, 17].

Since the levels of PKCs can determine their function, it is important to understand the mechanisms regulating PKC level. The novel PKC $\eta$  was upregulated in breast cancer tissues [18] and overexpression of PKC $\eta$  was associated with resistance to many chemotherapeutic agents [19-23]. We and others have shown that PKC $\eta$  resists downregulation by phorbol ester in various cell types [24-27]. PKC $\eta$  also contains three conserved phosphorylation sites at the A-loop (Thr513), TM (Thr655) and HM (Ser674) [28]. It is, however, not known how phosphorylation of PKC $\eta$  at conserved sites regulates PKC $\eta$  downregulation. In the present study, we have examined if phosphorylation of PKC $\eta$  protects it against phorbol ester-mediated downregulation. Our results show that PKC activators upregulate PKC $\eta$  whereas general PKC inhibitors trigger its downregulation. In addition, PKC inhibitor-mediated downregulation of PKC $\eta$  is blocked by protein phosphatase inhibitor calyculin A. Furthermore, mutation of PKC $\eta$  at the A-loop, TM and HM to Ala attenuates PKC $\eta$  level. Thus, our results suggest that phosphorylation of PKC $\eta$  at the A-loop (Thr513), TM (Thr655) and HM (Ser674) is important for its stability.

## EXPERIMENTAL PROCEDURES

### Materials

PDBu, TPA and ILV were purchased from Alexis Biochemicals (San Diego, CA). Gö 6983, Gö 6976, calyculin A and okadaic acid were purchased from Calbiochem (San Diego, CA). Polyclonal antibodies to PKC $\eta$ , PKC $\delta$ , PKC $\epsilon$  and monoclonal antibody against GAPDH were obtained from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA). Monoclonal antibody to PKC $\alpha$  was obtained from Upstate Bioechnology (Lake Placid, NY) and monoclonal antibody to PKC $\iota$  was obtained from Transduction Laboratories (San Jose, CA). Polyclonal antibody to phospho-PKC $\gamma$  (Thr514) was purchased from Cell Signaling Technology (Beverly, MA). Polyclonal antibodies to phospho-PKC $\eta$  were purchased from Biosource/Invitrogen (Carlsbad, CA). Monoclonal antibody against actin was obtained from Sigma (St. Louis, MO). Horseradish-peroxidase-conjugated donkey anti-rabbit and goat anti-mouse secondary antibodies were purchased from JacksonImmunoResearch Lab, Inc. (West Grove, PA). Poly(vinylidenedifluoride) membrane was obtained from Millipore (Bedford, MA). Enhanced chemiluminescence detection kit was purchased from Amersham (Arlington Heights, IL).

### Cell culture and transfection

MCF-7 breast cancer cells were maintained in RPMI medium supplemented with 10% heat-inactivated fetal bovine serum and 2 mM glutamine. Human embryonic kidney (HEK) 293 cells

were maintained in Dulbecco's modified minimal essential medium supplemented with 10% fetal bovine serum and 2 mM glutamine. Cells were kept in a humidified incubator at 37°C with 95% air and 5% CO<sub>2</sub>. HEK293 cells were plated one day before transfection. Cells were transfected with WT-PKC $\eta$  and phosphorylation site mutant constructs using Lipofectamine reagent (Invitrogen, Carlsbad, CA) and the manufacturer's protocol. One day post-transfection, the cells were re-plated for treatment with PDBu and Gö 6983.

### **Site-directed mutagenesis**

PKC $\eta$  was sub-cloned into pcDNA3 by PCR. Serine or threonine phosphorylation sites of PKC $\eta$  at T513, T655 and S674 were mutated to alanine or glutamate using the QuikChange site-directed mutagenesis kit (Stratagene, La Jolla, CA) following manufacturer's protocol. Mutations were confirmed by DNA sequencing.

### **Reverse Transcriptase PCR**

MCF-7 cells were treated with PDBu, ILV and Gö 6983 for 16 h. Total RNA was extracted using TRI Reagent from Molecular Research Center, Inc. (Cincinnati, OH). cDNA was synthesized using random primers and Improm II reverse transcriptase from Promega (Madison, WI). PCR amplification of cDNA was performed using Promega PCR Master Mix (Madison, WI), PKC $\eta$  and  $\beta$ -actin primers. The sequences of forward and reverse PKC $\eta$  primers were 5'-ATGCGGTGGAAGCTTGCCA-3' and 5'-CGTGACCACAGAGCATCTCATAGA-3' respectively. The sequences of the forward and reverse  $\beta$ -actin primers were 5'-

ACCCAGCACAATGAAGATCA-3' and 5'-GCGCAAGTTAGGTTTTGTCA-3'. After PCR cycling, a 750 bp product for PKC $\eta$  and 800-bp product for  $\beta$ -Actin was detected by gel electrophoresis.

### **Immunoblot Analysis**

Cells were lysed in extraction buffer containing 1 mM DTT, protease inhibitors and phosphatase inhibitors. Equal amounts of protein were separated by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and transferred on PVDF membranes. Western blot analysis was performed as described before [20].

### **Immunoprecipitation**

Cells were harvested and lysed in buffer containing 20 mM HEPES, pH 7.4, 0.15 M NaCl, 1 mM EDTA, 1% Nonidet P-40, 25 mM  $\beta$ -glycerophosphate, protease inhibitor cocktail, 10 mM NaF, and 0.1 mM sodium vanadate. After collecting total cell lysate (input), samples were immunoprecipitated with PKC $\eta$ -agarose conjugated polyclonal antibody or control rabbit IgG (Santa Cruz Biotechnology, Santa Cruz, CA). Immunocomplexes were processed as described previously [29] and subjected to SDS-PAGE and Western blotting.

## RESULTS

### Effects of PKC activators and inhibitors on PKC $\eta$ level

We have previously shown that prolonged treatment with phorbol 12,13-dibutyrate (PDBu) caused upregulation of PKC $\eta$  in MCF-7 breast cancer cells [25]. In the present study, we compared the ability of several PKC activators to upregulate PKC $\eta$  in MCF-7 cells (Figure 1). While PDBu and TPA belong to the same class of compounds, indolactam V (ILV) is structurally distinct from phorbol esters [30]. All three PKC activators caused substantial upregulation of PKC $\eta$  (Figure 1a). Based on the densitometric scanning of three separate experiments, PDBu, ILV and TPA caused 5-, 5- and 4-fold increase in PKC $\eta$  level, respectively (Figure 1b). In contrast, conventional PKC $\alpha$  and novel PKC $\delta$  were downregulated after prolonged treatment with PDBu and TPA (Figure 1a). ILV had little effect on PKC $\alpha$  downregulation. As expected, the phorbol ester-insensitive atypical PKC $\iota$  remained unaffected by the treatment with PKC activators. PDBu caused a time-dependent increase in downregulation of PKC $\alpha$  and PKC $\delta$  whereas treatment of MCF-7 cells with PDBu for 1 h was sufficient to increase PKC $\eta$  level, and it remained elevated even when cells were treated with PDBu for 8 h (Figure 1c). We also treated cells with different concentrations of PDBu. Figure 1d shows that a 12 h treatment with PDBu caused a concentration-dependent increase in PKC $\eta$

level whereas PKC $\delta$  was downregulated with increasing PDBu concentrations. Thus, the regulation of PKC $\eta$  is unique in comparison to other novel and conventional PKCs.

Since PKC activators caused upregulation of PKC $\eta$ , we examined if treatment with PKC inhibitors would lead to the downregulation of PKC $\eta$ . We examined the effects of the general PKC inhibitor Gö 6983 and conventional PKC inhibitor Gö 6976 on PKC $\eta$  downregulation. Gö 6983 but not Gö 6976 caused substantial downregulation of PKC $\eta$  (Figures 2a and 2b). The levels of PKC- $\alpha$ , - $\delta$  and - $\epsilon$  were not decreased by Gö 6983 treatment (Figure 2a). Thus, the effect of Gö 6983 on PKC $\eta$  downregulation was specific to this isozyme.

To determine if PKC activators and inhibitors alter PKC $\eta$  expression at the mRNA level, we treated MCF-7 cells with PDBu, ILV and Gö 6983 and analyzed mRNA expression by reverse-transcriptase PCR. As shown in Figure 3, treatment of MCF-7 cells with PKC activators and inhibitors did not alter PKC $\eta$  mRNA expression. Taken together, these results demonstrate that PKC $\eta$  level is altered post-transcriptionally following treatment with PKC activators and inhibitors.

### **Phosphatase inhibitor calyculin A prevents PKC $\eta$ downregulation by Gö 6983.**

To determine if phosphorylation of PKC $\eta$  confers PKC $\eta$  stability, we examined the effects of Ser/Thr phosphatase inhibitors okadaic acid and calyculin A on PKC inhibitor-induced downregulation of PKC $\eta$ . Calyculin A inhibits protein phosphatase 1 (PP1) and protein phosphatase 2A (PP2A), whereas okadaic acid preferentially inhibits PP2A [31]. As shown in

Figure 4, treatment of MCF-7 cells with calyculin A alone was sufficient to increase PKC $\eta$  level. Moreover, calyculin A but not okadaic acid prevented downregulation of PKC $\eta$  by Gö 6983. These results suggest that dephosphorylation of PKC $\eta$  by PP1 is important for its downregulation.

### **Phosphorylation of PKC $\eta$ at the conserved Ser/Thr sites regulates its stability.**

To determine if phospho-PKC $\eta$  resists PKC $\eta$  downregulation, we wanted to monitor PKC $\eta$  phosphorylation at all three conserved sites A-loop (Thr513), TM (Thr655) and HM (Ser674). There is no commercially available phospho-specific antibody against Thr513 at the A-loop of PKC $\eta$ . Although phospho-specific antibody against Ser674 at the HM is commercially available it also recognizes equivalent phosphorylation sites in conventional PKCs. We therefore monitored PKC $\eta$  phosphorylation following immunoprecipitation with PKC $\eta$  antibody. We have used phospho-specific antibody against Thr514 of PKC $\gamma$ , which also recognizes Thr513 site in PKC $\eta$ , to monitor A-loop phosphorylation. TM phosphorylation was monitored using phospho-specific antibody against Thr655 of PKC $\eta$ . Figure 5 shows that PDBu caused an increase in PKC $\eta$  level and this was associated with an increase in PKC $\eta$  phosphorylation at the A-loop, TM and HM sites.

To determine the importance of the A-loop (T513), TM (T655) and HM (S674) site phosphorylation in regulating PKC $\eta$  level, we substituted Ser/Thr residues for alanine (A) to prevent phosphorylation or glutamate (E) to mimic phosphorylation. We introduced wild-type



(WT) and mutant PKC $\eta$  constructs in HEK293 cells since these cells contain little endogenous PKC $\eta$  and they are easy to transfect. PDBu caused substantial upregulation of PKC $\eta$  in cells expressing WT PKC $\eta$ , and Gö 6983 caused a modest decrease in PKC $\eta$  (Figures 6a-c). Mutation of Thr513, Thr655 and Ser674 to Glu had little effect on PKC $\eta$  level (Figures 6a-c). However, the constitutive PKC $\eta$  level was substantially reduced in cells expressing T513A, T655A or S674A mutants (Figure 6a-c). Consequently, Gö 6983 did not have an additional effect in decreasing PKC $\eta$  level. Mutation of PKC $\eta$  at Thr513, Thr655 or Ser674 to Ala did not completely prevent upregulation of PKC $\eta$  by PDBu, although the level of PKC $\eta$  following PDBu treatment was much less in Ala mutant expressing cells compared to cells expressing WT or Glu mutants (Figures 6a-c). These results indicate that the phosphorylation at A-loop, TM and HM sites are important for the stability of PKC $\eta$ .

## DISCUSSION

The results of our present study demonstrate that the regulation of PKC $\eta$  is unique compared to other phorbol ester-sensitive PKC isozymes. Although tumor-promoting phorbol esters are potent activators of conventional and novel PKCs [8, 10], persistent treatment with phorbol esters leads to the downregulation and termination of PKC signaling [32]. In contrast, we have shown that treatment of cells with PKC activators induced upregulation of PKC $\eta$  whereas PKC-specific inhibitors triggered downregulation of PKC $\eta$ . Furthermore, phosphorylation of PKC $\eta$  at the conserved Ser/Thr sites were important for the stability of PKC $\eta$ .

It is generally believed that treatment with PKC activators leads to their membrane translocation followed by dephosphorylation [33]. The dephosphorylated PKCs are subject to downregulation by proteases [34, 35]. However, fully phosphorylated PKC $\alpha$  was shown to be downregulated at the plasma membrane via the proteasome-mediated pathway [36]. A recent report indicated that the fully phosphorylated and primed form of PKC $\epsilon$  was downregulated by phorbol ester treatment independent of its intrinsic kinase activity [37]. Although prolonged treatment with PDBu triggered downregulation of PKC $\alpha$  and PKC $\delta$  in MCF-7 cells, it caused upregulation of PKC $\eta$  (Figure 1a). Our results suggest that phosphorylation of PKC $\eta$  regulates its stability. First, treatment with several PKC activators, such as TPA, PDBu and ILV induced upregulation of PKC $\eta$  in MCF-7 cells (Figure 1a). Second, PDBu not only increased PKC $\eta$

level, but the increase in PKC $\eta$  was associated with an increase in its phosphorylation status. Third, PKC-specific inhibitors Gö 6983 (Figure 2a, b) and bisindolylmaleimide (data not shown) induced downregulation of PKC $\eta$ . Finally, phosphatase inhibitor calyculin A blocked PKC $\eta$  downregulation by Gö 6983 and increased constitutive level of PKC $\eta$ .

It has been, however, reported that active conformation of PKC $\eta$  is necessary for PKC $\eta$  downregulation since mutation of Ala161 at the pseudosubstrate domain of PKC $\eta$  to Glu (A161E) resulted in proteolysis of PKC $\eta$  in baby hamster kidney (BHK) cells whereas wild-type PKC $\eta$  was stable inside cells [38]. It is conceivable that the regulation of PKC $\eta$  depends on the cellular context. We have, however, found that the upregulation of PKC $\eta$  by PKC activator and downregulation by PKC inhibitor was not unique to MCF-7 cells, and was observed in other cell types, including HEK293 cells (Figures 5 and 6) and several other breast cancer cells, including BT-20, CAMA-1, SKBR-3 and HCC1806 (data not shown). Interestingly, the expression of A161E mutant in BHK cells resulted in distinct cleavage of full-length PKC $\eta$ , rather than its disappearance which usually follows downregulation of PKCs. Furthermore, the disappearance of the smaller cleavage products but not the full-length A161E PKC $\eta$  could be blocked by proteasome inhibitors, suggesting that the initial proteolysis of A161E PKC $\eta$  was proteasome-independent. In this study, mechanisms for PKC $\eta$  degradation were studied in the absence of phorbol ester treatment and the effects of PKC inhibitors were not tested. One possibility is that a change in conformation of PKC $\eta$  caused by mutation at the pseudosubstrate domain resulted in

a protease-mediated cleavage of PKC $\eta$  followed by further proteolysis via the ubiquitin proteasome-mediated pathway.

It is well established that the activity, maturation and stability of PKCs are regulated by phosphorylation and dephosphorylation events [11, 12, 39, 40]. It is generally believed that phosphorylation of PKCs at the activation loop primes them for activation whereas phosphorylation at the C-terminal hydrophobic motif confers stability. Phosphoinositide-dependent kinase-1 (PDK1) has been shown to phosphorylate PKCs at their activation loop sites [39, 41-44]. PDK1 has also been implicated in phosphorylating PKC $\eta$  at its Thr513 A-loop site. A recent report indicated that in mouse A9 fibroblasts infected with parvovirus, atypical PKC $\lambda$  (usually referred to as PKC $\iota$ ) phosphorylates PKC $\eta$  at the Ser674 hydrophobic site, allowing PDK1 to subsequently phosphorylate PKC $\eta$  at its activation loop site (42). However, knockdown of neither PDK1 nor PKC $\iota$  prevented upregulation of PKC $\eta$  by PDBu in MCF-7 cells (data not shown). We have found that mutation at the A-loop (Thr513), TM (Thr655) or the HM (Ser674) site to Ala was sufficient to decrease basal PKC $\eta$  level, suggesting the importance of PKC $\eta$  phosphorylation at these sites in regulating PKC $\eta$  level. Although the level of PKC $\eta$  in the PDBu-treated cells was much less in Ala mutant expressing cells compared to WT PKC $\eta$  expressing cells, single mutation at the A-loop, TM or HM sites was not sufficient to obliterate the effect of PDBu on PKC $\eta$  upregulation. Similarly, mutation of Ser/Thr to Glu did not block the effects of PDBu on PKC $\eta$  upregulation. It appears that although

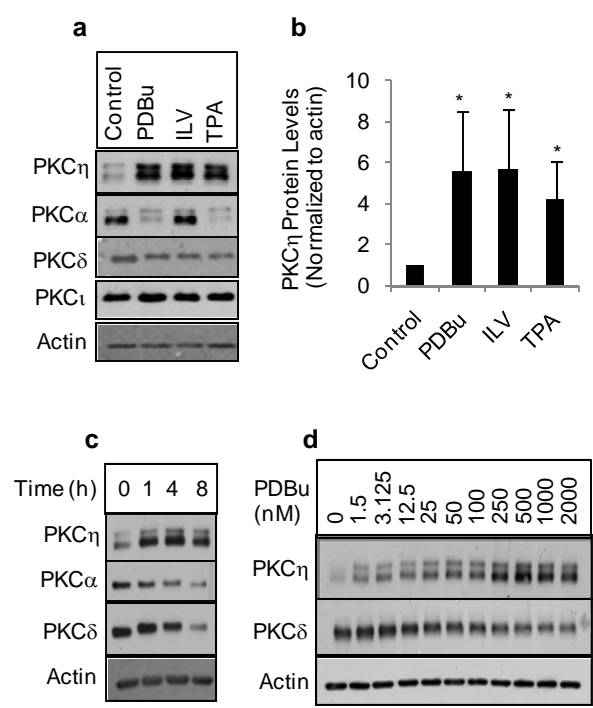
dephosphorylation at a single conserved phosphorylation site in PKC $\eta$  is enough to destabilize it, phosphorylation at multiple sites by PDBu can result in its upregulation.

In summary, we have made several novel observations that have important implications. The observation that PKC $\eta$  is the only PKC isozyme upregulated by tumor-promoting phorbol esters suggests that PKC $\eta$  may play an important role in tumorigenesis. We have also demonstrated that phosphorylations at the A-loop, TM and HM determine PKC $\eta$  level. Since PKC $\eta$  is often upregulated in breast cancer and overexpression of PKC $\eta$  confers resistance to chemotherapeutic drugs, future studies should determine how phosphorylation of PKC $\eta$  at these sites is regulated.

**Figure 1: Effects of PKC activators on upregulation of PKC $\eta$ .**

(a) MCF-7 cells were treated with 1  $\mu$ M PDBu, 10  $\mu$ M ILV and 1  $\mu$ M TPA for 15 h. (b) Densitometric quantification of PKC $\eta$  protein level from 3 separate experiments corrected for loading. Data represents the mean  $\pm$  s.e.m. The asterisk (\*) indicates significant difference from control ( $P < 0.01$ ) using Student's t-test. (c) MCF-7 cells were treated with 1  $\mu$ M PDBu for the indicated time periods and (d) indicated concentrations for 12 h. Western blot analysis was performed with total cell extract and probed with the indicated antibodies. Actin was used as a loading control.

Figure 1.

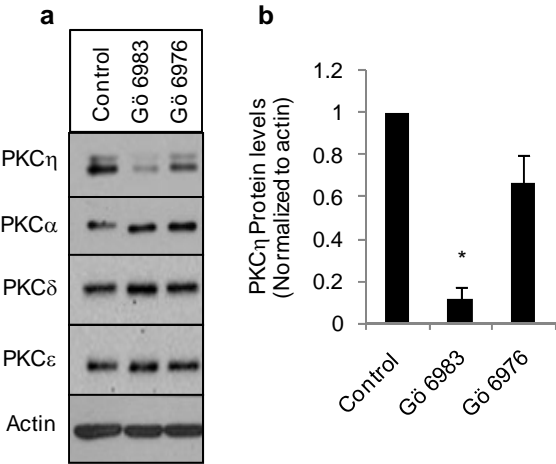


**Figure 2: Downregulation of PKC $\eta$  was mediated by the general PKC inhibitor Gö 6983.**

(a) MCF-7 cells were treated with 1  $\mu$ M Gö 6983 or 1  $\mu$ M Gö 6976 for 15 h. Total cell lysates were subjected to SDS-PAGE and western blot analysis was performed using the indicated antibodies. Actin was used as a loading control. (b) Densitometric quantification of PKC $\eta$  protein expression from 3 separate experiments corrected for loading. Data represents the mean  $\pm$  s.e.m. The asterisk (\*) indicates significant difference from the control ( $P < 0.01$ ) using Student's t-test.



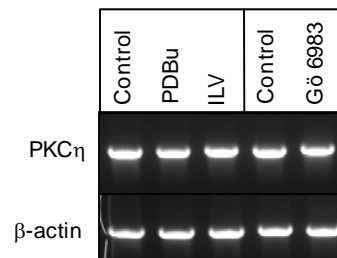
Figure 2.



**Figure 3: Effects of PKC activators and inhibitors on PKC $\eta$  mRNA expression.**

MCF-7 cells were treated with 1  $\mu$ M PDBu, 10  $\mu$ M ILV and 1  $\mu$ M Gö 6983 for 16 h. Total RNA was extracted and cDNA was synthesized by reverse transcriptase reaction. PKC $\eta$  and  $\beta$ -actin was amplified by PCR and electrophoresed. Results were representative of at least 2 independent experiments.

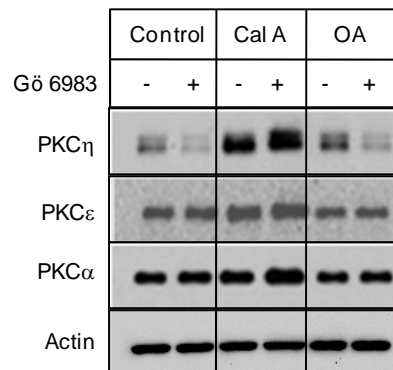
**Figure 3.**



**Figure 4: Effects of phosphatase inhibitors on PKC $\eta$  level.**

MCF-7 cells were pretreated with 10 nM calyculin A or 100 nM okadaic acid (OA) for 15 min and then treated with 1  $\mu$ M Gö 6983 for 3 h. Western blot analysis was performed with the indicated antibodies. Actin was used as a loading control. Results were representative of at least 2 independent experiments.

**Figure 4.**



**Figure 5: Effect of PDBu on PKC $\eta$  phosphorylation.**

HEK293 cells transfected with WT-PKC $\eta$  were treated with 1  $\mu$ M PDBu for 8 h or left unstimulated. Total cell lysates (input) were prepared and immunoprecipitated with PKC $\eta$  (IP) or control Rabbit IgG (IgG) antibodies overnight. Western blot analyses were performed using indicated antibodies.

**Figure 5.**

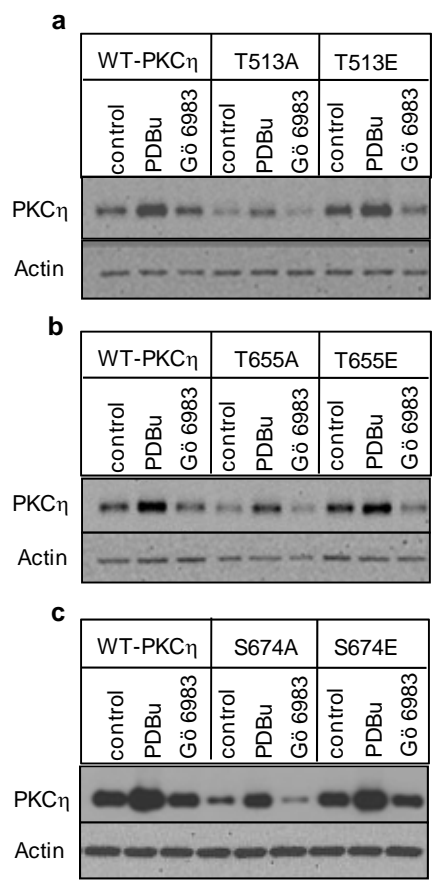
		Input	IP			
			IgG	PKC $\eta$	IgG	PKC $\eta$
PDBu		- +	- - + +			
T514-PKC $\gamma$						
T655-PKC $\eta$						
S674-PKC $\eta$						
PKC $\eta$						

**Figure 6: Effects of mutation of PKC $\eta$  at the A-loop, TM or HM on PKC $\eta$  level.**

HEK293 cells were transfected with WT-PKC $\eta$  or mutant PKC $\eta$  and treated with 1  $\mu$ M PDBu or 1  $\mu$ M Gö 6983 for 15 h or left unstimulated. (a) T513A or T513E; (b) T655A or T655E; (c) S674A or S674E. Western blot analysis was performed with indicated antibodies. Actin was used as a loading control. Results were representative of at least 2 independent experiments.



Figure 6.



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## CHAPTER III

### DOWNREGULATION OF PROTEIN KINASE C $\eta$ OCCURS VIA TWO DISTINCT MECHANISMS

#### SUMMARY

Protein kinase C (PKC) is a family of serine/threonine kinases that are key signaling proteins involved in regulating various cellular processes. PKC $\eta$ , a member of the novel group of PKC isozymes, plays an important role in regulating cell proliferation and differentiation. PKC $\eta$  is also upregulated in several cancers including breast cancer and overexpression of PKC $\eta$  is associated with resistance to chemotherapeutic agents. Persistent activation of PKCs by tumor-promoting phorbol esters leads to their degradation or downregulation. However, PKC $\eta$  resists activation-induced downregulation, suggesting that PKC $\eta$  may play a role in tumorigenesis. Targeting the downregulation of PKC $\eta$  may be an important strategy in cancer therapy. We have identified two pathways of PKC $\eta$  downregulation involving PKC inhibition and phosphoinositide 3-kinase (PI3K) inhibition by pharmacological inhibitors Gö 6983 and Ly294002, respectively. Both Gö 6983 and Ly294003-mediated downregulation of PKC $\eta$  depends on dephosphorylation by a calyculin A-sensitive phosphatase. However, only Ly294002-mediated downregulation was blocked by proteasome inhibitor, MG-132 and phorbol

12, 13 dibutyrate (PDBu). Therefore, dephosphorylation of PKC $\eta$  may induce its downregulation. In addition, downregulation of PKC $\eta$  is mediated via both proteasome-dependent and -independent pathways.

## INTRODUCTION

Protein kinase C (PKC) is a family of phospholipid-dependent serine/threonine kinases involved in multiple cellular functions including proliferation, differentiation and cell survival [1, 2]. The PKC family consists of 10 isozymes that differ in structure, function and biochemical properties [3-7]. The classical PKCs (cPKC $\alpha$ , - $\beta$ I,  $\beta$ II, and  $\gamma$ ) are activated by physiological second messengers  $\text{Ca}^{2+}$  and diacylglycerol (DAG), novel PKCs (nPKC $\delta$ , - $\epsilon$ , - $\eta$ , and - $\theta$ ) respond to DAG only and the atypical PKCs (aPKC $\iota/\lambda$  and - $\zeta$ ) respond to neither. Classical and novel PKCs are cellular receptors for phorbol esters which are pharmacological PKC agonists analogous to DAG [8, 9]. Phorbol esters promote membrane translocation and sustained activation of PKCs [10]. As a consequence of sustained activation, PKCs are downregulated resulting in signal termination [11]. Contrary to the other phorbol-ester sensitive PKCs, PKC $\eta$  resists phorbol ester-induced downregulation [12-14] suggesting that the termination of PKC $\eta$  signal occurs via a different mechanism.

Several degradation/downregulation pathways have been described for PKCs. Following membrane translocation,  $\text{Ca}^{2+}$  - activated neutral proteases (calpains) have been shown to downregulate cPKCs [15]. PKC $\alpha$ , - $\delta$  and - $\epsilon$  were shown to be degraded via the ubiquitin/proteasome-mediated pathway [11, 16, 17]. Vesicular trafficking can localize PKCs to lysosomal or membrane compartments, such as lipid rafts or caveolae where they can be degraded by proteases [18, 19]. It is generally believed that activated PKCs are not only sensitive



to protease-mediated degradation, but also to dephosphorylation by phosphatases [20]. The classical model of PKC downregulation involved chronic activation of PKC resulting in dephosphorylation, inactivation and subsequent degradation by accumulation in a cytoskeletal fraction of the cell [21]. Recent studies pose challenges to the classical model. Fully phosphorylated PKC $\alpha$  was shown to be downregulated at the plasma membrane via the proteasome-mediated pathway [17]. Moreover, PKC $\alpha$  was shown to be downregulated by two distinct mechanisms in the same cell type: 1) proteasome-dependent and 2) caveolar trafficking-dependent pathway [19]. These studies highlight the complexity of PKC downregulation mechanisms.

It has been reported that full-length PKC $\eta$  expressed in BHK cells was resistant to phorbol ester-induced downregulation and transfection of constitutively-active mutant at the pseudosubstrate site (A161EPKC $\eta$ ) resulted in the appearance of PKC $\eta$  degradation fragments [14]. Proteasome inhibitors had a modest effect in preventing downregulation of wild-type PKC $\eta$ , whereas they increased the abundance of PKC $\eta$  fragments. These results indicate that activation of PKC $\eta$  is necessary for downregulation by the proteasome-mediated pathway. These results could not be extended to other cell types since the A161EPKC $\eta$  constitutively-active mutant could not be expressed in HEK 293 cells [14]. Therefore, the exact mechanism of PKC $\eta$  downregulation remains unclear.

The purpose of the present study was to understand the mechanism of PKC $\eta$  downregulation in the breast cancer MCF-7 cell line. We report for the first time that PKC $\eta$  can be downregulated by PKC as well as phosphoinositide-3-kinase (PI3K) inhibitors. PKC $\eta$  downregulation mediated by PKC and PI3K inhibition occurs via dephosphorylation by a calyculin A-sensitive phosphatase..PKC $\eta$  downregulation by PI3K inhibition was proteasome-dependent whereas downregulation by Gö 6983 was proteasome-independent. These studies indicate that PKC $\eta$  can be downregulated by inhibition of both PI3K and PKC and the downregulation occurs by two distinct pathways.

## EXPERIMENTAL PROCEDURES

### Materials

Gö 6983, Ly294002, calyculin A, okadaic acid, and calpeptin A were purchased from Calbiochem (San Diego, CA). PDBu was purchased from Alexis Biochemicals (San Diego, CA). Polyclonal antibodies to PKC $\eta$ , PKC $\delta$  and PKC $\epsilon$ , and monoclonal antibody to GAPDH were from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA). Monoclonal antibody to PKC $\alpha$  was from Upstate Biotechnology, Inc. (Lake Placid, NY). Monoclonal antibody to actin was obtained from Sigma (St. Louis, MO). Non-targeting siRNA and siRNA SMARTpool against PTEN and PHLPP were obtained from Dharmacon (Lafayette, CO). Horseradish peroxidase conjugated goat anti-mouse and donkey anti-rabbit antibodies were obtained from JacksonImmunoResearch Lab. Inc. (West Grove, PA). Poly(vinylidenedifluoride) membrane was from Millipore (Bedford, MA) and enhanced chemiluminescence detection kit was from Amersham (Arlington Heights, IL).

### Cell Culture and Transfection

MCF-7 breast cancer cells were maintained in RPMI medium supplemented with 10% heat-inactivated fetal bovine serum and 2 mM glutamine. Cells were kept in a humidified incubator at 37°C with 95% air and 5% CO<sub>2</sub>. Human embryonic kidney (HEK) 293 cells were maintained in Dulbecco's modified minimal essential medium supplemented with 10% fetal bovine serum and 2 mM glutamine. Cells were kept in a humidified incubator at 37°C with 95% air and 5% CO<sub>2</sub>.

HEK293 cells were grown on glass coverslips one day before transfection. Cells were transfected with 0.3  $\mu$ g PKC $\eta$ -GFP using Lipofectamine reagent (Invitrogen, Carlsbad, CA) and the manufacturer's protocol. One day post-transfection, the cells were treated with PDBu, Gö 6983 and Ly294002.

### **Immunoblot Analysis**

Cells were lysed in extraction buffer containing 1 mM DTT, protease inhibitors and phosphatase inhibitors. Equal amounts of protein were separated by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and transferred on PVDF membranes. Western blot analysis was performed as described previously [22] .

### **siRNA transfection**

Control non-targeting siRNA or SMARTpool siRNA against PDK1, PTEN and PHLPP were introduced into MCF-7 cells using Lipofectamine 2000 (Invitrogen) and manufacturer's protocol. Briefly, cells were seeded one day before transfection. 48 h following siRNA transfection, cells were treated as indicated in the text and processed for Western blot analysis as described before [23].

### **Confocal microscopy**

HEK 293 cells were grown on glass coverslips and transfected with 0.3  $\mu$ g PKC $\eta$ -GFP construct. One day, post-transfection, cells were treated with 1  $\mu$ M PDBu, 1  $\mu$ M Gö 6983 and 25

$\mu$ M Ly294002 for 8 h. Cells were fixed and permeabilized with methanol and triton-X and nuclei were stained with DAPI (Molecular Probes, Eugene, OR). Coverslips were mounted on glass slides and cells were visualized on a Zeiss LSM 410 confocal microscope. Images were captured using LSM 4 software (Carl Zeiss Microimaging).

## RESULTS

### **PI3K and PKC inhibitors induce PKC $\eta$ downregulation**

We have previously reported that PKC $\eta$  resists phorbol ester-induced downregulation in MCF-7 breast cancer cells [12]. Therefore, persistent activation by phorbol esters does not lead to its downregulation. To determine if inhibition of PKC $\eta$  activity influences its downregulation, we compared the effect of the general PKC inhibitor (Gö 6983) and activation loop kinase, PI3K/phosphoinositide-dependent protein kinase-1 (PDK1) inhibitor (Ly294002) on PKC $\eta$  protein levels. Figure 1a, b shows that both Gö 6983 and Ly294002 caused a substantial decrease in PKC $\eta$  protein levels. The mitogen-activated protein kinase inhibitor U0126 did not alter PKC $\eta$  protein levels suggesting MAPK does not contribute to PKC $\eta$  stability. Moreover, the downregulation by Gö 6983 and Ly294002 was specific to PKC $\eta$  since the protein levels of other PKCs such as PKC $\epsilon$ ,  $-\delta$  and  $-\alpha$  were not affected. In Figure 2 a, b, PKC $\eta$  downregulation by both inhibitors was time-dependent. These results suggest that both PKC and PI3K pathways are involved in PKC $\eta$  downregulation.

### **PKC $\eta$ downregulation is mediated by two distinct mechanisms**

Since inactivation of PKC $\eta$  by Gö 6983 and Ly294002 leads to its downregulation, we next determined if PKC activators can reverse the effect of inhibitor-mediated downregulation of PKC $\eta$ . In Figure 3, pretreatment with phorbol 12, 13 dibutyrate, PDBu had a modest effect on blocking Gö 6983-mediated downregulation of PKC $\eta$ ; however, PDBu completely reversed the

effect of Ly294002-mediated downregulation. This suggests that activation of PKC $\eta$  by PDBu can protect PKC $\eta$  from downregulation by PI3K-inhibition but not PKC-inhibition. Therefore the downregulation of PKC $\eta$  by Gö 6983 and Ly294002 is mediated by different mechanisms.

It has been reported that PKC $\alpha$ , - $\delta$ , and - $\epsilon$  are downregulated by the ubiquitin/proteasome mediated pathway in response to phorbol ester treatment [11, 16, 17]. Therefore, we explored the possibility of PKC $\eta$  downregulation by Gö 6983 and Ly294002 via the ubiquitin/proteasome pathway. Interestingly, Ly294002-mediated but not Gö 6983-mediated downregulation was significantly blocked by the proteasome inhibitor, MG-132 (Figure 4a, b). Since PKCs can also be degraded by proteases such as calpains [15], we investigated the ability of calpains to degrade PKC $\eta$  using the calpain inhibitor, calpeptin. Figure 5 shows that inhibition of calpains did not affect downregulation of PKC $\eta$  by Gö 6983 or Ly294002 indicating PKC $\eta$  downregulation does not depend on calpains. These data further confirm two distinct pathways of PKC $\eta$  downregulation: proteasome-dependent downstream of PI3K inhibition and proteasome-independent in response to PKC inhibition.

### **Calyculin A sensitive phosphatase regulates downregulation of PKC $\eta$ by PKC and PI3K inhibitors**

It is generally believed that dephosphorylation precedes downregulation of PKCs [20]. To determine the involvement of phosphatases in PKC $\eta$  downregulation we depleted by siRNA two phosphatases involved in PKC signaling: phosphatase and tensin homologue deleted from

chromosome-10 (PTEN) and PH domain and leucine rich repeat protein phosphatase (PHLPP). PTEN opposes the activity of PI3K to negatively regulate Akt and PKC [24]. PHLPP has been reported to dephosphorylate both Akt and PKC at the hydrophobic motif to inactivate Akt and degrade PKC [25, 26]. Figure 6 shows that neither PTEN nor PHLPP depletion blocks PKC $\eta$  downregulation by Gö 6983 or Ly294002. Therefore, downregulation of PKC $\eta$  by Gö 6983 or Ly294002 is not mediated by PTEN or PHLPP dephosphorylation.

We next looked at the effect of Ser/Thr phosphatases on Gö 6983- and Ly294002-mediated downregulation of PKC $\eta$  by treating cells with Ser/Thr phosphatase inhibitors calyculin A which inhibits PP1 and PP2A and okadaic acid which inhibits PP2A at the 100 nM concentration tested. Figure 7 shows complete reversal of Gö 6983- and Ly294002-mediated downregulation of PKC $\eta$  with calyculin A, whereas okadaic acid had no apparent effect on PKC $\eta$  downregulation. This suggests that PP1 may be playing a role in regulating PKC $\eta$  dephosphorylation in the presence of Gö 6983 and Ly294002. Calyculin A also increased the levels of PKC $\alpha$  and PKC $\epsilon$  basally and in the presence of Gö 6983 indicating that PKC $\alpha$  and PKC $\epsilon$  may be dephosphorylated by PP1, but this dephosphorylation does not lead to degradation of PKC $\alpha$  and PKC $\epsilon$  as it does with PKC $\eta$ . This data indicates that dephosphorylation by a calyculin A-sensitive phosphatase is an important step in the downregulation of PKC $\eta$  by both Gö 6983 and Ly294002.



### **Treatment with PDBu, Gö 6983 and Ly294002 affects subcellular localization of PKC $\eta$ .**

Since we have seen that PDBu upregulates PKC $\eta$  levels and both Gö 6983 or Ly294002 downregulates PKC $\eta$  levels, we next determined if the localization of PKC $\eta$  is altered in response to these treatments. We transfected HEK 293 cells with PKC $\eta$ -GFP construct and monitored localization by confocal microscopy after treatment with PDBu, Gö 6983 and Ly294002 for 8 h. As shown in In Figure 8, PKC $\eta$ -GFP is concentrated in the perinuclear region in the control cells. Treatment with PDBu caused a dramatic increase in PKC $\eta$ -GFP expression with localization mostly in the cytosol, but also can be detected in the nucleus. Treatment with either Gö 6983 or Ly294002 caused a decrease in PKC $\eta$ -GFP expression and the localization was more dispersed throughout the cell with less concentration in the perinuclear region and more expression throughout the nucleus and cytoplasm. Therefore, the expression and localization of PKC $\eta$  is altered in response to treatment with PDBu, Gö 6983 and Ly294002.

## DISCUSSION

PKC $\eta$  upregulation has been linked to several cancer types including breast [12], renal [27] and glioblastoma [28]. In addition, overexpression of PKC $\eta$  has been linked to resistance to chemotherapeutic agents in breast cancer [22], prostate cancer [29], lung cancer [30] and Hodgkin's lymphoma [31]. Furthermore, PKC $\eta$  resists downregulation by chronic activation of tumor promoting phorbol esters [12, 13, 28], suggesting PKC $\eta$  plays a role in tumorigenesis. Therefore, elucidating the mechanism of PKC $\eta$  downregulation and desensitization is critical to improve cancer therapy. In the present study, we report that PKC $\eta$  is downregulated by two different inhibitors, the general PKC inhibitor Gö 6983 and PI3K inhibitor, Ly294002 rather than by prolonged activation as other PKCs (Figure 1a, b). Therefore, the inhibition of PKC $\eta$  kinase activity leads to downregulation.

We have developed a model of two distinct pathways of PKC $\eta$  downregulation (Figure 9). One pathway is proteasome-independent which mediates Gö 6983 induced downregulation and the other pathway is proteasome-dependent which mediates Ly294002 induced downregulation (Figure 4). Both pathways involve dephosphorylation by a calyculin A-sensitive phosphatase (Figure 7). The pathways differ in response to phorbol ester PDBu. Since Gö 6983 is a general PKC inhibitor, the kinase involved in phosphorylating and protecting PKC $\eta$  against downregulation is most likely a PKC. Since PDBu had no effect on PKC $\eta$  downregulation by Gö 6983 (Figure 3), the PKC involved may either be insensitive to phorbol esters, such as the

atypical PKCs or downregulated by PDBu treatment such as the conventional or novel PKC $\delta$ , - $\epsilon$  or  $\theta$ . PKC $\eta$  has been shown to directly phosphorylate PKC $\mu$ /PKD [32, 33] and PKC $\delta$  and PKC $\epsilon$  have been shown to phosphorylate each other on their activation loop or hydrophobic motif [34]. PKC $\eta$  has been reported to be phosphorylated at the hydrophobic motif by atypical PKC $\iota$  which stabilizes PKC $\eta$  and allows PDK1 to dock and phosphorylate the activation loop [35]. Preliminary results using PDK1 siRNA suggest that depletion of PDK1 can destabilize PKC $\eta$  basal levels (data not shown) indicating PDK1 may also be the potential target of Gö 6983 or Ly294002 in the downregulation of PKC. Furthermore, mammalian target of rapamycin complex 2 (mTORC2) was reported to phosphorylate and stabilize PKC $\epsilon$  at the turn motif and hydrophobic motif [36]. Recently, we have shown that depletion of PKC $\epsilon$  and mTORC2 enhanced downregulation of PKC $\delta$  [37]. Based on these reports, PKC $\epsilon$ , - $\delta$  or - $\iota$ , PDK1 or mTORC2 could be potential kinases involved in the Gö 6983 and Ly294002-mediated downregulation of PKC $\eta$ .

PHLPP has been shown to dephosphorylate and destabilize PKC $\alpha$  and PKC $\epsilon$  through removal of the hydrophobic motif phosphate, but not PKC $\eta$  [25, 26]. In this study, PHLPP depletion had no effect on blocking Gö 6983 or Ly294002 downregulation of PKC $\eta$  (Figure 6). However, since calyculin A but not okadaic acid blocked the downregulation of PKC $\eta$  by Gö 6983 and Ly294002, it is likely that PP1 is the potential phosphatase involved in

dephosphorylating PKC $\eta$ . Future studies should test the direct interaction of PP1 with PKC $\eta$  and the specific site of dephosphorylation of PKC $\eta$ .

The dual mechanisms of PKC downregulation was also reported for PKC $\alpha$  in response to downregulation by two different activators bryostatin and phorbol 12-myristate 13-acetate (PMA) [19]. One pathway involves ubiquitination of the fully phosphorylated, mature PKC $\alpha$  at the plasma membrane followed by proteasome-mediated degradation. In contrast, the second pathway involved caveolae-mediated trafficking to the perinuclear compartment, dephosphorylation and degradation via a proteasome-independent pathway. Therefore, both PKC $\eta$  and PKC $\alpha$  are downregulated via proteasome-dependent and independent mechanisms. For PKC $\eta$ , the proteasome-independent pathway does not involve calpains (Figure 5) nor does it involve cathepsins or lysosomal-mediated degradation since inhibitors of these mechanism had no effect on PKC $\eta$  downregulation by Gö 6983 or Ly294002 (data not shown). Therefore, further investigation is necessary to elucidate the proteasome-independent mechanism of PKC $\eta$  downregulation by Gö 6983.

We have shown that the localization of PKC $\eta$  is altered in response to treatment with PDBu, Gö 6983, or Ly294002 (Figure 8). It has been reported that PKC $\eta$  is localized in the Golgi, ER and nuclear envelope and translocates to the nuclear envelope upon treatment with PMA [38]. We have detected a striking upregulation of PKC $\eta$  in response to PDBu treatment with localization in the cytoplasm, nucleus and nuclear membrane. Similarly, treatment with inhibitors Gö 6983 and Ly294002 caused more nuclear and cytoplasmic localization of PKC $\eta$  and less perinuclear

concentration compared to the control unstimulated cells. It is possible that PKC $\eta$  is stabilized in the perinuclear region and translocation out of this region can lead to its destabilization and degradation.

In this study, we have identified two distinct mechanisms of PKC $\eta$  downregulation by two different inhibitors. Since overexpression of PKC $\eta$  has been associated with resistance to chemotherapeutic agents [31], Gö 6983 or Ly294002, which we have shown in this report leads to PKC $\eta$ -specific downregulation and not other PKCs, can be used in combination with chemotherapeutic agents to overcome chemotherapeutic-resistance associated with PKC $\eta$ .

**Figure 1. Effect of PKC and P13K inhibitors on PKC $\eta$  protein levels.**

(a) MCF-7 cells were treated with 1  $\mu$ M Gö 6983, 25  $\mu$ M Ly294002 and 10  $\mu$ M U0126 for 15h.

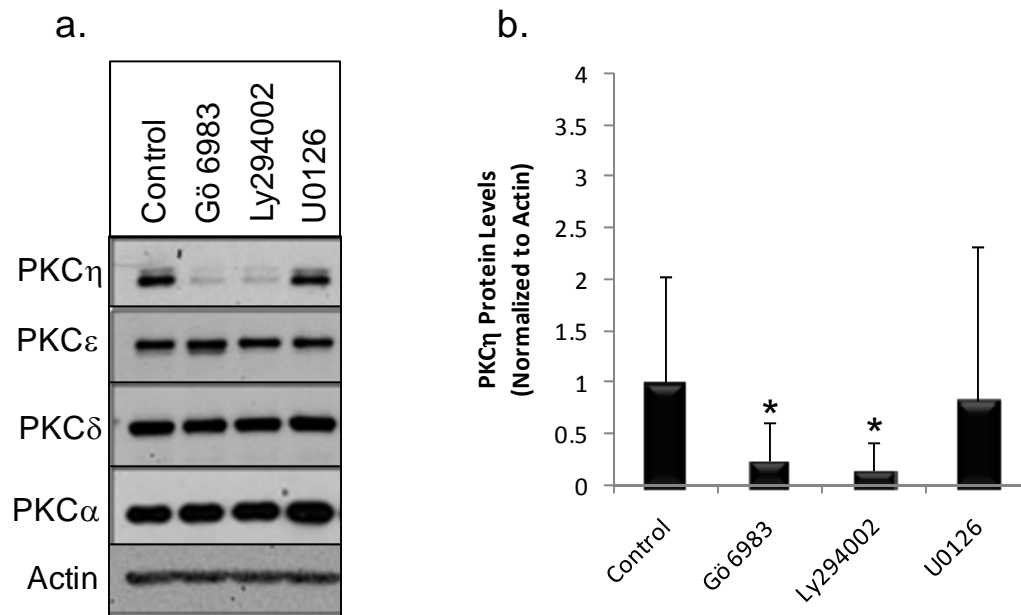
Western blot analysis was performed with total cellular extracts using the indicated antibodies.

Actin was used as a loading control. (b) Densitometric quantification of PKC $\eta$  protein levels

from 3 separate experiments corrected for loading. Data represents the mean  $\pm$  s.e.m. The

asterisk (\*) indicates significant difference from control ( $P < 0.01$ ) using Student's *t*-test.

**Figure 1.**



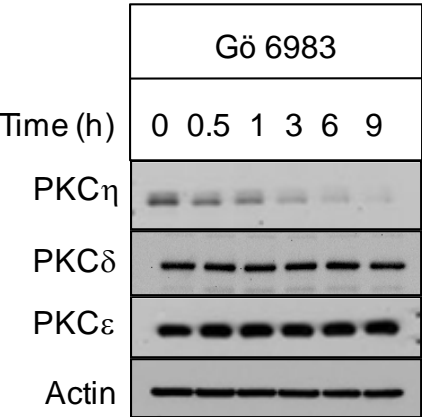
**Figure 2. Time-course comparison of PKC and P13K inhibitors on PKC $\eta$  protein levels.**

MCF-7 cells were treated with (a) 1  $\mu$ M Gö 6983 or (b) 25  $\mu$ M Ly294002 for the indicated time points. Western blot analysis was performed with total cellular extracts using the indicated antibodies. Actin was used as a loading control. Results were representative of at least 2 independent experiments.

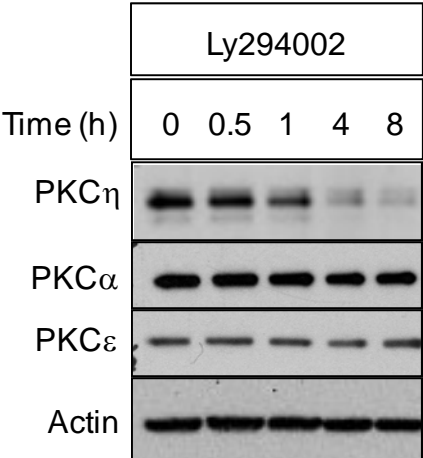


Figure 2.

a.



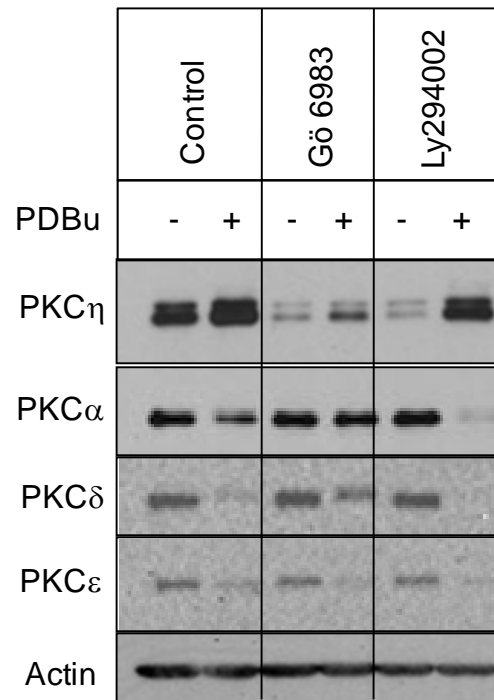
b.



**Figure 3. Effect of PDBu on Gö 6983- or Ly294002-mediated downregulation of PKC $\eta$ .**

MCF-7 cells were pre-treated with 1  $\mu$ M PDBu for 15 min, followed by treatment with 1  $\mu$ M Gö 6983 or 25  $\mu$ M Ly294002 for 15h. Western blot analysis was performed with total cellular extracts using the indicated antibodies. Actin was used as a loading control. Results were representative of 2 independent experiments.

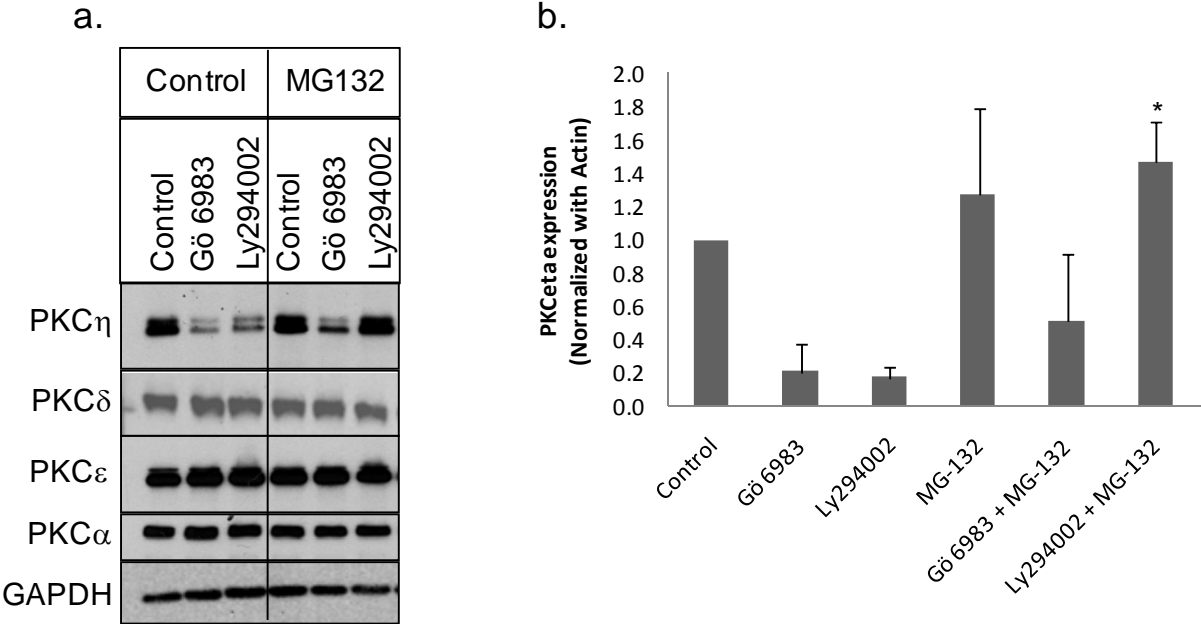
**Figure 3.**



**Figure 4. Effect of proteasome inhibitor, MG-132 on PKC $\eta$  downregulation by Gö 6983 or Ly294002.**

(a) MCF-7 cells were pretreated with 10  $\mu$ M MG-132 for 30 min, followed by treatment with 1  $\mu$ M Gö 6983 or 25  $\mu$ M Ly294002 for 12 h. Western blot analysis was performed with total cellular extracts using the indicated antibodies. GAPDH was used as a loading control. (b) Densitometric quantification of PKC $\eta$  protein levels from 3 separate experiments corrected for loading. Data represents the mean  $\pm$  s.e.m. The asterisk (\*) indicates significant difference of MG-132 treated cells from control or treatment with the inhibitors alone ( $P < 0.01$ ) using Student's *t*-test.

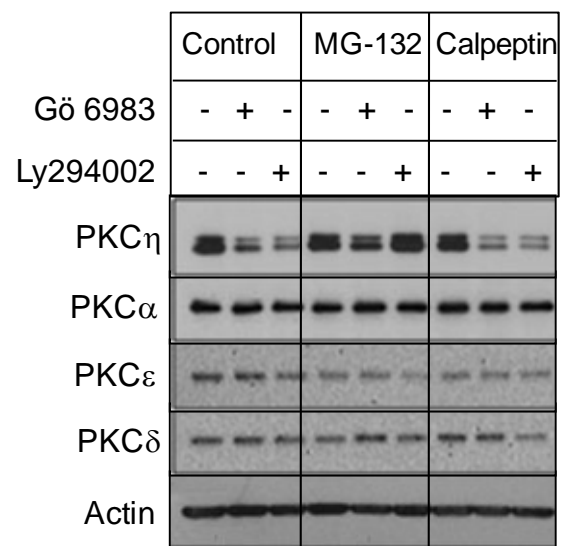
**Figure 4.**



**Figure 5. Effect of calpain inhibitor, Calpeptin on Gö 6983- or Ly294002-mediated downregulation of PKC $\eta$ .**

MCF-7 cells were pretreated with 50  $\mu$ M Calpeptin for 30 min, followed by treatment with 1  $\mu$ M Gö 6983 or 25  $\mu$ M Ly294002 for 12 h. Western blot analysis was performed with total cellular extracts using the indicated antibodies. Actin was used as a loading control. Results were representative of 2 independent experiments.

**Figure 5.**

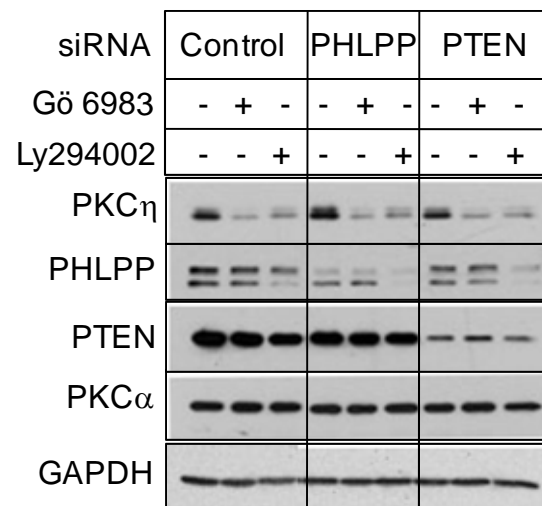


**Figure 6. Effect of PHLPP or PTEN phosphatase depletion on Gö 6983- or Ly294002-mediated downregulation of PKC $\eta$ .**

MCF-7 cells were transfected with non-targeting siRNA (Control) or siRNA against PTEN or PHLPP. Cells were treated with 1  $\mu$ M Gö 6983 or 25  $\mu$ M Ly294002 for 15 h. Western blot analysis was performed with total cellular extracts using the indicated antibodies. GAPDH was used as a loading control. Results were representative of 2 independent experiments.



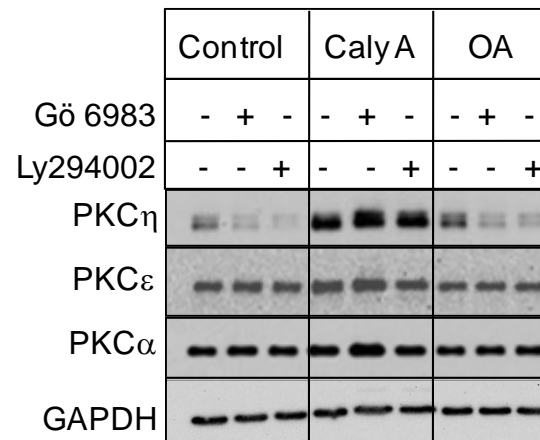
**Figure 6.**



**Figure 7. Effect of phosphatase inhibitors, calyculin A and okadaic acid on Gö 6983- or Ly294002-mediated downregulation of PKC $\eta$ .**

MCF-7 cells were pretreated with 10 nM calyculin A (Caly A) or 100 nM okadaic acid (OA) for 15 min, followed by treatment with 1  $\mu$ M Gö 6983 or 25  $\mu$ M Ly294002 for 3 h. Western blot analysis was performed with total cellular extracts using the indicated antibodies. GAPDH was used as a loading control. Results were representative of 2 independent experiments.

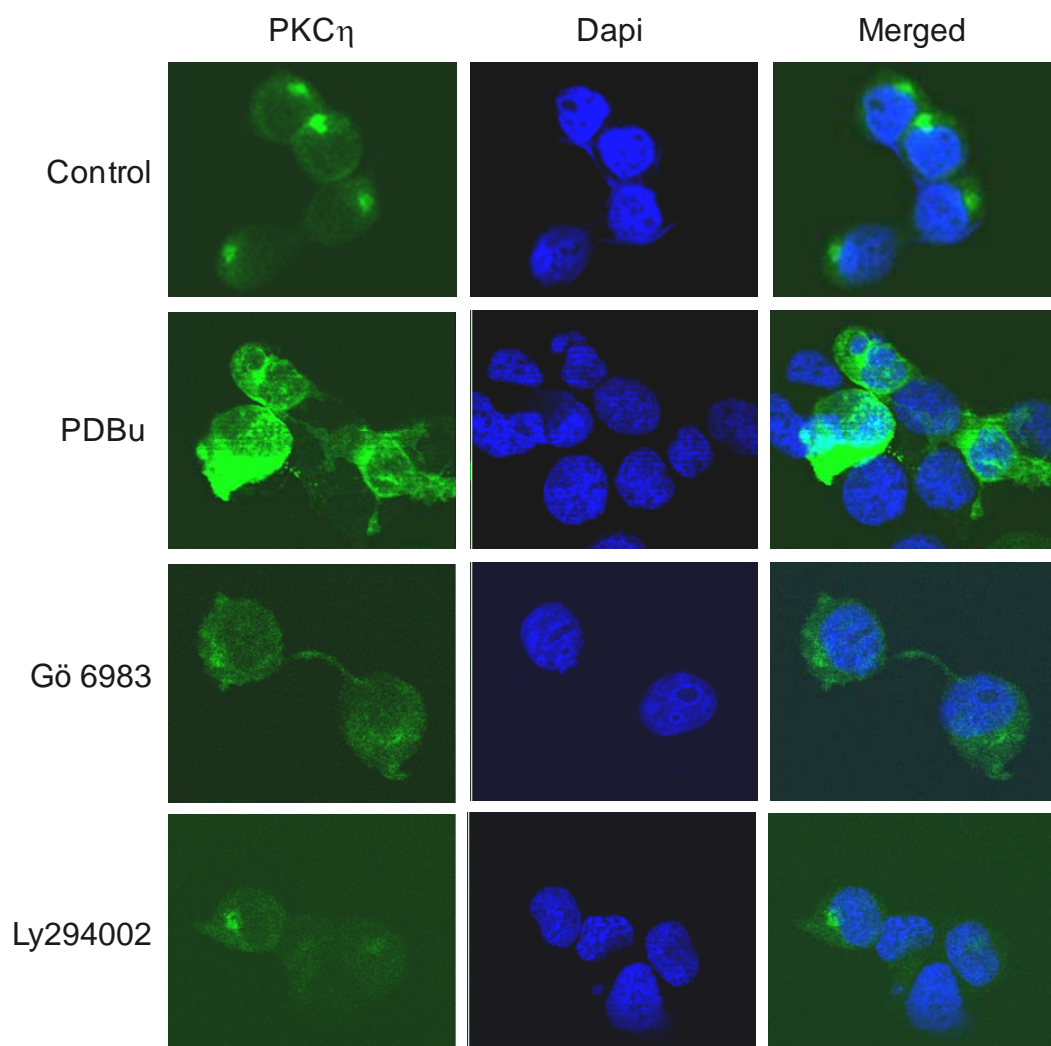
**Figure 7.**



**Figure 8. Effect of PDBu, Gö 6983 or Ly294002 treatment on localization of PKC $\eta$ .**

PKC $\eta$ -GFP construct was transiently transfected in HEK 293 cells and treated with 1  $\mu$ M PDBu, 1  $\mu$ M Gö 6983 and 25  $\mu$ M Ly294002 for 8 h. Cells were fixed and imaged with confocal microscopy. PKC $\eta$ -GFP was visualized as green fluorescent signals mostly in the perinuclear, cytoplasmic and nuclear regions. Nuclei staining with DAPI were visualized in blue.

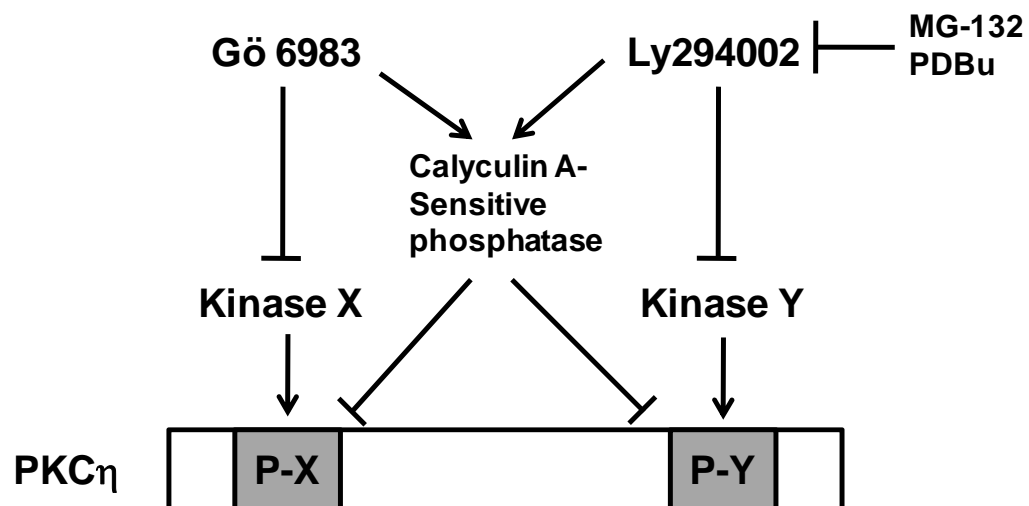
**Figure 8.**



**Figure 9. Model of two distinct pathways of PKC $\eta$  downregulation by Gö 6983 or Ly294002.**

PKC $\eta$  can be downregulated by treatment with the PKC inhibitor, Gö 6983 or PI3K inhibitor, Ly294002. Gö 6983 inhibits hypothetical (Kinase X) and Ly294002 inhibits hypothetical (Kinase Y) which can phosphorylate and stabilize PKC $\eta$  possibly at two different sites (P-X or P-Y). Activation of a calyculin A-sensitive phosphatase by both inhibitors can dephosphorylate and downregulate PKC $\eta$ . Ly294002 mediated downregulation of PKC $\eta$  is blocked by proteasome inhibitor, MG-132 or PKC activator PDBu indicating proteasome-dependent downregulation. Downregulation of PKC $\eta$  by Gö 6983 occurs independently of the proteasome degradation pathway.

Figure 9.



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## CHAPTER IV

### FUNCTIONAL SIGNIFICANCE OF PROTEIN KINASE C $\eta$ DOWNREGULATION

#### SUMMARY

A deregulation in apoptosis or programmed cell death can contribute to cancer progression and resistance to chemotherapeutic agents. The protein kinase C (PKC) family plays an important role in regulating apoptosis. Several anti-apoptotic PKC isozymes such as PKC $\epsilon$  and PKC $\eta$  have been shown to be overexpressed in cancers and contribute to resistance against TNF or TRAIL-induced cell death. In this study, we have investigated the anti-apoptotic function of PKC $\eta$  in breast cancer cells and report that increased PKC $\eta$  protein level plays a role in breast cancer progression and confers resistance to TRAIL-induced cell death. Depletion of PKC $\eta$  altered the protein levels of two Bcl-2 family members, pro-apoptotic Bax and anti-apoptotic Mcl-1. PKC $\eta$  depletion increased the dimerization of Bax and decreased the induction of Mcl-1 in response to TRAIL. MCF-7 breast cancer cells were sensitized to TRAIL with PKC $\eta$  or Mcl-1 depletion. This study highlights the potential role of PKC $\eta$  in regulating proteins involved in the intrinsic mitochondrial pathway of TRAIL-induced cell death.

## INTRODUCTION

Apoptosis or programmed cell death plays an important role in the development and homeostasis of normal tissues [1, 2]. An imbalance between cell proliferation and cell death has been linked to several human diseases including cancer, autoimmune disease and neurodegenerative disorders [3-6]. Current cancer therapies are based on their ability to induce cell death in rapidly growing cells [7]. Therefore, deciphering the mechanisms of signaling pathways involved in apoptosis is crucial to develop more efficient and specific cancer therapeutics. Two major apoptotic signaling pathways have been described which are the extrinsic (death receptor-mediated) and intrinsic (mitochondrial-mediated) pathways [8] (Figure 3 from Introduction). The extrinsic pathway involves death receptors belonging to the tumor necrosis factor- $\alpha$  receptor (TNFR) superfamily. Ligands such as TNF or TNF-related apoptosis-inducing ligand (TRAIL) can bind to death receptors and recruit adaptor molecules to form the death-inducing signaling complex (DISC). The second pathway, intrinsic pathway is mediated by Bcl-2 family of proteins which regulate mitochondrial membrane integrity in response to apoptotic stimuli such as DNA damage or other cytotoxic insults [9]. Both pathways further recruit cysteine aspartic acid specific proteases (caspases) to activate apoptosis [8, 10, 11].

Several signaling pathways controlling apoptosis are commonly altered in cancer [12]. The protein kinase C (PKC) family of isozymes play a major role in regulating cell proliferation and cell death processes [13]. Anti-apoptotic PKC isozymes such as PKC $\epsilon$  and PKC $\eta$  have been

reported to be associated with resistance to TNF or TRAIL-induced cell death [14-18]. Overexpression of anti-apoptotic Bcl-2 family members is also found in many types of human cancers [12]. Therefore, both PKC and Bcl-2 protein families can be exploited as potential targets for cancer therapy [19-21]. We have reported that PKC $\epsilon$  exerts its anti-apoptotic effect by downregulating the pro-apoptotic Bcl-2 member Bid and upregulating anti-apoptotic Bcl-2 to confer resistance to TRAIL [17]. Others have found that PKC isozymes can regulate pro- or anti-apoptotic members of the Bcl-2 family to influence TRAIL resistance [22, 23]. For instance, activation of PKC by phorbol-12-myristate-13-acetate (PMA) induced the expression of pro-apoptotic Bad and anti-apoptotic Mcl-1 in the pancreatic cancer cell line PANC-1 [23]. Furthermore, the activation of Bad was attributed to conventional and not novel or atypical PKC isozymes since pretreatment with conventional PKC inhibitors prevented Bad induction [23]. Activation of PKC also increased the expression of TRAIL receptors to provide a potential mechanism to sensitize pancreatic cancer cells to TRAIL [23]. The mechanism by which PKC $\eta$  exerts its anti-apoptotic effect in response to TRAIL is not well established.

In this study, we report that increased protein levels of PKC $\eta$  is associated with breast tumor progression using an isogenic model of breast epithelial cells that progress from benign to pre-malignant to metastatic stages. Overexpression of PKC $\eta$  was associated with resistance to TRAIL-induced cell death in breast adenocarcinoma MCF-7 cells. Knockdown of PKC $\eta$  by itself did not sensitize cells to TRAIL-induced apoptosis via cleavage of caspase substrate poly (ADP-ribose) polymerase (PARP), but enhanced the dimerization of pro-apoptotic Bax and

blocked the induction of anti-apoptotic Mcl-1. These data suggest that PKC $\eta$  is an upstream effector of the Bcl-2 family in response to TRAIL. Mcl-1 depletion by itself caused cell death in MCF-7 cells and further enhanced TRAIL-induced cell death. PKC $\eta$  depletion resulted in a modest increase in cell death suggesting there may be a compensatory effect of other anti-apoptotic proteins due to PKC $\eta$  depletion. These results suggest that PKC $\eta$  may exert its anti-apoptotic effect by regulating Bcl-2 family proteins upstream of the mitochondria-mediated cell death pathway.

## EXPERIMENTAL PROCEDURES

### Materials

Human recombinant TRAIL was purchased from R&D systems (Minneapolis, MN). Polyclonal antibodies to PKC $\eta$ , PKC $\delta$  and PKC $\epsilon$ , and monoclonal antibodies to glyceraldehydes-3-phosphate dehydrogenase (GAPDH), Bcl-2 and Bax (6A7) were purchased from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA). Polyclonal antibody to Bid and monoclonal antibodies to PARP and caspase-7 were purchased from Pharmingen (San Diego, CA). Polyclonal antibody to Mcl-1 was purchased from Cell Signaling Technologies (Beverly, MA). Monoclonal antibody to PKC $\alpha$  was from Upstate Biotechnology, Inc. (Lake Placid, NY). Monoclonal antibody to actin was obtained from Sigma (St. Louis, MO). Non-targeting siRNA and siRNA SMARTpool against PKC $\eta$  and Mcl-1 were obtained from Dharmacon (Lafayette, CO). YO-PRO-1 dye was obtained from Molecular Probes (Eugene, OR). Horseradish peroxidase conjugated goat anti-mouse and donkey anti-rabbit antibodies were obtained from JacksonImmunoResearch Lab. Inc. (West Grove, PA). Poly(vinylidenedifluoride) membrane was from Millipore (Bedford, MA) and enhanced chemiluminescence detection kit was from Amersham (Arlington Heights, IL).

### Cell Culture

MCF10A and MCF10AT1 cells were maintained in DMEM /F12 medium supplemented with 5% horse serum, 15 mM HEPES buffer, 10 mg/ml insulin, 20 ng/ml EGF, 100 ng/ml cholera toxin and 0.5 mg/ml hydrocortisone. MCF10CA1d and MCF10CA1a cells were



maintained in DMEM/ F12 medium supplemented with 5% horse serum. MCF-7 breast cancer cells were maintained in RPMI medium supplemented with 10% heat-inactivated fetal bovine serum and 2 mM glutamine. Cells were kept in a humidified incubator at 37°C with 95% air and 5% CO<sub>2</sub>.

### **Transfection**

MCF-7 cells were transfected with 1 µg of pcDNA3 or vector containing wild-type PKC $\eta$  (pcDNA3-PKC $\eta$ ) using FuGENE 6 (Roche, NJ). Briefly, cells were seeded 1 day before transfection. 24 h following transfection, cells were treated with Geneticin (G418) (Gibco) and resistant cells were pooled and re-plated after 3 days. Cells were treated with the indicated concentrations of TRAIL and processed for immunoblot analysis.

### **Immunoblot Analysis**

Cells were lysed in extraction buffer containing 1 mM DTT, protease inhibitors and phosphatase inhibitors. Equal amounts of protein were separated by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and transferred on PVDF membranes. Western blot analysis was performed as described previously [24] .

### **siRNA**

Control non-targeting siRNA or SMARTpool siRNA against PKC $\eta$  or Mcl-1 were introduced into MCF-7 cells using Lipofectamine 2000 (Invitrogen) and manufacturer's protocol. Briefly, cells were seeded one day before transfection. 48 h following siRNA

transfection, cells were treated as indicated in the text and processed for Western blot analysis as described before [25].

#### **Assessment of Cell Death by YO-PRO-1 Assay**

MCF-7 cells transfected with non-targeting control, PKC $\eta$  or Mcl-1 siRNA. Two days after transfection, cells were treated with TRAIL for 12 h and analyzed for the number of apoptotic and dead cells using YO-PRO-1 staining. Live cells were stained with 0.5  $\mu$ M YO-PRO-1 for 15 min in the dark. Fluorescent staining was then visualized using a Zeiss Axiovert 40 inverted microscope with the AxioVision Rel 4.6 software (Zeiss, Göttingen, Germany). Cells staining positively for YO-PRO-1 binding (green fluorescence) were scored as apoptotic, since YO-PRO-1 permeates early apoptotic cells. [26].

## RESULTS

### **Overexpression of PKC $\eta$ confers resistance to TRAIL-induced cell death in MCF-7 cells.**

Since we have previously reported that overexpression of PKC $\eta$  attenuated TNF-induced cell death in MCF-7 cells [24], we examined if overexpression of PKC $\eta$  can also confer resistance to TRAIL. MCF-7 cells overexpressing PKC $\eta$  was previously generated [24]. Apoptotic cell death was monitored by processing of caspase 7 and cleavage of caspase 7 substrate, poly (ADP-ribose) polymerase (PARP). PARP cleavage and decrease in full-length caspase 7 was detected in MCF-7 cells transfected with empty vector in response to TRAIL in a concentration dependent manner (Figure 1). In contrast, PKC $\eta$  overexpressing cells were completely resistant to TRAIL-induced cell death. This data suggests that PKC $\eta$  is involved in resistance to TRAIL-induced cell death in MCF-7 cells.

### **Depletion of PKC $\eta$ blocks TRAIL-induced Mcl-1 expression.**

Since it was reported that overexpression of PKC $\epsilon$  conferred resistance to TRAIL-induced cell death by regulating members of the Bcl-2 family [17], we wanted to determine if PKC $\eta$  also exerts its protective effect via the Bcl-2 family. We depleted PKC $\eta$  by siRNA using non-targeting siRNA as a control and treated MCF-7 cells with TRAIL. As shown in Figure 2a, PKC $\eta$  siRNA successfully depleted PKC $\eta$  protein levels without affecting the levels of PKC $\delta$ , PKC $\epsilon$  and PKC $\alpha$ . In Figure 2b, PKC $\eta$  knockdown increased Bax dimerization indicating PKC $\eta$

may play a role in the intrinsic apoptotic pathway. PKC $\eta$  depletion also blocked the induction of Mcl-1, an anti-apoptotic Bcl-2 family member by TRAIL. PKC $\eta$  depletion had no detectable affect on Bcl-2 or Bid protein levels. This data suggests that PKC $\eta$  may exert its anti-apoptotic affect by targeting Bax and Mcl-1.

### **Mcl-1 knockdown sensitized cells to TRAIL-induced cell death**

To further investigate the role of PKC $\eta$  and Mcl-1 in TRAIL-induced cell death, we depleted PKC $\eta$  or Mcl-1 in MCF-7 cells and monitored apoptotic cell death in response to TRAIL by YO-PRO-1 Assay. YO-PRO-1 is a green fluorescent nucleic acid dye that can permeate apoptotic cells. As shown in Figure 3 a, b, PKC $\eta$  depletion modestly sensitized cells to TRAIL-induced cell death compared to the control non-targeting siRNA transfected cells. In contrast, Mcl-1 depletion by itself increased cell death compared to the control and further enhanced TRAIL-induced cell death (Figure 3 a, b). This data suggests that Mcl-1 depletion is sufficient in sensitizing MCF-7 cells to TRAIL-induced cell death.

### **PKC $\eta$ protein level increases with breast tumor progression**

Since PKC $\eta$  overexpression conferred resistance to TRAIL (Figure 1) and depletion of PKC $\eta$  modestly sensitizes MCF-7 cells to TRAIL-induced apoptosis (Figure 3), we next wanted to compare the protein levels of PKC $\eta$  in normal breast epithelial cells and breast cancer cells. We utilized a series of isogenic human breast cancer cells [27] representing a tumor progression

model to determine if increased PKC $\eta$  expression is associated with breast tumor progression. The MCF-10A series consists of cells that have the same genotype, but different phenotype. The MCF-10A cells are immortalized benign breast epithelial cells. The MCF-10AT1 cells are pre-malignant and were obtained by xenograft from cells that were transformed by HRAS. The MCF10CA1a and MCF10CA1d cells are metastatic clones. Since these cells lines are isogenic, they represent an advantageous model system for studying specific protein expression in breast tumor progression by eliminating genetic variations. Figure 4 shows a comparison of PKC isozyme protein levels in the MCF10A series. Compared to the normal MCF10A breast epithelial cells, PKC $\alpha$  levels remained similar in the cell lines, whereas PKC $\epsilon$  and PKC $\delta$  levels increased in MCF10CA1d cells, but decreased in the metastatic cell line MCF10CA1a. PKC $\eta$  increased ~2-fold in the pre-malignant MCF10AT1 cells and ~5-fold in both metastatic cell lines (Figure 4b). This data shows that increased protein level of the PKC $\eta$  isozyme is associated with breast cancer progression.

## DISCUSSION

The role of PKC $\eta$  in tumor progression is cell type specific. PKC $\eta$  was reported to be associated with renal carcinoma [28] whereas PKC $\eta$  null mice were more susceptible to skin tumor formation [29]. In breast [24], lung [30], prostate [18] and Hodgkins lymphoma [31], PKC $\eta$  was associated with resistance to chemotherapeutic agents. We have previously shown that overexpression of PKC $\eta$  confers resistance to TNF-induced cell death; however, the mechanism by which PKC $\eta$  exerts its anti-apoptotic effect is not well-established. This study substantiates the anti-apoptotic role of PKC $\eta$  in breast cancer cells by the following observations. First, overexpression of PKC $\eta$  was associated with resistance to TRAIL-induced cell death (Figure 1). Second, depletion of PKC $\eta$  increased pro-apoptotic Bax dimerization and decreased anti-apoptotic Mcl-1 induction by TRAIL (Figure 2). Third, PKC $\eta$  depletion modestly increased TRAIL induced cell death (Figure 3). Finally, using a series of cell lines representing a breast tumorigenesis model, PKC $\eta$  protein level increased in the metastatic cells versus the normal/benign cells (Figure 4)

The Bcl-2 family of proteins consists of at least 20 members with opposing activities to regulate cell death [32]. The ratio of anti-apoptotic members ( *e.g.*, Bcl-2, Bcl-xl, Mcl-1 and Bcl-w) to pro-apoptotic members (*e.g.*, Bax, Bad, and Bid) can decide the fate of the cell. There have been several reports linking PKC activation with alterations in expression of Bcl-2 family members leading to protection or resistance against apoptotic stimuli [22, 23, 33]. PKC $\epsilon$  has

been shown to regulate several Bcl-2 family members to exert its anti-apoptotic effect [15]. Overexpression of PKC $\epsilon$  increased anti-apoptotic Bcl-2 mRNA and protein level while decreasing pro-apoptotic Bid resulting in a net anti-apoptotic response contributing to TRAIL resistance [17]. PKC $\epsilon$  also prevented Bax translocation to the mitochondrial membrane to protect MCF-7 cells from TNF-induced apoptosis [16]. Bax exists as a monomer in the cytosol and during induction of apoptosis, Bax translocates to the mitochondria, integrates into the outer mitochondrial membrane and undergoes dimerization [34] resulting in cytochrome c release and apoptotic cell death [34]. In the present study, PKC $\eta$  depletion also regulated two opposing members of the Bcl-2 family, Bax and Mcl-1 (Figure 2). Depletion of PKC $\eta$  by itself increased Bax dimer formation which was further increased in the presence of TRAIL. We also detected a concomitant decrease in Mcl-1 induction by TRAIL. TRAIL induces NF- $\kappa$ B-mediated transcriptional induction of Mcl-1 in TRAIL-resistant cells [35]. Expression of c-myc reduced the induction of Mcl-1 by TRAIL and sensitized cells to TRAIL-induced cell death [35] suggesting Mcl-1 plays an important role in TRAIL resistance [36].

Tumor resistance to apoptotic cell death is often a hallmark of cancer and contributes to resistance to chemotherapeutic agents [5]. Although TRAIL has been used in clinical trials as a promising anti-cancer agent for its ability to target cancer cells while sparing normal cells [37, 38]; recombinant TRAIL therapy or anti-TRAIL-R therapies are limited to patients with TRAIL-sensitive tumors resulting in low overall efficacy [39-41]. Therefore, for patients demonstrating a

partial response to TRAIL therapy, combination therapy with TRAIL and agents targeting specific apoptosis signaling pathways can be beneficial.

In this study, we have shown that PKC $\eta$  can potentially target two Bcl-2 family members, pro-apoptotic Bax and anti-apoptotic Mcl-1 in response to TRAIL (Figure 2). Whether or not PKC $\eta$  can regulate Bax or Mcl-1 directly is subject to further investigation. It has been reported that Mcl-1 can be phosphorylated and inactivated by a pro-apoptotic member of the mitogen-activated protein kinase (MAPK) family, c-Jun NH(2)-terminal kinase (JNK) in response to oxidative stress [42]. Moreover, a recent report indicated that overexpression of PKC $\eta$  inhibited JNK activity and its pro-apoptotic function in MCF-7 cells to confer protection against DNA-damage induced apoptosis [43]. Therefore, it is conceivable that the link between the anti-apoptotic function of PKC $\eta$  and Mcl-1 may be via JNK inhibition.

We have shown that Mcl-1 depletion had more of an effect in enhancing TRAIL-induced cell death than PKC $\eta$  (Figure 3). This could be explained in part by the role of Mcl-1 in regulating cell death. Depending on the cellular conditions, Mcl-1 plays two major roles in regulating apoptosis [44]. Under survival conditions, Mcl-1 binds and sequesters pro-apoptotic Bak on the mitochondrial membrane. Upon receiving apoptotic stimuli, Mcl-1 is displaced from Bak by BH3-only proteins leading to Bak oligomerization and release of cytochrome c. Mcl-1 can also heterodimerize with BH3-only proteins such as tBid, PUMA and Bim under survival conditions. During apoptosis, NOXA displaces Mcl-1 which releases BH3-only proteins, allowing them to interact with Bax which inserts into the mitochondrial membrane and causes the release of



cytochrome c. Therefore, Mcl-1 when present in sufficient amounts in the cell, acts as an anti-apoptotic protein by sequestering pro-apoptotic proteins. However, apoptotic stimuli can lead to the rapid downregulation and inactivation of Mcl-1. Thus, in cells that are resistant to apoptosis due to overexpression of Mcl-1, depletion of Mcl-1 can cause a robust apoptotic response in response to apoptotic stimuli.

In addition to inducing apoptosis, TRAIL can also induce survival pathways through the activation of transcription factor, nuclear factor- $\kappa$ B (NF- $\kappa$ B) [45]. The activity of NF- $\kappa$ B is sequestered by binding to the inhibitor of  $\kappa$ B (I $\kappa$ B) [46]. Upon phosphorylation of I $\kappa$ B by I $\kappa$ B kinase  $\beta$  (IKK $\beta$ ), NF- $\kappa$ B is released, translocates to the nucleus and induced transcription of survival proteins [46]. Therefore, small molecule inhibitors of IKK $\beta$  can have toxic properties [47, 48]. It was reported in B-cell lymphoma cells resistance to IKK $\beta$  inhibitors was due to a compensatory effect of I $\kappa$ B kinase  $\alpha$  which phosphorylated I $\kappa$ B in the absence of IKK $\beta$  [49]. Depletion of IKK $\alpha$  in combination with IKK $\beta$  inhibitors successfully sensitized resistant B-cell lymphoma cells to cell death [49]. Therefore, cancer cells may engage in several compensatory signaling pathways to promote survival or sustain proliferation. We have shown that depletion of PKC $\eta$  caused only a modest sensitization to TRAIL-induced cell death, which may be due to compensatory effects from other anti-apoptotic proteins.

Using the MCF-10A series representing a breast tumor progression model, we have observed that PKC $\eta$  protein levels increase in the metastatic cell lines versus the normal cell line (Figure 4). It is possible that these cells utilize PKC $\eta$  to advance to the metastatic state and further

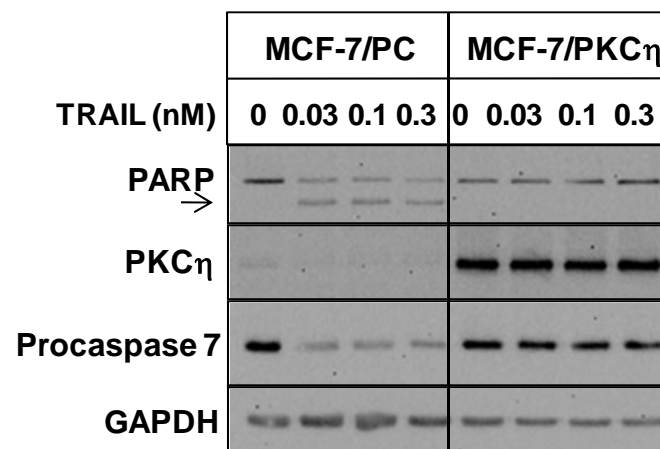
studies should elucidate the mechanism by which PKC $\eta$  can promote tumorigenesis in these cells. The expression and activation of PKC $\epsilon$  has been reported to be decreased in malignant breast [50] and pancreatic [51] compared to the adjacent normal tissue. It is possible that PKC $\eta$  and PKC $\epsilon$  can play differential roles in normal versus breast cancer cells where PKC $\epsilon$  has a predominant role in the normal cells and PKC $\eta$  a predominant role in metastatic cells.

PKC $\eta$  and Mcl-1 have been implicated as anti-apoptotic proteins whose overexpressions confer resistance to TRAIL-induced cell death. The results from this study provide a potential mechanism by which PKC $\eta$  exerts its anti-apoptotic effect by regulating the Bcl-2 family members Bax and Mcl-1. This study provides valuable insight to target PKC $\eta$  via the mitochondrial cell death pathway to sensitize breast cancer cells to TRAIL-induced cell death.

**Figure 1. Effect of PKC $\eta$  overexpression on TRAIL-induced apoptosis**

MCF-7 cells were transfected with pcDNA3 empty vector and PKC $\eta$ -pcDNA3 constructs. G418 resistant pooled cells were treated with the indicated concentrations of TRAIL for 12 h. Western blot analysis was performed with total cellular extracts using the indicated antibodies. GAPDH was used as a loading control. Arrow indicates cleaved PARP band. Results were representative of at least 2 independent experiments.

**Figure 1.**

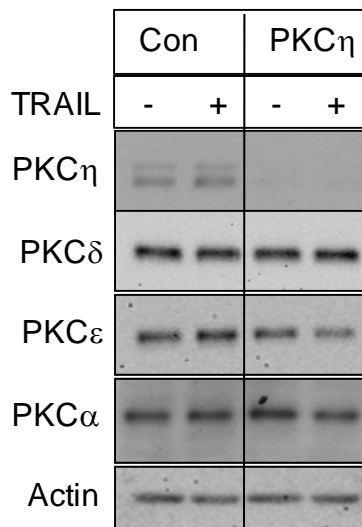


**Figure 2. Effect of PKC $\eta$  depletion on TRAIL-induced cell death.**

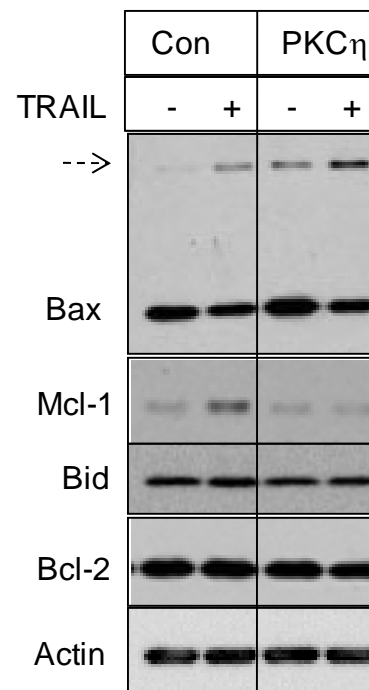
MCF-7 cells were transfected with non-targeting siRNA (Con) or siRNA against PKC $\eta$ . 48 h after transfection, cells were treated with 0.1 nM TRAIL for 12 h. (a) Western blot analysis was performed with total cellular extracts using PKC antibodies. (b) Western blot analysis was performed using Bax, Mcl-1, Bid and Bcl-2, Dotted arrow indicates Bax dimer. Actin was used as a loading control. Results were representative of 2 independent experiments.

**Figure 2.**

**a.**



**b.**

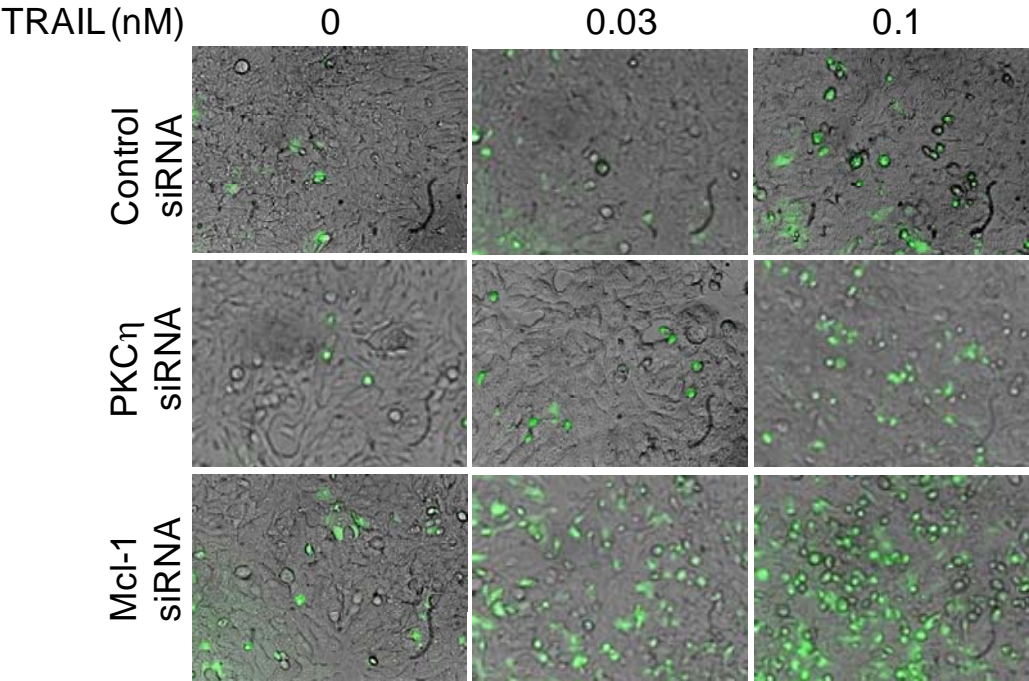


**Figure 3. Effect of PKC $\eta$  or Mcl-1 depletion on TRAIL-induced cell death**

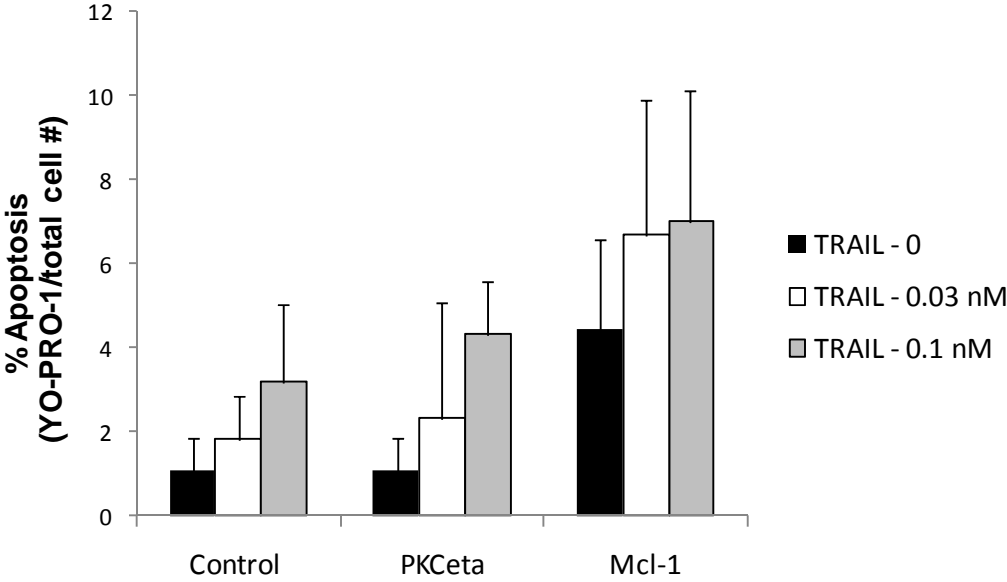
(a) MCF-7 cells were transfected with non-targeting siRNA (Con) or siRNA against PKC $\eta$  or Mcl-1. Two days after transfection, cells were treated with the indicated concentrations of TRAIL for 12 h. Cells were stained with YO-PRO-1 dye for 15 mins and visualized under 20X magnification using the fluorescent Zeiss Axiovert 40 inverted microscope. YO-PRO positive cells were detected with green fluorescence. (b) Densitometric quantification of apoptotic cells as the ratio of YO-PRO<sup>+</sup> cells to total cell number. Results represent at least 2 independent experiments.

Figure 3.

a.



b.

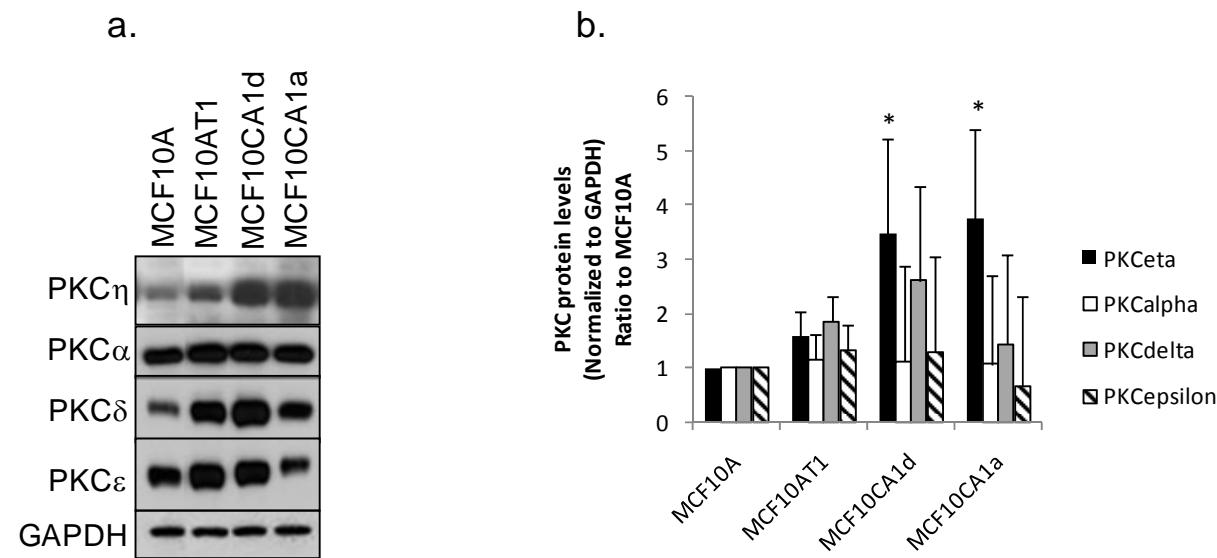




**Figure 4. Comparison of PKC isozyme protein levels in MCF10A series.**

(a) Western blot analysis was performed with total cellular extracts using the indicated antibodies. GAPDH was used as a loading control. (b) Densitometric quantification of PKC $\eta$ ,  $-\alpha$ ,  $-\delta$  and  $-\epsilon$  protein levels from 3 separate experiments corrected for loading and compared as a ratio to MCF10A cells. The asterisk (\*) indicates significant difference from MCF10A ( $P < 0.01$ ) using Student's *t*-test.

Figure 4.



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## CHAPTER V

### CONCLUSIONS

Protein kinase C (PKC) is the receptor for tumor-promoting phorbol esters and plays a major role in regulating signaling events involved in cell proliferation and cell death [1, 2]. Prolonged treatment with phorbol esters leads to activation and downregulation of PKCs [3]. Downregulation of PKC $\delta$  by phorbol esters was associated with tumor promotion [4]. We and others have reported that in contrast to other PKCs, PKC $\eta$  is the only isozyme that is upregulated by prolonged treatment with phorbol esters [5-8] and downregulated by treatment with PKC inhibitors [6] indicating PKC $\eta$  may play a role in tumor-promotion. An understanding of the cellular and molecular mechanisms of proteins involved in cancer progression is critical in developing effective cancer therapies. PKC $\eta$  plays a role in cell proliferation, cell-cycle control and resistance to chemotherapeutic agents in various cancer types [9-12]. The purpose of this dissertation was to investigate the molecular mechanisms of PKC $\eta$  upregulation and downregulation by PKC activators and inhibitors. The results described here demonstrated that (i) phosphorylation of PKC $\eta$  protects it from downregulation (ii) downregulation of PKC $\eta$  is mediated by two distinct mechanisms: proteasome-dependent and proteasome-independent and (iii) PKC $\eta$  downregulation moderately sensitizes breast cancer cells to TRAIL-induced cell death via inhibition of Mcl-1 and increased dimerization of Bax.



Phosphorylation of PKCs can regulate their maturation, stability and function [13-17]. PKCs are generally targeted for downregulation after prolonged treatment with activators and the downregulation was usually associated with dephosphorylation of PKCs [18-22]. The first part of this dissertation investigated if the phosphorylation status of PKC $\eta$  regulates its stability in response to activation by phorbol esters. We found that prolonged treatment with phorbol ester PDBu increased phosphorylation of PKC $\eta$  at conserved serine/threonine sites in the activation loop, turn motif and hydrophobic motif. Furthermore, substitution of a single phosphorylation site from a serine/threonine to alanine which renders PKC $\eta$  “non-phosphorylatable” resulted in destabilization of PKC $\eta$ . Thus, phosphorylation plays an important role in protecting PKC $\eta$  from downregulation. It has been shown that phosphorylation at the turn motif and hydrophobic motif sites stabilize PKC and other AGC kinases in a form that is resistant to degradation by proteases and phosphatases [13, 23]. Our results suggest that phosphorylation of all three sites is important for PKC $\eta$  stability and mutation at just one site can destabilize the protein. It is not clear whether the phosphorylation at one site of PKC $\eta$  can affect the phosphorylation of another site and this phenomenon should be tested in further experiments.

PKC $\eta$  has been shown to be upregulated in various cancers and promotes resistance to chemotherapeutic agents [9, 10, 24-26]. In the second part of the dissertation, we focused on elucidating the downregulation mechanisms of PKC $\eta$ . Our results show that contrary to other PKC isozymes, PKC $\eta$  is downregulated by two inhibitors: the general PKC inhibitor Gö 6983 and PI3K inhibitor Ly294002. Both inhibitors promote dephosphorylation of PKC $\eta$  by a

calyculin A-sensitive phosphatase, most likely protein phosphatase 1 (PP1). The inhibitors are distinct in their ability to degrade PKC $\eta$  through the ubiquitin/proteasome-mediated pathway. Downregulation by Gö 6983 is proteasome-independent, whereas downregulation by Ly294002 is proteasome-dependent. Based on these studies, PKC $\eta$  can be targeted for downregulation by dephosphorylation via inhibition of two separate upstream pathways: PKC and PI3K. PKC $\alpha$  downregulation is also mediated by two distinct mechanisms involving a proteasome-dependent pathway that does not require dephosphorylation and a proteasome-independent pathway requiring dephosphorylation and caveolar trafficking to degradation compartments [27]. Activation of PKC $\alpha$  by two different activators can trigger both downregulation pathways at the same time [27]. In the case of PKC $\eta$ , the two inhibitors have two distinct downregulation mechanisms indicating the inhibitors may affect different kinases or phosphatases to act on distinct sites on PKC $\eta$ . One limitation of using pharmacological inhibitors is the toxic side effects caused by non-specific targeting. Since these the two inhibitors downregulate only PKC $\eta$  and not other PKC isozymes, non-specific effects are reduced.

Downregulation of PKC $\eta$  was associated with sensitization of lung [28] and prostate cancers to chemotherapeutic agents [29]. We have previously shown that overexpression of PKC $\eta$  protected MCF-7 breast cancer cells from TNF-induced apoptosis [24]. The third part of the dissertation investigated the anti-apoptotic role of PKC $\eta$  in the breast adenocarcinoma MCF-7 cells in response to TRAIL-induced cell death. The results demonstrate that overexpression of

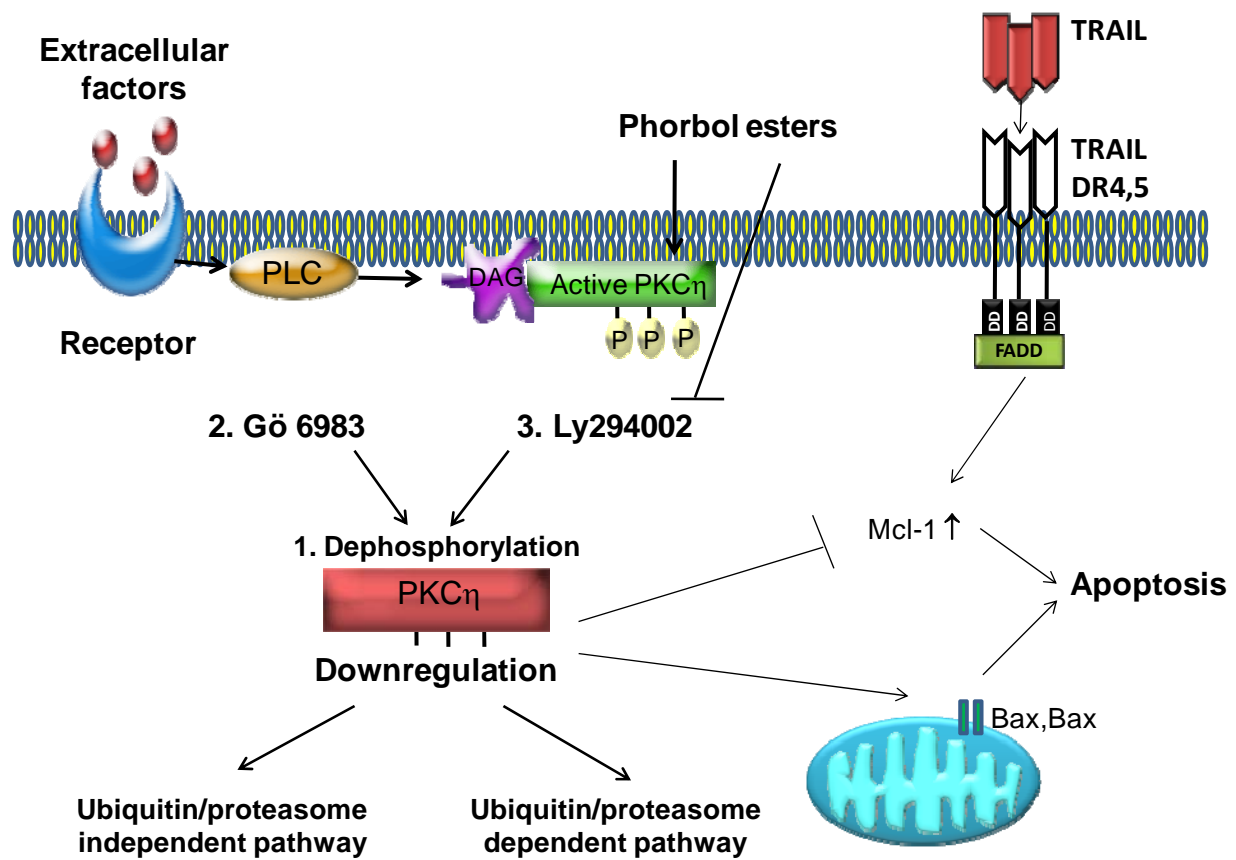
PKC $\eta$  confers resistance to TRAIL-induced cell death in MCF-7 cells. Depletion of PKC $\eta$  increased Bax dimer formation and decreased induction of Mcl-1 to sensitize MCF-7 cells to TRAIL-induced cell death. Therefore, Bax and Mcl-1 could be potential downstream targets of PKC $\eta$  in TRAIL-induced cell death. Since PKC $\eta$  depletion by itself did not enhance cell death in MCF-7 cells, this indicates that in MCF-7 cells, PKC $\eta$  may not directly regulate cell death signaling and other anti-apoptotic proteins may compensate of the loss of PKC $\eta$ . Similarly, although Akt plays a major role in survival, its involvement in cancer metastasis depends on the specific Akt isoform [30]. Thus, it is important to understand the mechanism of regulation for specific isozymes in order to develop more specific and specialized therapies.

In summary, this dissertation demonstrated that PKC $\eta$  can be specifically targeted for downregulation by three pathways: 1) dephosphorylation at conserved sites 2) inhibition by Gö 6983 and 3) inhibition by Ly294002. We have shown that depletion of PKC $\eta$  blocks the induction of Mcl-1 by TRAIL and increases Bax dimer formation indicating Mcl-1 and Bax may be potential targets of PKC $\eta$  (Figure 1). This dissertation provides novel information about PKC $\eta$  regulation by phosphorylation, downregulation and potential downstream targets. The information honed from this study makes PKC $\eta$  an attractive target for cancer therapy in cancers that upregulate PKC $\eta$  to promote cell proliferation and cell survival. We have identified downregulation and upregulation mechanisms that are specific to PKC $\eta$  and not other PKCs which can be pivotal in developing inhibitors of PKC $\eta$  for therapeutic intervention.

## **Figure 1. Conclusion**

We have reported that upon prolonged treatment with phorbol esters such as PDBu, PKC $\eta$  is upregulated and phosphorylated at three conserved sites: activation loop, turn motif and hydrophobic motif. PKC $\eta$  is downregulated by two inhibitors, the PKC inhibitor, Gö 6983 and PI3K inhibitor, Ly294002. Both inhibitors lead to dephosphorylation of PKC $\eta$  by a calyculin A-sensitive phosphatase. Downregulation of PKC $\eta$  by these two inhibitors occurs by two distinct mechanisms: proteasome-dependent and proteasome-independent. Gö 6983-mediated downregulation of PKC $\eta$  occurs via a proteasome-independent pathway, whereas Ly294002-mediated downregulation of PKC $\eta$  occurs by a proteasome-dependent pathway. Ly294002-mediated downregulation of PKC $\eta$  is also inhibited by PDBu treatment. Depletion of PKC $\eta$  by siRNA can block the induction of anti-apoptotic protein Mcl-1 by TRAIL and increase dimer formation of pro-apoptotic Bax which can lead to apoptosis.

Figure 1.



## FUTURE DIRECTIONS

We have demonstrated that phosphorylation of PKC $\eta$  by phorbol esters protects PKC $\eta$  from downregulation. The kinases or phosphatases involved in the regulation of PKC $\eta$  by phosphorylation remain to be identified. Since we have shown that both Gö 6983 and Ly294002 leads to dephosphorylation and downregulation of PKC $\eta$ ; it is likely that autophosphorylation or transphosphorylation events may be involved. Several PKC isozymes including PKC $\eta$  have already been reported to cross-regulate and phosphorylate one another [31-35]. Thus, investigating the transphosphorylation of PKC $\eta$  by other PKCs may be worthwhile approach to identify the kinase involved in PKC $\eta$  phosphorylation in response to phorbol esters. PKC $\iota/\lambda$  has been reported to phosphorylate PKC $\eta$  at the hydrophobic motif site allowing PDK1 to dock and phosphorylate PKC $\eta$  at the activation loop in mouse fibroblasts in response to parvovirus infection [31]. Whether or not PKC $\eta$  can be phosphorylated by PKC $\iota/\lambda$  in response to phorbol esters in human cancers is subject to future investigation. In addition to identifying the kinase involved in phosphorylating PKC $\eta$ , identification of the phosphatase involved in dephosphorylating and downregulating PKC $\eta$  can also have important implications in PKC $\eta$  regulation. In the second chapter, we identified that PP1 may be the potential phosphatase regulating PKC $\eta$  dephosphorylation since it is sensitive to calyculin A inhibition, but not okadaic acid. It would be worthwhile to investigate the role of PP1 in regulating PKC $\eta$  dephosphorylation and downregulation in cancer cells that promote survival by upregulating

PKC $\eta$ . Studies investigating the mechanism of PKC $\epsilon$  dephosphorylation at the hydrophobic Ser729 site reported that dephosphorylation was not mediated by PP1, PP2A or PP2B, but was mediated by mTOR, MAPK and PKC $\delta$  [16, 36, 37]. Therefore the involvement of mTOR, MAPK and other PKCs should also be investigated in the downregulation of PKC $\eta$ . In addition to identifying the kinase or phosphatase involved in regulating PKC $\eta$  phosphorylation, identification of specific PKC $\eta$  phosphorylation sites that are important for its stability could be beneficial for the development of PKC $\eta$ -specific therapeutic agents.

We have identified two potential downstream targets of PKC $\eta$  (Bax and Mcl-1) involved in sensitizing MCF-7 cells to TRAIL-induced apoptosis. Further experiments should confirm if PKC $\eta$  can directly interact with Bax or Mcl-1 by coimmunoprecipitation or fluorescent resonance energy transfer (FRET) microscopy. PKC $\epsilon$  was reported to directly interact with and phosphorylate components of the cardiac mitochondrial pore in mice to inhibit pore opening contributing to its cardioprotective function [38]. PKC $\epsilon$  was also reported to interact with Bax and prevent its dimerization and translocation to the mitochondria to protect MCF-7 cells from TNF-induced apoptosis [39]. Since PKC $\eta$  shares the most structural similarity to PKC $\epsilon$  [40], further studies should identify the subcellular localization of PKC $\eta$  in response to TRAIL-induced cell death to determine if PKC $\eta$  can translocate to the mitochondria to exert its anti-apoptotic effect.

Since depletion of PKC $\eta$  had a modest effect on cell death by apoptosis, further studies should determine if PKC $\eta$  may play a role in other cell death pathways such as autophagy. PKC $\eta$  was shown to mediate cell proliferation in glioblastoma cells by regulating the Akt and mTOR signaling pathways [41]. Both Akt and mTOR pathways have been reported to play a key role in regulating autophagy [42]; therefore it is conceivable that PKC $\eta$  may mediate autophagy or cell proliferation in breast cancer cells via Akt or mTOR. We have shown in Chapter II that PKC $\eta$  can be downregulated by the inhibitor of PI3K/Akt, Ly294002 in MCF-7 cells suggesting PKC $\eta$  can act via the PI3K pathway. Given the role of PKC $\eta$  in glioblastoma proliferation [5] and cell cycle control in MCF-7 cells and NIH-3T3 cells [43], depletion of PKC $\eta$  could result in an anti-proliferative effect in MCF-7 breast cancer cells. Further studies should elucidate if PKC $\eta$  depletion decreases cell proliferation in response to TRAIL in MCF-7 cells. Since MCF-7 cells contain a moderate level of PKC $\eta$  protein, it may be worthwhile to test the effect of PKC $\eta$  depletion in other cell lines expressing higher levels of PKC $\eta$  such as MCF10CA1a or MCF10CA1d to determine its effect on cell death.

The mechanism of PKC $\eta$  downregulation in response to inhibitors and increased phosphorylation in response to inhibitors has been limited to breast cancer cells and HEK 293 cells in this study. Future studies should investigate if the regulation of PKC $\eta$  described in this dissertation can be applied to other cancer cell types such as lung[28], prostate [29], renal [25] and Hodgkins lymphomas [9] where PKC $\eta$  plays a role in resistance or tumor progression.



The findings of this dissertation provide valuable insight on the mechanism of PKC $\eta$  downregulation and its anti-apoptotic function in breast cancer. This information can lead to potential therapeutic agents targeting PKC $\eta$  downregulation to overcome resistance to TRAIL in breast cancer cells.

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