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Protein kinase C-eta (PKCn) is a novel member of the PKC family that is important for several cellular processes. PKCn is overexpressed in breast cancer and has been associated with chemotherapeutic resistance. PKC<sub>η</sub> is the only phorbol ester-sensitive PKC isozyme that resists downregulation upon prolonged treatment with tumorpromoting phorbol esters suggesting its unique regulation. The purpose of this dissertation is to elucidate the mechanism of PKCn regulation and its functional relevance in breast cancer. We have shown that PKC<sub>1</sub> is upregulated by several structurally and functionally distinct PKC activators in contrast to other PKC isozymes. Activator-induced upregulation of PKC<sub>n</sub> was associated with its phosphorylation. Our results indicate that novel PKCs are involved in the upregulation of PKCn by PKC activators. We also made a novel observation that PKC $\eta$  is downregulated via two distinct mechanisms. While inhibition of PKC caused the downregulation of PKC<sub>1</sub> via proteasome-independent pathway, inhibition of PDK1 led to PKCn downregulation via proteasome-dependent pathway. We further demonstrated that PKC<sub>η</sub> is important for the growth and survival of breast cancer cells. The unique regulation of PKC<sub>1</sub> and its implications on breast cancer growth and survival suggests that this pathway could be selectively exploited for targeted therapies for breast cancer.

# PROTEIN KINASE C-ETA SIGNALING IN BREAST CANCER

DISSERTATION

Presented to the Graduate Council of the Graduate School of Biomedical Sciences University of North Texas Health Science Center at Fort Worth

In Partial Fulfillment of the Requirements

For the Degree of

# DOCTOR OF PHILOSOPHY

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Deepanwita Pal, M.S. Fort Worth, Texas November, 2013

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# LIST OF ABBREVIATIONS

aPKC	Atypical protein kinase C
ATP	Adenosine triphosphate
Bax	Bcl-2 associated X protein
Bcl-2	B-cell lymphoma 2
Bid	BH3-interacting domain death agonist
BIM	Bisindolylmaleimide
Cdk	Cyclin-dependent kinase
сРКС	Conventional protein kinase C
DAG	Diacylglycerol
DGK	Diacylglycerol kinase
ER	Endoplasmic reticulum
ER	Estrogen receptor
ERK	Extracellular signal-regulated kinase
GFP	Green fluorescent protein
HEK	Human embryonic kidney

Hsp	Heat shock protein
IFN	Interferon
ILV	Indolactam V
IP3	Inositol triphosphate
JNK	c-Jun N-terminal kinase
МАРК	Mitogen activated protein kinase
Mcl-1	Myeloid cell leukemia sequence 1
MDR1	Multidrug resistance protein 1
mTOR	Mammalian target of Rapamycin
MTT	3-[4,5-dimethylthiazol-2-yl]-2,5-diphenyltetrazolium bromide
NF-κB	Nuclear factor kappa B
nPKC	Novel protein kinase C
PB1	Phox and Bem 1
PDBu	Phorbol 12, 13-dibutyrate
PDK1	Phosphoinositide-dependent kinase 1
PDZ	Post synaptic density protein (PSD95), Drosophila disc large tumor
	suppressor (Dlg1) and Zonula occudens-1 protein (zo-1)
PHLPP	PH domain and leucine rich repeat protein phosphatase

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РІЗК	Phosphatiylinositol 3-kinase
Pin1	Peptidyl prolyl isomerase
РКА	Protein kinase A
РКС	Protein kinase C
PLC	Phospholipase C
РМА	Phorbol 12-myristate 13-acetate
Pro	Proline
RACK	Receptors for activated C kinase
Rb	Retinoblastoma
Ser	Serine
siRNA	Short interfering RNA
Thr	Threonine
TLR2	Toll-like receptor 2
TNF	Tumor necrosis factor
TPA	12-O-tetradecanoylphorbol 13-acetate.
uORF	Upstream open reading frame
UTR	Untranslated region

VEGF	Vascular endothelial growth factor
XIAP	X-linked inhibitor of apoptosis

# **CHAPTER I**

## **INTRODUCTION**

#### **Breast Cancer**

Breast cancer is the second leading cause of death in American women (1). In the United States, about 1 in 8 women develop invasive breast cancer during the course of their lifetime claiming around 40,000 lives each year (1). While surgery, radiation, hormonal treatment, chemo- and targeted therapies are the conventional modes of treatment, they are associated with several problems like toxicity, lack of specificity and acquisition of resistance (2). Thus, understanding the regulation of signaling molecules that promote cancer and chemotherapeutic resistance will facilitate the development of effective therapeutics.

# Protein Kinase C (PKC)

Protein kinase C was originally identified by Nishizuka and colleagues as a cyclic nucleotideindependent, Ca<sup>2+</sup>- and lipid-dependent kinase from bovine and rat cerebellum (3, 4). Results from southern hybridization experiments later revealed a multi-gene family of related isoforms (5). The PKC family has since been established as a family of serine/threonine kinases that play diverse roles in fundamental cellular processes including cell proliferation, cell death and differentiation (6, 7). PKCs respond to extracellular signals that promote phospholipid hydrolysis and facilitate the generation of diacylglycerol (DAG) and release of Ca<sup>2+</sup> from intracellular stores. Ca<sup>2+</sup> and DAG act as cofactors for PKCs and subsequently initiate membrane translocation and activation of PKC (7). Based on the structural features and cofactor requirements, the PKC family consists of 10 isozymes categorized as the conventional or the classical (c) PKCs ( $\alpha$ ,  $\beta$ I,  $\beta$ II,  $\gamma$ ), the novel (n) PKCs ( $\delta$ ,  $\varepsilon$ ,  $\eta$ ,  $\theta$ ) and the atypical (a) PKCs ( $\zeta$ ,  $\lambda/\iota$ ) (6).

# PKC isoform structure

Protein kinase C is a member of a larger superfamily of protein kinases, the AGC family that shares basic structural features (8). All PKC isozymes contain a common structural backbone comprised of a highly conserved catalytic domain at the C-terminal and a regulatory domain at the N-terminal (Figure 1). The catalytic domain consists of motifs that are required for ATP/substrate binding and catalysis. PKCs possess 4 conserved modules (C1–4): C1 and C2 are the membrane targeting modules that along with the pseudosubstrate region form the regulatory domain; C3 and C4 comprise the catalytic domain (9). A proteolytically labile hinge region connects the regulatory domain to the catalytic domain (3).

The N-terminal contains the autoinhibitory pseudosubstrate sequence that contains an alanine in place of the serine/threonine phosphoacceptor site, but otherwise resembles a PKC substrate. The pseudosubstrate thus holds the enzyme in an inactive conformation by occupying the catalytic site (10). The membrane targeting modules regulate the spatial distribution of the PKC isozymes. The C1 domain is a globular structure that contains cysteine-rich motifs. The conventional and the novel PKCs have a tandem C1 domain (C1A and C1B) (11). The physiological stimulator

diacylglycerol and the pharmacological activators, such as tumor-promoting phorbol esters bind to the C1 domain. In addition, C1 domain confers selectivity for phosphatidylserine that acts as the activator for PKCs (12). Atypical PKCs have only one cysteine-rich motif in their C1 domain which renders them incapable of binding to DAG or phorbol esters (11). C2 domain can also serve as the recognition site for anionic lipids such as phosphatidylserine and in some enzymes, the calcium binding site. The C2 domain of novel PKCs lacks the key aspartic residues to bind calcium. Consequently, cPKCs are Ca<sup>2+</sup>- and DAG/phorbol ester-sensitive, nPKCs are Ca<sup>2+</sup>insensitive, but they are activated by DAG/phorbol esters and aPKCs are insensitive to both Ca<sup>2+</sup> and DAG/phorbol esters. Their function is driven by protein–protein interactions mediated via the N-terminal Phox and Bem 1 (PB1) domain and the carboxyl-terminal PDZ ligand motif (9). The distinct structural and biochemical features of the PKC isozymes pave the way for the differential cellular responses attributed to the PKC family.

# Modes of regulation

The PKC isozymes are under tight structural and spatial regulation that underlies their biochemical functions, intracellular localization and tissue distribution (9). PKCs can be regulated by phosphorylation, cofactor binding and membrane targeting through interaction with scaffold proteins (13).

# Regulation by phosphorylation

PKCs have to be first processed by a series of ordered phosphorylation events before it can become catalytically competent (13). PKCs have three conserved phosphorylation sites: *activation loop* (which is located in a cleft in the kinase domain at the entrance of the catalytic site), *turn motif* (which is at a turn in the structure) and the *hydrophobic motif* (which is

surrounded by hydrophobic residues). It is generally believed that first of the phosphorylation events occurs at the activation loop site followed by subsequent phosphorylations at the turn motif and the hydrophobic motif on the C-terminal (14). The priming phosphorylation is mediated by phosphoinositide-dependent kinase 1 (PDK1) (15, 16). When PKC is newly synthesized, it remains associated with the membrane in an open conformation that allows PDK1 access to the activation loop site and the substrate binding pocket. Phosphorylation of PKC at the activation loop by PDK1 triggers additional phosphorylations at the C-terminus (14). There are, however, controversies regarding the phosphorylation of novel PKCs at the activation loop (17-19). For example, PKC $\varepsilon$  rather than PDK1 has been reported to phosphorylate PKC $\delta$  and PKC $\varepsilon$ at the activation loop (18, 19). Although activation loop phosphorylation is considered an early event in the priming of PKCs, recent studies have identified an earlier step in PKC maturation which involves chaperone proteins (20). Heat shock protein-90 (Hsp90) and co-chaperone Cdc37 bind to a molecular clamp in the kinase domain of PKC, an event that is essential for the subsequent priming phosphorylations (20). Activation loop phosphorylation serves two purposes- it allows for the proper positioning of the residues for catalysis and it unmasks the substrate binding site (21). Although activation loop phosphorylation is crucial for the maturation of PKC, once PKC is phosphorylated at the C-terminal sites, phosphorylation at the activation loop is dispensable (22). Unlike the activation loop phosphorylation, phosphorylation at the turn motif is absolutely essential for the function of PKC. Negative charge at the turn motif is pre-requisite and sufficient for the function of the mature PKC (22). It is generally accepted that this site is modified by autophosphorylation (23). It also serves as the docking site for protein-protein interactions with other effectors such as 14-3-3 class of proteins (24). The phosphorylation at the turn motif is followed by phosphorylation at the hydrophobic motif. The

mTORC2 complex has been implicated in the regulation of the hydrophobic motif (25, 26). The hydrophobic site phosphorylation determines subcellular localization and stability but is not necessary for its catalytic function (22, 27, 28). This series of phosphorylation events lead to a conformation of PKC that is primed for activation by cofactors (14).

#### Regulation of PKC by cofactors and membrane targeting

Once PKC is phosphorylated, it localizes to the cytosol in an inactive form with the pseudosubstrate bound to the catalytic site (13). Engagement of growth factor or cytokine to their receptors activates phospholipase C that cleaves phosphatidylinositol 4, 5-bisphosphate to generate the second messengers: DAG and inositol trisphosphate (IP3). IP3 facilitates the release of calcium from intracellular stores. The production of DAG recruits PKCs to the plasma membrane through the action of receptors for activated C kinases (RACKs), where they become activated by acidic phospholipids, such as phosphatidylserine (29). RACKs bind to the PKC isozymes and serve as anchoring proteins thus facilitating proper spatial localization of PKCs (30). Binding of DAG and Ca<sup>2+</sup> to the C1 and C2 domains respectively, changes the conformation of PKC releasing the pseudosubstrate from the substrate binding pocket and allows for the downstream signaling of PKCs (12, 31) (Figure 2).

# Pharmacological modulators of PKC

PKCs are the receptors for tumor-promoting phorbol esters which are potent activators of PKCs and mimic the action of DAG (32, 33). While membrane recruitment and activation of PKCs by DAG is transient, phorbol esters induce sustained activation of PKCs. However, chronic activation of PKCs by phorbol esters ultimately leads to desensitization and downregulation of the PKCs (13). Diterpene esters like mezerein have also been shown to activate PKC by

mimicking the action of DAG (34). PKCs can also be activated by synthetic analogs (indolactams) related to the tumor promoter teleocidin (35, 36). Besides tumor-promoting phorbol esters, other non-tumor-promoting agents can also activate PKCs like bryostatins, ingenol mebutate and the relatively newer class of synthetic analogs of DAG known as DAG-lactones (37-39). Bryostatins, belonging to the family of macrocyclic lactones however, act as partial agonists of PKCs and can counteract the action of phorbol esters and have been widely investigated in clinical trials for cancer therapy (40, 41).

The function of PKCs can also be modulated by PKC inhibitors that can be either categorized as ATP-competitive inhibitors or regulatory site inhibitors. Bisindolylmaleimide and its analogs and staurosporine derivatives such as Gö 6983 compete for the ATP-binding site and serve as potent inhibitors of PKC activity (42-45). Calphostin C acts as regulatory site inhibitor by interaction with the DAG/phorbol ester binding domains (46). Peptide inhibitors or antisense oligonucleotides such as aprinocarsen can also inhibit PKC function by interfering in the interaction of PKCs with anchoring proteins (40, 47). Recent studies have also described bisubstrate-based inhibitors, which are capable of binding both the ATP binding site as well as the substrate binding groove by use of a pseudosubstrate analog ensuring better selectivity (48, 49).

## Signal termination and downregulation of PKC isozymes

Termination of PKC signaling can occur via different mechanisms such as release of PKC isozymes from the membrane, metabolism of DAG by DAG kinases (DGKs) (50, 51), agonist-induced degradation or the removal of priming phosphorylation which leads to downregulation and rapid degradation (29, 50, 52). Desensitization of G-protein coupled receptors by

autophosphorylation facilitates reverse translocation and leads to the release of PKCs from the membrane and subsequent downregulation (51). Since co-factors such as DAG are important for PKC regulation, the removal of these second messengers leads to inactivation of PKC signaling. DGKs phosphorylate DAG to generate phosphatidic acid, thereby effectively depleting the levels of DAG in the cell, thus inducing downregulation of PKC (51). While the interaction of PKC with DAG is transient (53), high-affinity binding of phorbol esters leads to sustained activation of PKC (54). This renders PKC in an open conformation and predisposes them to the action of proteases (55). In the open conformation, the sensitivity of PKC to dephosphorylation is also increased (13). Dephosphorylation of PKCs is believed to precede their downregulation (56) although it was reported that phosphorylation of PKCS is required for activation-induced downregulation (57). In addition, fully phosphorylated PKCa was shown to undergo downregulation (52). PKCs are also susceptible to phosphatases such as PHLPP which can target PKCs for ubiquitin-mediated degradation (58). However, dephosphorylated PKCs can be rescued by the action of heat-shock proteins such as Hsp70 (59). PKCs can be stabilized by the binding of Hsp70 to the dephosphorylated turn motif which allows rephosphorylation of PKC, thereby prolonging its lifetime (59). Recently, the peptidyl-prolyl isomerase (Pin1) was implicated in the downregulation of conventional protein kinase C isozymes (60). Binding of Pin1 to the conventional PKCBII led to conformational changes in the Thr-Pro peptidyl bond in the Cterminal tail facilitating downregulation. In novel PKCs, the absence of the Pro residue in the turn motif prevents this conformation-dependent degradation switch. However, PKCn is the only novel isozyme which has the Thr-Pro peptidyl bond in its turn motif (60).

Several mechanisms of degradation have been proposed for the PKC isozymes. Conventional PKCs are believed to be downregulated by calcium-activated proteases, such as calpains (61, 62)

whereas PKC $\alpha$ , - $\delta$  and - $\epsilon$  were shown to be degraded via proteasome-mediated pathway (63-65). PKCs are also subject to caspase-mediated cleavage and can be subsequently degraded by other proteases (66-68). Studies have reported that PKCs are trafficked to the endosomal compartments upon activation with phorbol esters (56, 69, 70) and subsequently accumulate in the perinuclear region by a caveolae-dependent process where it is dephosphorylated and degraded (56, 70).

#### Role of PKC isozymes in breast cancer

Since their discovery as receptors for tumor promoters, PKC isozymes have been attractive targets for cancer therapy (33, 40). Individual PKC isozymes exhibit distinct biochemical properties, tissue distribution and subcellular localization which lead to divergent responses in distinct cancers and sometimes even within the same cancer type (71, 72). While PKC $\alpha$  was shown to be overexpressed in human breast tumor samples (73), downregulation of PKC $\alpha$  in breast cancer has also been reported (74). However, several lines of evidence have implicated PKCa in promoting migration and epithelial-mesenchymal transition of breast cancer cells thereby implicating PKC $\alpha$  in invasion and metastasis of breast cancer cells (75, 76). Numerous reports have established PKC $\beta$  as a potential therapeutic target in breast cancer (77). While both PKCBI and PKCBII are important for cell cycle progression and cell proliferation (78), PKCBII has been reported to be a key mediator of vascular endothelial growth factor (VEGF)-induced proliferation thereby suggesting a role in angiogenesis (79, 80). Similar to PKC $\alpha$ , PKC $\delta$  also has conflicting roles in breast cancer; it can facilitate both tumorigenesis and tumor suppression (81, 82). It is well documented that PKCδ mediates survival of breast cancer cells (83) through the NF- $\kappa$ B and the MEK pathways (84, 85) and promotes metastasis (86). In contrast, PKC $\delta$ promotes an anti-proliferative response via suppression of Akt and the ERK pathways as well as

by regulating hypophosphorylation of Rb (87). While the proteolytic cleavage of PKC $\delta$  is generally believed to be important for apoptosis, depending on the apoptotic stimulus, the catalytic fragment can elicit both pro- and anti-apoptotic functions (88-90). On the other hand, PKC $\epsilon$  promotes oncogenic signaling in several cancers including breast cancer (91). Overexpression of PKC $\epsilon$  correlates with high tumor-grade, ER negative status and poor survival in breast cancer patients, thus serving as a predictive biomarker for breast cancer aggressiveness (92). Similarly, PKC $\iota$  is believed to be an oncogenic kinase with crucial roles in transformation and tumorigenicity (93, 94). Immunohistochemical analysis has revealed increased expression of PKC $\zeta$  has been reported in breast carcinomas (96). In mouse mammary cells, PKC $\zeta$  was shown to activate the mitogen-activated protein kinase (MAPK)/extracellular signal-regulated kinase (ERK) pathway, leading to cell proliferation and migration (97). Studies have also implicated PKC $\zeta$  in breast cancer cell chemotaxis and cell motility (98, 99). Thus, the PKC isozymes exhibit pleiotropic functions in cancer.

# Regulation of Bcl-2 family members by PKC isozymes

The PKC isozymes are known to exert their effects in cancer signaling via several mechanisms including the regulation of the Bcl-2 family members which are central regulators of cell survival and apoptosis and are frequently deregulated in cancer (7, 81, 100). It is well documented that PKC $\alpha$  can promote cell survival by the suppression of apoptosis (75). Overexpression of PKC $\alpha$  has been shown to inhibit apoptosis via the phosphorylation of Bcl-2 at Ser-70 which leads to stabilization of Bcl-2 (101). In SKBR3 breast cancer cells, inhibition of PKC $\alpha$  augmented apoptosis by downregulation of Bcl-2 (102). On the other hand, PKC $\delta$  acts downstream of Syk kinase and stabilizes anti-apoptotic Mcl-1 through inhibition of GSK3 $\beta$  thereby inhibiting

apoptosis (103). PKC $\delta$  can also exert its anti-apoptotic effect by promoting the proteasomal degradation of pro-apoptotic Bim (104). In contrast, the catalytic fragment of PKCδ was shown to phosphorylate Mcl-1 and target it for degradation, thus facilitating cell death (88). PKCδ can also inhibit cell survival through the activation of Bax and Bak proteins through interaction with the p38/MAPK pathway (105). PKC $\varepsilon$  is believed to protect against apoptosis and has been implicated in chemotherapeutic resistance in tumor cells (106). In lung cancer, PKC $\varepsilon$  was shown to upregulate the pro-survival factors X-linked inhibitor of apoptosis (XIAP) and Bcl-xL (107). We have previously reported that PKCE overexpression in breast cancer cells increased the Bcl-2 expression at the mRNA and protein levels with concomitant decrease in the levels of proapoptotic Bid (106). Recent evidence has also showed that downregulation of PKCE by miR-31 sensitized breast cancer cells to apoptosis which was accompanied by decrease in NF-kB activity and Bcl-2 expression (108). Sequestration of PKC1 and PKC2 by the pro-apoptotic Par-4 protein has been demonstrated to induce apoptosis (109). PKC has been shown to phosphorylate and inhibit the pro-apoptotic Bax in lung cancer (110) while PKC<sub>1</sub> promotes cell survival through inhibition of Bad in glioblastoma (111). Although limited evidence is available for the role of PKCθ in the regulation of the Bcl-2 family, PKCθ-deficient mice displayed reduced expression of Bcl-2 and Bcl-xL (112).

## Protein kinase C-eta

Protein kinase C-eta (PKC $\eta$ ) is a novel member of the PKC family. It is classified as a calciumindependent but DAG/phorbol ester-dependent PKC (113). It was first isolated from a cDNA library of mouse epidermis (113). PKC $\eta$  is assigned to human chromosome 14 (14q22-23) and mouse chromosome 12 (12C3-D2) (114, 115) and contains an open reading frame encoding 683 amino acid residues (116). Contrary to other PKCs which are primarily enriched in the brain tissue, PKCη is mainly expressed in lung, skin and heart tissues (117). PKCη participates in diverse cellular processes including proliferation, differentiation, secretion and apoptosis (118-124). Recent reports have revealed the role of PKCη in immune function (125, 126). PKCη was shown to be important for T-cell proliferation and homeostasis (127). PKCη was also implicated in the regulation of toll-like receptor-2 (TLR-2) responses in macrophages (128).

# Structure, regulation and localization of PKCn

The structure of PKC<sub>n</sub> comprises of the catalytic domain and the regulatory domain similar to other PKCs (9). A characteristic cysteine-rich region is present in the C1 domain of PKCn along with a protein kinase domain, both of which are conserved features in the PKC family (129). PKC<sub>1</sub> shares greatest homology with PKC<sub>2</sub>, another member of the novel PKC family (117). Similar to other PKC isozymes, PKCn has three conserved phosphorylation sites- activation loop (Thr-513), turn motif (Thr-655) and hydrophobic domain (Ser-674) (9). Although the order of priming phosphorylations of PKCn is not well established, PDK1 is believed to phosphorylate PKC<sub>1</sub> at the activation loop in vitro (130). In mouse A9 fibroblasts infected with parovirus, Lachmann et.al demonstrated that PKC<sup>\lambda</sup> phosphorylates PKC<sup>\lambda</sup> at the hydrophobic site thus allowing PDK1 access to the activation loop (131). The C2 domain structure of PKCn was found to be similar to PKCE with significant differences at the putative lipid binding site. Mass spectrometric analysis of the C2 domain of PKCn revealed two autophosphorylation sites at Ser-28 and Ser-32 (132). The autophosphorylation site at Ser-28 but not Ser-32 is conserved in PKCE (132). It has been speculated that autophosphorylation at these sites could affect the lipid-binding of PKC<sub>1</sub> (132).

Anionic phospholipids like phosphatidylserine and DAG/phorbol esters regulate PKC $\eta$  (113, 117). However, contrary to other phorbol-ester sensitive PKC isozymes, PKC $\eta$  resists downregulation by prolonged treatment with phorbol esters (119, 133, 134). PKC $\eta$  is specifically activated by cholesterol sulfate and sulfatide (135). It was reported that cholesterol sulfate-mediated activation of PKC $\eta$  involved casein kinase I (136). In addition, PKC $\eta$  was shown to be activated by treatment with type I interferons (IFNs) like IFN $\alpha$  or IFN $\beta$  in chronic myeloid leukemia cells (137). Interestingly, other novel PKC isozymes like PKC $\delta$ , - $\varepsilon$  and - $\theta$  are also activated by Type I and Type II IFNs and participate in Type I and/or Type II IFN-induced responses (138-141). PKC $\eta$  is also elevated in response to estradiol treatment in estrogensensitive breast cancer cells in a time- and concentration-dependent manner (142). Differential expression analysis in the neoplastic cell line 8701-BC demonstrated that PKC $\eta$  downregulation can be induced by type V collagen (143).

Furthermore, PKC $\eta$  is subject to translational regulation under both normal and stressed conditions caused by amino acid starvation (144). Raveh-Amit and colleagues reported that the 5'-UTR of PKC $\eta$  is unusually long (659 nucleotides) and rich in GC content and identified two upstream open reading frames (uORF) in the 5'-UTR which function as repressive elements under normal growth conditions. However, under amino acid starvation, the repression is removed by leaky scanning leading to the translational upregulation of PKC $\eta$  (144). PKC $\epsilon$  is the only other PKC isozyme for which the presence of a regulatory uORF has been reported (145).

PKC $\eta$  is localized in the Golgi, endoplasmic reticulum (ER) and the nuclear envelope (146). Although the C1A domain of PKC $\eta$  lacks a Golgi localization signal similar to the other members of the novel PKC family, the C1B domain of PKC $\eta$  facilitates its translocation to the Golgi complex (146). In response to serum starvation and PMA, PKC $\eta$  translocates to the nuclear envelope. While C1B domain is sufficient to drive Golgi translocation of PKC $\eta$ , both the C1 and the pseudosubstrate region are required for the localization at the nuclear envelope and ER (146). Furthermore, a recent study reported that in hepatocellular carcinoma cells, PKC $\eta$  is targeted to lipid droplets where it limited the formation of larger lipid droplets (147).

### Role of PKC<sub>η</sub> in breast cancer

The role of PKC $\eta$  in cancer is controversial owing to its diverse responses in different cancers. Although, PKC $\eta$ -deficient mice were more susceptible to tumor promotion in two-stage skin carcinogenesis model (148), PKC $\eta$  mediates chemotherapeutic resistance in breast cancer (118, 149), glioblastoma (150), lung cancer (151) and several other cancers (152, 153). It has been reported that PKC $\eta$  is downregulated in hepatocellular carcinoma (154), however, it is associated with the progression of renal cell carcinoma (155). Thus, PKC $\eta$  may promote or inhibit malignant growth depending on the cellular context.

PKC $\eta$  is a regulator of mammary gland development (156). It is upregulated in the rat mammary gland during the transition from the resting to the pregnant state (156). Furthermore, a marked decrease in PKC $\eta$  levels was observed during gland regression which is typically characterized by the onset of apoptotic processes leading to involution (156). Qualitative and quantitative alterations in PKC $\eta$  have been reported in human breast cancer tissues (157). PKC $\eta$  expression was increased in locally invasive breast tumor tissues and high levels of PKC $\eta$  were detected in invasive tumors associated with significant lymph node metastases which suggests a role of PKC $\eta$  in cancer progression (157). This is consistent with a report which demonstrated the importance of PKC $\eta$  in maintaining tight junction integrity via interaction and subsequent phosphorylation of occludin on its C-terminal domain (158). Since key changes in the barrier

function of tight junctions have been shown to be critical in cancer progression (159), it is likely that PKCn may have potential roles in survival and progression of cancer cells.

PKCn mRNA is elevated in multidrug-resistant breast tumors (160). Overexpression of PKCn has been shown to protect against apoptosis (118, 119, 123). We have previously reported that overexpression of PKCn attenuated caspase activation and TNF-induced cell death in breast cancer cells (118). PKCn also protects against camptothecin-induced DNA damage by activating NF-kB and promoting nuclear localization of RelA/p65 in breast cancer (123). Upon etoposideinduced stress, PKCn is tethered to the nuclear membrane and confers protection against cell death (161). Moreover, PKCn was effective in blocking apoptosis via the suppression of c-Jun N-terminal kinase (JNK) activity upon UV irradiation (149). PKCn is also critical for cell cycle control. Although PKCn induced growth arrest in NIH3T3 fibroblasts and keratinocytes (162, 163), it enhanced cell cycle progression in breast cancer cells (120). Induced expression of PKCn led to an increase in the levels of cyclin E and cyclin D (120). While the levels of the cell cycle inhibitor p27 (kip1) were unaltered by PKCn overexpression, it however, facilitated the removal of the cell cycle inhibitor p27 (kip1) from the cyclin E/cdk2 complex thereby activating the cyclin E/cdk2 complex (120). While these studies implicate PKCn in breast cancer, the mechanism by which PKCn contributes to breast cancer development is largely unknown.

# **Objectives of the present study**

Deregulation of cellular processes is the hallmark of cancer. The signaling pathways that are altered in cancer can greatly influence clinical outcome. The protein kinase C (PKC) family is critical for the regulation of cellular processes like cell proliferation, cell survival and tumor promotion (6, 7). Thus, they serve as potent targets for cancer therapy. Protein kinase C (PKC) serves as the receptor for tumor promoting phorbol esters, which are activators of conventional and novel PKCs and can substitute for the physiological activator DAG (33). However, persistent treatment with phorbol esters leads to downregulation of these PKCs (13). PKC $\eta$ , a novel PKC isozyme, resists downregulation by tumor-promoting phorbol esters, suggesting that the regulation of PKC $\eta$  is unique (119, 133, 134). PKC $\eta$  levels were found to be altered in human breast tumors and correlated with positive lymph node metastases in invasive tumors (157). Moreover, significant positive correlations were established between PKC $\eta$  expression and MDR1 (multidrug resistance-associated protein 1) genes in breast cancer (160). However, little is known about how PKC $\eta$  level is regulated. The objective of this study is to examine the regulation of PKC $\eta$  and to elucidate its role in breast cancer.

# Hypothesis and specific aims

Our preliminary studies demonstrate that PKC $\eta$  is the only isozyme that resists downregulation in response to persistent treatment with tumor-promoting phorbol esters in contrast to the other PKCs which are either downregulated or remain unaltered. The unique upregulation of PKC $\eta$  in response to tumor-promoters suggests its role in tumor development. Furthermore, we have observed that the protein levels of PKC $\eta$  increased with the aggressiveness of breast cancer in the progressive MCF-10A series, suggesting that PKC $\eta$  may contribute to the survival of breast cancer cells leading to breast cancer progression. Overexpression of PKCη has been observed in human breast tumors and it contributes to chemoresistance in several cancers including breast cancer (118, 119, 123). Hence, we hypothesize that *the upregulation of PKCη contributes to breast cancer cell survival*. We will pursue the following specific aims in order to test our hypothesis.

Aim 1. To determine the mechanism of upregulation of PKC<sub>η</sub> in breast cancer

Aim 2. To elucidate how inhibition of PKC<sub>1</sub> phosphorylation leads to its downregulation

Aim 3. To determine the consequence of PKC<sub>η</sub> downregulation on breast cancer cell survival

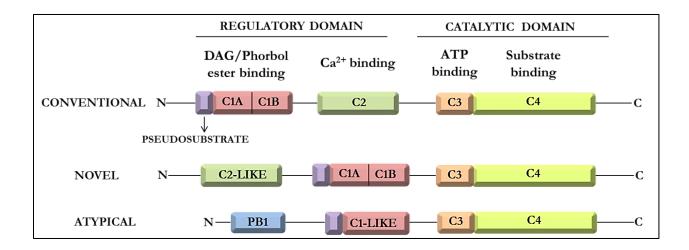
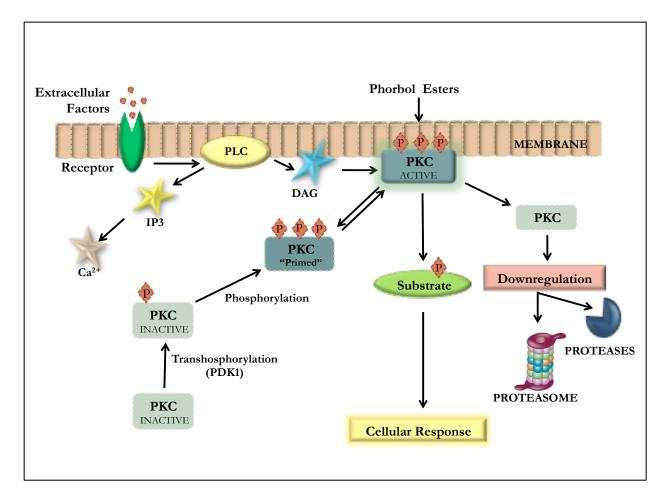


Figure 1. Domain structure of PKC isozymes. The PKC family comprises of three classesconventional, novel and atypical. Each isozyme has a regulatory domain (C1, C2) and a catalytic domain (C3, C4). The C1 domain binds phosphatidylserine for all PKCs and consists of motifs that form the DAG/phorbol ester binding site for the conventional and novel PKCs while C2 domain binds anionic lipids and  $Ca^{2+}$  for conventional PKCs. Atypical PKCs possess a PB1 module for protein-protein interactions. C3 and C4 form the ATP and the substrate binding domains of PKCs respectively.



**Figure 2. Regulation of PKC.** Inactive PKCs are localized in the cytosol where they are processed by ordered phosphorylations which prime them for activation. Signals that promote phospholipid hydrolysis facilitate the generation of DAG and  $Ca^{2+}$  which induce the translocation of the PKCs from the cytosol to the membrane leading to activation. Upon activation, the pseudosubstrate is released which allows substrate binding thus eliciting a cellular response. The open, active conformation of PKC is susceptible to dephosphorylation and degradation. Persistent activation by phorbol esters can also lead to downregulation of PKCs.

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## **CHAPTER II**

### NOVEL REGULATION OF PROTEIN KINASE C-η

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## ABSTRACT

Protein kinase C (PKC) is the receptor for tumor promoting phorbol esters, which are potent activators of conventional and novel PKCs, but persistent treatment with phorbol esters leads to downregulation of these PKCs. However, PKCy, a novel PKC isozyme, resists downregulation by tumor-promoting phorbol esters, but little is known about how PKCn level is regulated. Phosphorylation and dephosphorylation play an important role in regulating activity and stability of PKCs. In the present study, we have investigated the molecular mechanism of PKCn regulation. Several PKC activators, including phorbol 12, 13-dibutyrate, 12-0tetradecanoylphorbol-13-acetate and indolactam V caused upregulation of PKCn whereas the general PKC inhibitor Gö 6983, but not the conventional PKC inhibitor Gö 6976 led to the Upregulation of PKCn was associated with an increase in downregulation of PKC<sub>η</sub>. phosphorylation of PKC<sub>η</sub>. Silencing of phosphoinositide-dependent kinase-1, which phosphorylates PKC<sub>1</sub> at the activation loop, failed to prevent PKC activator-induced

upregulation of PKC $\eta$ . Knockdown of PKC $\epsilon$  but not PKC $\alpha$  inhibited PKC activator-induced upregulation of PKC $\eta$ . Thus, our results suggest that the regulation of PKC $\eta$  is unique and PKC $\epsilon$  is required for the PKC activator-induced upregulation of PKC $\eta$ .

## 1. Introduction

Protein kinase C, a family of phospholipid-dependent serine/threonine kinases, plays a critical role in signal transduction and cell regulation (1, 2). On the basis of their structural features, the PKC family is categorized into three groups, conventional ( $\alpha$ ,  $\beta$ I,  $\beta$ II, and  $\gamma$ ), novel ( $\delta$ ,  $\varepsilon$ ,  $\eta$ ,  $\theta$ ) and atypical ( $\zeta$ ,  $\lambda/\iota$ ). While conventional PKCs require Ca<sup>2+</sup> and diacylglycerol (DAG) for their activities, novel PKCs are Ca<sup>2+</sup>-insensitive but DAG-dependent whereas atypical PKCs are insensitive to both Ca<sup>2+</sup> and DAG (1). PKC isozymes differ in biochemical properties, tissue-specific distribution and intracellular localization. Most cells express multiple PKC isozymes and they exhibit overlapping as well as distinct functions (3).

PKC serves as the receptor for tumor-promoting phorbol esters, which are potent activators of conventional and novel PKCs, and can substitute for the physiological activator DAG (3, 4). Sustained stimulation of PKCs by phorbol esters, such as TPA, has implicated the PKC isozymes in tumor promotion (2, 5). Prolonged treatment with tumor-promoting phorbol esters eventually leads to the downregulation of the phorbol ester-sensitive PKCs (6). Both activation and downregulation of PKCs have been implicated in regulating cellular functions.

PKCs are not only subject to regulation by cofactors, but also via phosphorylation (3). PKCs are phosphorylated at the conserved residues in the activation loop, turn motif and hydrophobic motif. The phosphorylation of PKCs primes them for activation and regulates their stability and subcellular localization (3, 5, 7, 8). PKCs are regulated by both autophosphorylation (9) and transphosphorylation (10). It is generally believed that the priming phosphorylation of PKC occurs at the activation loop by phosphoinositide-dependent kinase-1 (PDK1) and is followed by autophosphorylation at the turn and the hydrophobic motifs (6). Recent studies, however, suggest that PKCs may also be transphosphorylated by other members of the PKC family (3, 6, 7, 11). For example, PKCδ has been shown to be transphosphorylated by PKCε and *vice versa* (12). This cross-regulation of PKCs may be an important way to integrate signals by various PKC isozymes.

PKCη is a member of the novel PKC isozymes that regulates cell proliferation, differentiation, secretion and apoptosis (13-17). It is primarily expressed in epithelial cells and shares highest homology with PKCε (18). PKCη is upregulated in breast cancer tissues (19) and overexpression of PKCη has been associated with resistance to chemotherapeutic agents (20-24). Although PKCs have been implicated in tumor promotion, PKCη is the only phorbol estersensitive PKC isozyme that resists downregulation upon prolonged treatment with phorbol esters (20, 25, 26). Little is known about the unique regulation of PKCη. In the present study, we have investigated the mechanism by which PKCη level is regulated. Our results indicate that in contrast to conventional and novel PKCs, which undergo downregulation following persistent treatment with PKC activators, PKCη is upregulated in response to PKC activators and is downregulated upon treatment with PKC inhibitors. We demonstrate for the first time that the PKC activator-induced upregulation of PKCη is regulated by PKCε, another member of the novel PKC family.

#### 2. Materials and Methods

#### 2.1. Materials

PDBu and TPA were purchased from Alexis Biochemicals (San Diego, CA). ILV was obtained from LC Laboratories (Woburn, MA) and Sigma (St. Louis, MO). Gö 6983 and Gö 6976 were purchased from Calbiochem (San Diego, CA). Polyclonal antibodies to PKCη, PKCδ and PKCE were obtained from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA). Polyclonal antibody against PDK1 was purchased from Cell Signaling Technology, Inc. (Danvers, MA). Monoclonal antibody to PKCa was obtained from Upstate Biotechnology (Lake Placid, NY) and monoclonal antibody to PKCi was from BD Transduction Laboratories (San Jose, CA). Monoclonal antibody against actin was obtained from Sigma (St. Louis, MO). Horseradishperoxidase-conjugated donkey anti-rabbit and goat anti-mouse secondary antibodies were purchased from Jackson ImmunoResearch Laboratories, Inc. (West Grove, PA). <sup>32</sup>P]Orthophosphate was purchased from PerkinElmer, (Waltham, MA). Inc. Poly(vinylidenedifluoride) membrane was obtained from Millipore (Bedford, MA). Enhanced chemiluminescence detection kit was purchased from Amersham (Arlington Heights, IL).

## 2.2. Cell culture

Breast cancer cells were maintained in RPMI medium supplemented with 10% fetal bovine serum and 2 mM glutamine. Human embryonic kidney (HEK) 293T 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>.

## 2.3. Transfection

Control non-targeting siRNA or SMARTpool siRNA against PKC isozymes, and PDK1 were introduced into MCF-7 or T47D cells using Lipofectamine 2000 or Lipofectamine RNAiMax (Invitrogen, Carlsbad, CA) and manufacturer's protocol. 48 h following siRNA transfection, cells were treated as indicated in the text and processed for Western blot analysis.

#### 2.4. Reverse Transcriptase PCR

MCF-7 cells were treated with or without PDBu, ILV or 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), PKCη and β-actin primers. The sequences of forward and reverse PKCη primers were 5'-ATGCGGTGGAACTTGCCA-3' and 5'-CGTGACCACAGAGCATCTCATAGA-3' respectively. The sequences of the forward and reverse β-actin primers were 5'-ACCCAGCACAATGAAGATCA-3' and 5'-GCGCAAGTTAGGTTTTGTCA-3'. After PCR cycling, a 750 bp product for PKCη and 800-bp product for β-actin was detected by gel electrophoresis.

#### 2.5. 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 (17).

### 2.6. Metabolic labeling

HEK293T cells were transiently transfected with either pcDNA3 or vector containing PKCη construct and radiolabeled with [<sup>32</sup>P]orthophosphate. Cells were treated with or without PDBu and immunoprecipated with either rabbit IgG or anti-PKCη antibody. Immunocomplexes were processed as described previously (27) and subjected to SDS-PAGE and autoradiography.

### 3. Results

## 3.1. Effect of PKC activators and inhibitors on PKC $\eta$ levels

We have previously demonstrated that persistent treatment with phorbol 12, 13- dibutyrate (PDBu) caused upregulation of PKC $\eta$  in MCF-7 breast cancer cells (20). In the present study, we compared the effect of several structurally and functionally distinct PKC activators on PKC $\eta$  level. While PDBu and TPA belong to the same class of compounds, indolactam V (ILV) is structurally distinct from phorbol esters. All three PKC activators caused substantial upregulation of PKC $\eta$  (Fig. 1A and 1B). Based on the densitometric quantification of several independent experiments, PKC activators caused a significant increase in PKC $\eta$  level (Fig. 1B). PKC $\eta$  appeared as a doublet in the Western blot since it contains two major transcription initiation sites (28). Prolonged treatment with PDBu and TPA caused downregulation of conventional PKC $\alpha$  and novel PKC $\delta$  although PKC $\epsilon$  was less susceptible to PKC activator-induced downregulation (Fig. 1A). The level of phorbol ester-insensitive atypical PKC $\iota$  remained unaltered, as expected (Fig. 1A). Consistent with our earlier reports, ILV had little effect on the downregulation of PKC $\alpha$  (29). Thus, the regulation of PKC $\eta$  is unique in comparison to other conventional and novel PKCs.

Since PKC activators led to PKC $\eta$  upregulation, we examined whether PKC inhibitors would induce downregulation of PKC $\eta$ . We compared the effects of the general PKC inhibitor Gö 6983 and conventional PKC inhibitor Gö 6976. Gö 6983 but not Gö 6976 caused substantial downregulation of PKC $\eta$  (Fig. 1C and 1D). The levels of PKC- $\alpha$ , - $\delta$  and - $\epsilon$  were not decreased by Gö 6983 treatment (Fig. 1C). The general PKC inhibitor bisindolylmaleimide also induced selective downregulation of PKC $\eta$  (data not shown). Since atypical PKCs are phorbol esterinsensitive, these results suggest that the level of PKC $\eta$  may be regulated by novel PKCs.

To determine if PKC activators and inhibitors alter PKC $\eta$  expression at the mRNA level, we treated MCF-7 cells with PDBu, ILV or Gö 6983 and examined the mRNA expression by reverse-transcriptase PCR. As shown in Fig. 2A, the treatment of MCF-7 cells with PKC activators and inhibitors did not alter the mRNA expression of PKC $\eta$ . Taken together, these results suggest that PKC $\eta$  level is altered at the post-transcriptional level following treatment with PKC activators and inhibitors.

## 3.2. Effect of PKC activator and inhibitor on PKCn phosphorylation

Since persistent treatment with PKC activators cause activation of PKCs followed by dephosphorylation and downregulation of PKCs, we examined if upregulation of PKCη by PKC activators was associated with an increase in PKCη phosphorylation. We introduced PKCη in HEK293T cells, labeled with [<sup>32</sup>P]orthophosphate and immunoprecipitated PKCη following treatment with or without PDBu. We did not detect a phosphorylated band corresponding to PKCη in vector-transfected HEK293T cells (Fig. 2B). PKCη was constitutively phosphorylated in HEK293T cells expressing wild-type PKCη and PDBu further increased the level of phospho-PKCη (Fig. 2B). The densitometric scanning from three separate experiments indicated a significant increase in the phosphorylation status of PKCη in response to PDBu (Fig. 2C). These results suggest that upregulation of PKCη is associated with an increase in PKCη phosphorylation.

# 3.3. Regulation of PKC<sub>η</sub> level by transphosphorylation

PDK1 is believed to phosphorylate the activation loop of AGC kinases, including PKC isozymes (7, 8). Recent evidence has also implicated PDK1 in phosphorylating PKC $\eta$  at the activation loop (30). We therefore examined whether PDK1 was involved in the activator-induced upregulation of PKC $\eta$ . Fig. 3A shows that the silencing of PDK1 by siRNA decreased the basal level of PKC $\eta$  but had little effect on the upregulation of PKC $\eta$  by phorbol esters.

Since cross-regulation of PKC isozymes by other PKC family members has been suggested by several studies (11, 12, 31), we examined if the knockdown of a particular PKC isozyme affects PKC $\eta$  level. As shown in Fig. 3B, the depletion of conventional PKC $\alpha$  had little effect on phorbol ester-induced upregulation of PKC $\eta$ . While knockdown of PKC $\delta$  had a modest effect, the knockdown of novel PKC $\epsilon$  substantially decreased the ability of PKC activators to enhance PKC $\eta$  level in both MCF-7 (Fig. 4A) and T47D (Fig. 4B) cells. These results suggest that transphosphorylation of PKC $\eta$  by novel PKC $\epsilon$  may be responsible for PKC $\eta$  upregulation.

### 4. Discussion

The results of our present study demonstrate that the regulation of PKCη is unique compared to other PKC isozymes. Although tumor-promoting phorbol esters are potent activators of conventional and novel PKCs (4), persistent treatment with phorbol esters leads to the downregulation of phorbol ester-sensitive PKCs causing termination of PKC signaling (32). Downregulation of PKCs has important implications in regulating long-term cellular responses, such as cell proliferation, differentiation and tumor promotion (2, 13). We have shown that in contrast to other PKCs, prolonged treatment with PKC activators led to upregulation of PKCη whereas PKC-specific inhibitors triggered downregulation of PKCη. Furthermore, we made a novel observation that novel PKCs are involved in PKC activator-induced upregulation of PKCη.

It is generally believed that treatment with PKC activators leads to membrane translocation of PKCs followed by dephosphorylation (33). The dephosphorylated PKCs are subject to downregulation by proteases (34). However, fully phosphorylated PKC $\alpha$  was shown to be downregulated at the plasma membrane via the proteasome-mediated pathway (35). In addition, the phosphorylated primed form of PKC $\epsilon$  was downregulated by phorbol ester treatment independent of its intrinsic kinase activity (36). It has been reported that active conformation of PKC $\eta$  is necessary for its downregulation in baby hamster kidney (BHK) cells although TPA failed to downregulate PKC $\eta$  in these cells (37). Our results show that prolonged treatment with structurally distinct PKC activators, such as phorbol esters and ILV, caused an upregulation of PKC $\eta$  in MCF-7 cells (Fig. 1A and 1B). The upregulation of PKC $\eta$  by PKC activators was not unique to MCF-7 cells, and was observed in several cell types, including T47D, BT-20 and MCF-10CA1d cells (Fig. 4A, 4B and data not shown).

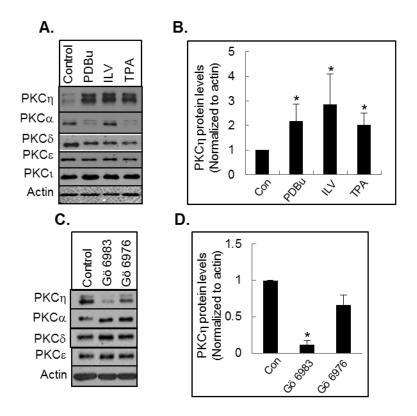
The activity, maturation, stability and localization of PKCs are regulated by phosphorylation and dephosphorylation events (7, 8). Our study suggests that PKCη level is regulated by phosphorylation. First, treatment with several PKC activators, such as TPA, PDBu and ILV induced upregulation of PKCη (Fig. 1A and 1B) but this upregulation was not associated with an increase in PKCη mRNA (Fig. 2A). Second, PKC-specific inhibitors Gö 6983 (Figs. 1C and 1D) and bisindolylmaleimide (data not shown) led to downregulation of PKCη. Third, upregulation of PKCη by PDBu was associated with an increase in PKCη phosphorylation (Fig. 2B and 2C).

Phosphorylation of PKCs is regulated by both autophosphorylation and transphosphorylation (3) and phosphorylation of PKCs at the activation loop is believed to prime them for activation (8). Phosphoinositide-dependent kinase-1 (PDK1) has been shown to phosphorylate PKCs, at the activation loop and contributes to the stability of cPKCs and PKCε (32, 33, 38) PDK1 was also shown to phosphorylate PKCη at the activation loop (30). However, knockdown of PDK1 did not prevent PKC activator-induced upregulation of PKCη (Fig. 3A).

PKCs can also undergo transphosphorylation by other members of the PKC family (3, 12). For example, PKCε rather than PDK1 was shown to phosphorylate PKCδ and PKCε at the activation loop whereas PKCδ induced autophosphorylation as well as transphosphorylation of PKCε at the hydrophobic motif (12). We recently reported that depletion of PKCε enhanced PDBu-induced downregulation of PKCδ in HeLa cells (11). Since the general PKC inhibitor Gö 6983 but not the conventional PKC inhibitor Gö 6976 induced PKCη downregulation (Fig. 1C and 1D) and atypical PKCs are phorbol ester insensitive, it is likely that PKCη is also regulated by novel PKC isozyme(s). Consistent with this notion, we found that depletion of cPKC $\alpha$  had little effect on PKC activator-induced upregulation of PKC $\eta$  whereas knockdown of nPKC $\epsilon$  attenuated PKC $\eta$  upregulation (Fig. 4A and 4B).

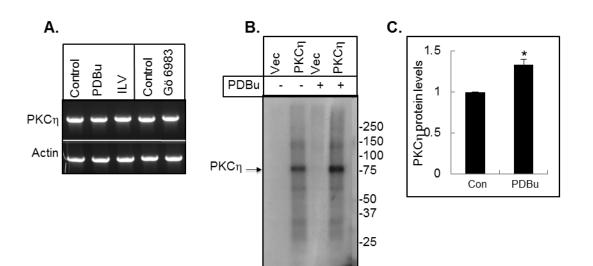
The observation that PKC $\eta$  is the only PKC isozyme upregulated by tumor-promoting phorbol esters suggests that PKC $\eta$  may play an important role in tumorigenesis. Depending on the cellular context, PKC $\eta$  may suppress tumorigenesis or promote malignant cell growth. For example, PKC $\eta$  knockout mice were more susceptible to tumor promotion in two-stage skin carcinogenesis model (39). In contrast, PKC $\eta$  has also been implicated in breast cancer (19, 20), glioblastoma (21), Hodgkin's lymphoma (40), lung cancer (22, 41) and hepatocellular carcinoma (42). This contrasting function of PKC $\eta$  in different cell types is not unique to PKC $\eta$  and has been noted with other novel PKCs, such as PKC $\delta$  (5) and PKC $\epsilon$  (43). PKC $\eta$  is often overexpressed in breast cancer (19) and the level of PKC $\eta$  is upregulated by estradiol in hormone-sensitive breast cancer cells (44). Moreover, overexpression of PKC $\eta$  confers resistance to chemotherapeutic drugs (20-24). Thus, understanding the mechanism of PKC $\eta$ upregulation has significant implications in cancer therapy. **Figure 1.** Effects of PKC activators and inhibitors on PKC $\eta$  level. MCF-7 cells were treated with 1  $\mu$ M PDBu, 10  $\mu$ M ILV and 100 nM TPA for 15 h. (A) Western blot analysis was performed with total cell extract and probed with the indicated antibodies. Actin was used as a loading control. (B) Densitometric quantification of PKC $\eta$  protein level from 3 separate experiments corrected for loading. Data represents the mean +/- s.e.m. The asterisk (\*) indicates significant difference from control (P<0.05) using paired Student's t-test. (C) MCF-7 cells were treated with 1  $\mu$ M Gö 6983 for 15 h. Total cell lysates were subjected to SDS-PAGE and Western blot analysis was performed using the indicated antibodies. (D) Densitometric quantification of PKC $\eta$  protein expression from 3 separate experiments corrected for loading.

Figure 1.



**Figure 2.** Effects of PKC modulators on PKC $\eta$  mRNA expression and phosphorylation. (A) MCF-7 cells were treated with 1  $\mu$ M PDBu, 10  $\mu$ M ILV or 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 cDNA were amplified by PCR and electrophoresed. Results are representative of at least 2 independent experiments. (B) HEK293T cells expressing empty vector or vector containing PKC $\eta$  were radiolabeled with [<sup>32</sup>P]orthophosphate and immunoprecipitated with PKC $\eta$  following treatment with or without PDBu. The arrow indicates PKC $\eta$ . (C) Densitometric quantification of PKC $\eta$  protein level from 3 separate experiments corrected for loading. Data represents the mean +/- s.e.m. The asterisk (\*) indicates significant increase with PDBu treatment (P<0.05) using paired Student's t-test.

Figure 2.



**Figure 3.** Effect of PDK1 and PKC $\alpha$  knockdown on PKC $\eta$  upregulation. (A) and (B) MCF-7 cells were transfected with the indicated siRNAs and then treated with or without 1 $\mu$ M PDBu, 100 nM TPA or 10  $\mu$ M ILV for 16 h. Western blot analysis was performed with indicated antibodies. Actin was used as a loading control. Results are representative of 3 independent experiments.

Figure 3.

Α.

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PDK1	i.	-	-	-	-
Actin	i	-	-	-	ļ

В.

siRNA	Con			ΡΚCα			
Treatment	Con	PDBu	١L٧	Con	PDBu	١٢٧	
ΡΚϹη	-	1	1	-	1	1	
ΡΚCα	-	-	-	· And			
Actin	1	-	-	-	-	-	

**Figure 4.** Effects of novel PKC isozyme knockdown on PKC $\eta$  upregulation. MCF-7 (A) and T47D (B) cells were transfected with indicated siRNAs. Cells were treated with or without 1  $\mu$ M PDBu, 10  $\mu$ M ILV or 100 nM TPA for 16 h. Western blot analyses were performed using indicated antibodies. Results are representative of 3 independent experiments.

Figure 4.

A	۱.							_			
	siRNA	Con		ΡKCδ			ΡΚϹε				
	Treatment	Con PDBu	TPA TPA	Con	PDBu	۲ ۲	TPA	Con	PDBu	IL<	TPA
	ΡΚϹη	-		1	-	-	-	1	-	-	-
	ΡΚϹδ	1	-	-		-	-	-	-	-	-
	ΡΚϹͽ		-	0			1	1	-	-	-
	Actin			-	-	-	-	-	-	-	-

В.					
	siRNA	ΡΚCα	ΡKCδ	ΡΚϹε	Con
	Treatment	Con TPA ILV	Con TPA ILV	Con TPA ILV	Con TPA ILV
	ΡΚϹη				8
	ΡΚCα				
l	PKCδ		-		
	ΡΚϹε		1		1
	Actin				1

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#### **CHAPTER III**

## UPREGULATION OF PKCη BY PKCε AND PDK1 INVOLVES TWO DISTINCT MECHANISMS AND PROMOTES BREAST CANCER CELL SURVIVAL

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#### ABSTRACT

**Background:** Protein kinase C (PKC) serves as the receptor for tumor-promoting phorbol esters, which are potent activators of conventional (c) and novel (n) PKCs. We recently showed that these activators induced selective upregulation of PKC $\eta$  in breast cancer cells. The objective of this study is to understand unique regulation of PKC $\eta$  and its importance in breast cancer.

*Methods*: The levels of PKC isozymes were monitored in breast cancer cells following treatment with inhibitors of kinases, proteasome and proteases by Western blotting. PKC $\varepsilon$  was introduced by adenoviral delivery. PKC $\eta$  and PDK1 were depleted by siRNA silencing. Cell growth was determined by the MTT or clonal assay.

**Results:** The general PKC inhibitors Gö 6983 and bisindolylmaleimide but not cPKC inhibitor Gö 6976 led to substantial PKC $\eta$  downregulation, which was partly rescued by the introduction of nPKC $\epsilon$ . Inhibition of phosphoinositide-dependent kinase-1 (PDK1) by Ly294002 or knockdown of PDK1 also led to downregulation of basal PKC $\eta$  but had no effect on PKC activator-induced upregulation of PKC $\eta$ . Proteasome inhibitors blocked PKC $\eta$  downregulation triggered by PDK1 inhibition/depletion but not by Gö 6983. PKC $\eta$  level increased in malignant but not in non-tumorigenic or pre-malignant cells in the progressive MCF-10A series associated with activated PDK1, and knockdown of PKC $\eta$  inhibited breast cancer cell growth and clonogenic survival.

*Conclusion*: Upregulation of PKCη contributes to breast cancer cell growth and targeting either PKCε or PDK1 triggers PKCη downregulation but involves two distinct mechanisms.

*General significance*: The status of PKCη may serve as a potential biomarker for breast cancer malignancy.

#### 1. Introduction

Protein kinase C, a family of phospholipid-dependent serine/threonine kinases, plays a critical role in growth factor signal transduction pathways (1, 2). The PKC family is classified into conventional ( $\alpha$ ,  $\beta$ I,  $\beta$ II,  $\gamma$ ), novel ( $\delta$ ,  $\varepsilon$ ,  $\eta$ ,  $\theta$ ) and atypical PKCs ( $\zeta$ ,  $\lambda/\iota$ ) based on their structural features and cofactor sensitivity (1, 2). Diacylglycerol (DAG) and Ca<sup>2+</sup> are required for the activity of conventional PKCs whereas novel PKCs are insensitive to Ca<sup>2+</sup> but dependent on DAG; atypical PKCs are insensitive to both Ca<sup>2+</sup> and DAG (1, 2).

Tumor-promoting phorbol esters are potent activators of PKCs and can substitute for DAG. However, sustained activation by phorbol esters leads to downregulation of PKCs causing termination of the PKC signaling. Calcium-activated proteases, such as calpains and ubiquitin proteasome-mediated pathways have been implicated in PKC activator-induced downregulation of PKCs. Calpains are believed to downregulate cPKCs (3, 4) whereas PKC $\alpha$ , - $\delta$  and - $\epsilon$  were shown to be degraded via proteasome-mediated pathway (5-7). Downregulation of PKCs has important implications in regulating long-term cellular responses such as cell proliferation, differentiation and tumor promotion (1, 8, 9).

PKC $\eta$  is a member of the novel PKC family and shares highest homology with PKC $\epsilon$ (10). However, the regulation of PKC $\eta$  appears to be unique. We have recently shown that several different PKC activators, including tumor-promoting phorbol esters, induce upregulation rather than downregulation of PKC $\eta$  (11). Moreover, phosphorylation of PKC $\eta$  by novel PKC $\epsilon$ appears to be responsible for PKC activator-induced upregulation of PKC $\eta$  (11). Depending on the cellular context, inhibition of PKC $\eta$  could either promote or suppress tumor promotion (12-19). Since PKC $\eta$  is upregulated by tumor promoters, we examined the mechanism of PKC $\eta$  downregulation. Our results indicate that inhibition of either PKC or PDK1 induces PKCη downregulation but involves two distinct mechanisms. While inhibition of PKC resulted in PKCη downregulation via proteasome-independent pathway, inhibition of PDK1 led to PKCη downregulation via proteasome-dependent pathway. We also showed that PKCη level is increased in malignant but not in non-tumorigenic or pre-malignant cells in the progressive MCF-10A series and knockdown of PKCη inhibited breast cancer cell growth.

#### 2. Materials and Methods

#### 2.1. Materials

PDBu was purchased from Alexis Biochemicals (San Diego, CA). Ly294002 was purchased from Calbiochem (San Diego, CA) and Cell Signaling Technology, Inc (Danvers, MA). Gö 6983, Gö 6976, KT5720, Rottlerin, PD98059, BIM, U0126, MG-132, lactacystin, calpeptin and cathepsin inhibitor I were obtained from Calbiochem (San Diego, CA). Polyclonal antibodies to PKC $\eta$ , PKC $\delta$ , PKC $\epsilon$  and monoclonal antibody to GAPDH were obtained from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA). Monoclonal antibody to PKC $\alpha$  was obtained from Upstate Biotechnology (Lake Placid, NY). Polyclonal antibody against PDK1 was purchased from Cell Signaling Technology, Inc. (Danvers, MA). 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 Jackson ImmunoResearch Laboratories, Inc. (West Grove, PA). Control non-targeting siRNA and siRNA specific for PDK1 and PKC $\eta$  were obtained from Dharmacon (Lafayette, CO). Poly(vinylidenedifluoride) membrane was from Millipore (Bedford, MA) and enhanced chemiluminescence detection kit was from Amersham (Arlington Heights, IL).

#### 2.2. Cell culture

MCF-7 and T47D cells were maintained in RPMI 1640 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>. The MCF-10A series developed by Dr. Fred Miller and colleagues (20), was obtained from the Barbara Ann Karmanos Cancer Institute (Detroit, MI). They were cultured as described previously (21).

#### 2.3. Transfection

Control non-targeting siRNA or SMARTpool siRNA against PDK1 or PKC $\eta$  were introduced into cells using Lipofectamine RNAiMax (Invitrogen, Carlsbad, CA) and manufacturer's protocol. Cells were treated as indicated in the text and processed for Western blot analysis.

#### 2.4. 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).

#### 2.5. Clonogenic assay

Cells transfected with or without control non-targeting or PKC $\eta$  siRNA were cultured at 37°C in a humidified incubator with 5% CO<sub>2</sub> until there were at least 50 cells per colony. At the end of the incubation, the cells were washed with PBS and incubated with 0.025% crystal violet solution for 15 minutes. Colonies were counted using ImageJ software (http://rsbweb.nih.gov/ij/), and the plate was photographed using the BioChemi System (BioImaging System, UVP, Upland, CA).

#### 2.6. MTT assay

Cells transfected with or without control non-targeting or PKCη siRNA were plated in microtiter plates and incubated at 37°C and 5% CO<sub>2</sub>. After 4 days, the number of viable cells was determined using 3-[4,5-dimethylthiazol-2-yl]-2,5-diphenyltetra-zolium bromide (MTT) as described previously (23).

### 2.7. Statistical analysis

Statistical significance was determined by Student's t test by using PASW Statistics (SPSS, Inc.). p values < 0.05 were considered statistically significant.

#### 3. Results

#### 3.1. Inhibitors of PKC and PI3K induce downregulation of PKC \eta

We have previously shown that the regulation of PKC $\eta$  is unique since it is upregulated rather than downregulated by PKC activators in breast cancer cells (11). In the present study, we examined if inhibition of PKC induces its downregulation. Figure 1A shows that the general PKC inhibitor bisindolylmaleimide caused substantial downregulation of PKC $\eta$  whereas rottlerin, which inhibits novel PKC $\delta$ , had no effect; the conventional PKC inhibitor Gö 6976 caused only a modest decrease in PKC $\eta$  level in MCF-7 cells. The PI3K inhibitor Ly294002 also induced PKC $\eta$  downregulation whereas rapamycin, PD98059 and KT5720, which inhibit mTOR, MAPK and PKA, respectively had little or no effect (Fig. 1A). To determine if the ability of PKC or PI3K inhibitor to downregulate PKC $\eta$  is a general phenomenon, we tested several different breast cancer cell lines. Figure 1B shows that similar to MCF-7 cells, bisindolylmaleimide and Ly294002 induced substantial downregulation of PKC $\eta$  in T47D cells whereas mTOR inhibitor rapamycin had a modest effect and MEK inhibitor U0126 had no effect. These results suggest that both PKC and PI3K pathways are involved in regulating PKC $\eta$ level.

#### 3.2. PKC and PI3K inhibitors induce PKC downregulation via two distinct pathways.

Since PKC activators induce upregulation of PKC $\eta$ , we examined if the general PKC inhibitor Gö 6983 or the PI3K inhibitor Ly294002 could block PKC activator-induced upregulation of PKC $\eta$ . Figure 2 shows that while the PKC activator PDBu induced downregulation of PKC $\alpha$ , - $\delta$  and - $\epsilon$ , it caused upregulation of PKC $\eta$ . Consistent with the notion that PKC activity is required for PKC activator-induced downregulation of PKCs (5, 7, 24), the

general PKC inhibitor Gö 6983 prevented PDBu-induced downregulation of PKC $\alpha$  and PKC $\delta$ . However, Gö 6983 was able to induce PKC $\eta$  downregulation in PDBu-treated cells. The PI3K inhibitor Ly294002 caused a substantial decrease in basal PKC $\eta$  level but the constitutive levels of PKC $\alpha$ , - $\delta$  and - $\epsilon$  were not altered by the Ly294002 treatment. In contrast to Gö 6983, Ly294002 was unable to induce PKC $\eta$  downregulation in PDBu-treated cells. These results suggest that Gö 6983 and Ly294002 induced PKC $\eta$  downregulation via two distinct pathways.

#### 3.3. Ly294002 induces PKC downregulation via ubiquitin proteasome-mediated pathway

Both calcium-activated proteases, such as calpains as well as ubiquitin proteasome-mediated pathway have been implicated in the activation-induced downregulation of PKCs (4, 5, 7). Therefore, we examined the ability of calpain inhibitor calpeptin, cathepsin inhibitor I and proteasome inhibitor MG-132 or lactacystin in preventing downregulation of PKCη by Gö 6983 or Ly294002. Figure 3 shows that neither calpain inhibitor nor cathepsin inhibitor blocked PKCη downregulation induced by either Gö 6983 or Ly294002. Although the proteasome inhibitor MG-132 prevented PKCη downregulation by Ly294002, it had only a modest effect on Gö 6983-mediated downregulation of PKCη (Figs. 4A & 4B). Similar results were observed in T47D cells where two different proteasome inhibitors MG-132 and lactacystin blocked Ly294002-mediated but not Gö 6983-mediated downregulation of PKCη (Fig. 4C). These results demonstrate that Ly294002 but not Gö 6983 induces PKCη downregulation via the proteasome-mediated pathway.

#### 3.4. Inhibition of PDK1 and PKC $\varepsilon$ triggers PKC $\eta$ downregulation

Since PDK1 is believed to phosphorylate PKC $\eta$  at the activation loop (25) and Ly294002 inhibits PDK1 which acts downstream of PI3K, we examined if knockdown of PDK1 induces

downregulation of PKCη. Figure 5A shows that similar to Ly294002, depletion of PDK1 by siRNA decreased basal PKCη level. The proteasome inhibitors MG-132 and lactacystin caused a modest increase in PKCη level in cells transfected with control non-targeting siRNA or in untransfected cells, and blocked PKCη downregulation by both Ly294002 and PDK1 knockdown (Fig. 5A). These results suggest that inhibition of PDK1 by Ly294002 targets PKCη to proteasome-mediated downregulation.

Since we have previously shown that novel PKC $\varepsilon$  was responsible for PKC activator-induced upregulation of PKC $\eta$  (11), we speculated that the general PKC inhibitor Gö 6983 triggers PKC $\eta$  downregulation by inhibiting PKC $\varepsilon$ . Since T47D cells were more dependent on PKC $\varepsilon$ -mediated upregulation of PKC $\eta$  (11), we infected T47D cells with adenoviral vector expressing either GFP or PKC $\varepsilon$ . Figure 5B shows that adenoviral delivery of PKC $\varepsilon$  but not GFP increased basal PKC $\varepsilon$  level and partially blocked Gö 6983-induced downregulation of PKC $\eta$ . Taken together, these results suggest that inhibition of PDK1 and novel PKC $\varepsilon$  by Ly294002 and Gö 6983, respectively triggers PKC $\eta$  downregulation via two distinct pathways.

# 3.5. *PKC* $\eta$ is progressively increased in MCF-10A series and promotes breast cancer cell survival

Since PKC $\eta$  level is regulated by PKC and PI3K/PDK1 pathways that have been implicated in breast cancer (26-28), we compared PKC $\eta$  level in non-tumorigenic MCF-10A cells and breast cancer cells. The level and activation status of PDK1 was increased in the progressive MCF-10A series (21) that includes spontaneously immortalized non-tumorigenic mammary epithelial MCF-10A cells, premalignant MCF-10AT cells, ductal carcinoma in situ (DCIS) and highly malignant MCF-10CA1d cells (20). Figure 6A shows that PKC $\eta$  is expressed only in malignant breast cancer cells but not in non-tumorigenic MCF-10A or premalignant MCF-10AT cells. The levels of other PKCs, such as PKC $\alpha$ , PKC $\delta$ , PKC $\epsilon$  or PKC $\zeta$  were not altered with the malignancy of the MCF-10A series. Similar to MCF-7 and T47D cells, both Gö 6983 and Ly294002 led to PKC $\eta$  downregulation in CA1d cells (Fig. 6B).

To determine the functional significance of PKCη upregulation in breast cancer cells, we determined the consequence of PKCη depletion on the viability of breast cancer cells. Depletion of PKCη by siRNA (Fig. 7A) decreased MCF-7 cell survival in a long-term clonogenic assay (Figs. 7B & 7C). Knockdown of PKCη also inhibited the growth of both T47D (Fig. 7D) and DCIS (Fig. 7E) cells. These results suggest that PKCη contributes to the viability of breast cancer cells.

#### 4. Discussion

Because of the pivotal role of the PKC family members in signal transduction and cell regulation, there have been significant efforts in understanding their function and regulation. Among the novel PKCs, most of the studies thus far have been focused on PKC $\delta$  and - $\epsilon$  but little is known about the regulation of novel PKC $\eta$ . Our results suggest that the regulation of PKC $\eta$  is unique. We recently reported that persistent treatment with PKC activators induce upregulation of PKC $\eta$  rather than downregulation which is seen with other phorbol ester-sensitive conventional and novel PKCs. In the present study, we show that downregulation of PKC $\eta$  can be achieved via two distinct pathways. While inhibition of PKC induces PKC $\eta$  downregulation via a proteasome-independent pathway. We also made a novel observation that PKC $\eta$  is the only PKC isozyme which is upregulated in breast cancer cells compared to non-malignant cells and downregulation of PKC $\eta$  inhibits breast cancer cell growth.

PKC $\eta$  has been implicated in both tumor promotion and tumor suppression. For example, PKC $\eta$  expression was decreased in hepatocellular carcinoma (16), and PKC $\eta$  deficiency enhanced susceptibility to tumor formation in a two-stage skin carcinogenesis model (12, 13). Moreover, overexpression of PKC $\eta$  induced differentiation in keratinocytes (17, 19). In contrast, PKC $\eta$  has been implicated in breast cancer (29), glioblastoma (15), lung cancer (14) and renal cell carcinoma (18). In addition, overexpression of PKC $\eta$  induced anchorage-independent growth in NIH3T3 cells (30) and provided proliferative advantage in astrocytic tumor cells (31). The contrasting function of PKC $\eta$  is not unique and several other PKC isoforms have been shown to exert opposite effects depending on the cell type (1, 9, 27, 32). Thus, it is important to understand how PKC $\eta$  is regulated in a particular cellular context in order to understand its function.

We recently reported that the regulation of PKC $\eta$  in breast cancer cells is distinct from other PKC isozymes. While brief exposure to PKC activators, such as tumor-promoting phorbol esters leads to activation of conventional and novel PKCs, persistent treatment with these activators leads to their downregulation (1, 2). We showed that prolonged treatment with several structurally and functionally distinct PKC activators caused upregulation rather than downregulation of PKC $\eta$  and a general PKC inhibitor led to PKC $\eta$  downregulation (11). When we compared the effects of pharmacological inhibitors of several different kinases, we found that not only PKC inhibitors but also the PI3K inhibitor Ly294002 induced PKC $\eta$  downregulation.

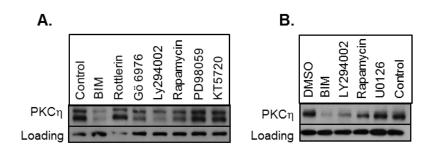
PKCs are phosphorylated by autophosphorylation and transphosphorylation by other members of the PKC family as well as PDK1 (33-35). We recently reported that transphosphorylation of PKC $\eta$  by novel PKC $\varepsilon$  is responsible for its upregulation (11). Since two different general PKC inhibitors bisindolylmaleimide and Gö 6983 induced PKC $\eta$ downregulation whereas the conventional PKC inhibitor Gö 6976 had only a modest effect, it is likely that inhibition of PKC $\eta$  phosphorylation by novel PKC $\varepsilon$  leads to its downregulation. Our observation that adenoviral delivery of PKC $\varepsilon$  increased PKC $\eta$  level both in control and Gö 6983-treated cells supports this notion. We, however, found that overexpression of PKC $\varepsilon$  was unable to completely prevent Gö 6983-mediated downregulation of PKC $\eta$ ; presumably because Gö 6983 could inhibit PKC $\varepsilon$  in PKC $\varepsilon$ -overexpressing cells albeit to a lesser extent compared to endogenous PKC $\varepsilon$ . It has been reported that PDK1 directly phosphorylates PKCη resulting in its activation (25) but knockdown of PDK1 had little effect on PKC activator-induced upregulation of PKCη (11). Although PDK1 was not required for PKC activator-induced upregulation of PKCη, depletion of PDK1 by siRNA or its inhibition by the PI3K inhibitor Ly294002 decreased basal PKCη level, suggesting that phosphorylation of PKCη by PDK1 also protects it from downregulation. However, the mechanism by which Gö 6983 and Ly294002 induced PKCη downregulation was distinct. While both Gö 6983 and Ly294002 decreased basal PKCη level, only Gö 6983 but not Ly294002 could induce PKCη downregulation in the presence of PDBu. Moreover, two distinct proteasome inhibitors MG-132 and lactacystin could prevent PKCη downregulation caused by Ly294002 or PDK1 knockdown but not by Gö 6983. These results suggest that while inhibition of PKCη triggers PKCη downregulation via proteasome-independent pathway.

Both PKC and PI3K/PDK1/Akt signaling pathways play important roles in the development and progression of breast cancer (1, 26-28). It has been reported that the level and activation status of PDK1 is progressively increased in the MCF-10A series (21) which includes spontaneously immortalized non-tumorigenic mammary epithelial MCF-10A, premalignant MCF-10AT and MCF10AT3G, ductal carcinoma in situ DCIS and fully malignant MCF10CA1a and MCF10CA1d cells (20, 21). The MCF-10A series provides a unique cell culture model system to study the alterations in signaling molecules leading to breast cancer since these cells share common genetic background. We made a novel observation that PKC $\eta$  is the only PKC isozyme that is progressively increased in the MCF-10A series but there was no correlation between the levels of conventional PKC $\alpha$ , novel PKC $\delta$  and - $\varepsilon$  and atypical PKC $\zeta$  and the malignant status of MCF10A-derived cells. Our results suggest that while PKCη level correlates with the level/activation status of PDK1 in the MCF10 cell series, there is no correlation between PKCη level and hormone receptor status. For example, it is difficult to detect PKCη in triple-negative MDA-MB-231 cells (data not shown). However, both PKC inhibitor Gö 6983 and PI3K/PDK1 inhibitor Ly294002 induced downregulation of PKCη in basal type MCF-10CA1d cells (Fig. 6B) and MCF-10CA1a cells (data not shown).

To determine the functional significance of PKC $\eta$  in breast cancer cells we depleted PKC $\eta$  using siRNA since a selective inhibitor of PKC $\eta$  is currently not available. Silencing of PKC $\eta$  by siRNA decreased the growth of both DCIS and T47D cells. Knockdown of PKC $\eta$  also reduced the long-term clonogenic survival of MCF-7 cells, which express very high level of PKC $\eta$ . Moreover, since PKC $\eta$  is regulated by PKC $\epsilon$  and PDK1 that play critical roles in breast cancer, PKC $\eta$  may serve as an important target for breast cancer therapy.

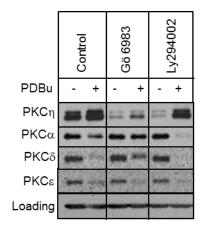
**Figure 1.** Effects of kinase inhibitors on PKC $\eta$  levels. MCF-7 (A) or T47D (B) cells were treated with or without 10  $\mu$ M BIM, 10  $\mu$ M rottlerin, 1  $\mu$ M Gö 6976, 25  $\mu$ M Ly294002, 50 nM rapamycin, 50  $\mu$ M PD98059, 10  $\mu$ M U0126 or 2  $\mu$ M KT5720 for 15 h. Western blot analysis was performed with total cellular extracts using the indicated antibodies. Actin was used as a loading control.

Figure 1.



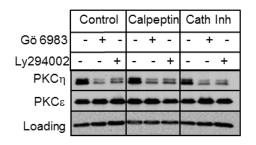
**Figure 2.** Effect of PKC activators on PKC $\eta$  downregulation by PKC and PI3K inhibitors. MCF-7 cells were pretreated with 1  $\mu$ M PDBu for 15 min, followed by treatment with or without 1 $\mu$ M Gö 6983 or 25  $\mu$ M Ly294002 for 15 h. Western blot analysis was performed with total cellular extracts using the indicated antibodies. Actin was used as a loading control.

Figure 2.



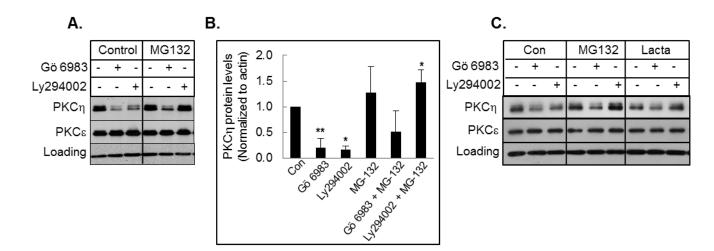
**Figure 3.** Effect of protease inhibitors on PKC $\eta$  downregulation in MCF-7 cells. MCF-7 cells were pretreated with or without 50  $\mu$ M calpeptin or 50  $\mu$ M cathepsin inhibitor I for 30 min, followed by treatment with 1  $\mu$ M Gö 6983 or 25  $\mu$ M Ly294002 for 12 h. Western blot analysis was performed with total cellular extracts using the indicated antibodies. GAPDH was used as a loading control. Results are representative of 2 independent experiments.





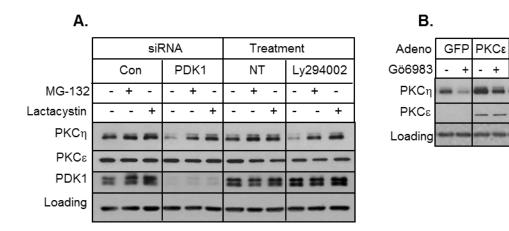
**Figure 4.** Effect of proteasome inhibitors on PKC $\eta$  downregulation. A, MCF-7 cells were pretreated with 10 µM MG-132 for 30 min, followed by treatment with 1 µM Gö 6983 or 25 µM Ly294002 for 12 h. Western blot analysis was performed with total cellular extracts using the indicated antibodies. 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 +/- s.e.m. The asterisk (\*) indicates significant difference of MG-132 treated cells from control or treatment with the inhibitors alone using Student's *t*-test. \*, *P*<0.05; \*\*, *P*<0.005 C, T47D cells were pretreated with 10 µM MG-132 or 10 µM lactacystin for 30 min, followed by treatment with 1 µM Gö 6983 or 10 µM Ly294002 for 15 h. Western blot analysis was performed with total cellular extracts using the indicated antibodies. Actin was used as a loading control.

Figure 4.



**Figure 5.** Effect of PDK1 and PKC $\varepsilon$  on PKC $\eta$  downregulation. A, MCF-7 cells were transfected with control non-targeting siRNA, PDK1 siRNA or were left non-transfected (NT). Cells were then pre-treated with either 10  $\mu$ M MG-132 or 10  $\mu$ M lactacystin, followed by treatment with 25  $\mu$ M Ly294002. Western blot analysis was performed with indicated antibodies. Actin was used as a loading control. B, T47D cells were infected with adenovirus vector containing GFP or PKC $\varepsilon$  construct and then treated with 1  $\mu$ M Gö 6983 for 15 h. Western blot analysis was carried out with indicated antibodies.



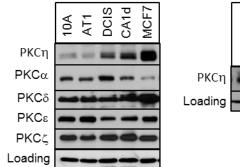


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**Figure 6.** Comparison of PKC $\eta$  levels in MCF10A series. A, Western blot analysis was performed with total cellular extracts from 10A, AT1, DCIS, CA1d and MCF-7 cells and probed with the indicated antibodies. B, CA1d cells were treated with or without 1  $\mu$ M Gö 6983 or 25  $\mu$ M Ly294002 for 16 h. Western blot analysis was performed with total cellular extracts using the indicated antibodies. Actin was used as a loading control.

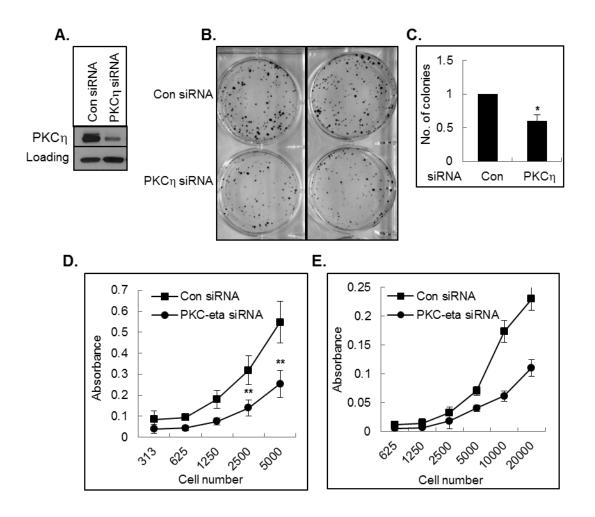
## Figure 6.





**Figure 7.** Effect of PKC $\eta$  on cell growth. A, MCF-7 cells were transfected with control nontargeting siRNA or PKC $\eta$  siRNA and total cell extracts were used for Western blot analysis. Actin was used as a loading control. B, Clonogenic assay was performed with MCF-7 cells transfected with either control non-targeting siRNA or PKC $\eta$  siRNA as described in the Materials and Methods. C, Quantification of the number of colonies as determined by the clonogenic assay. The results are representative of 3 independent experiments. \**P* < 0.05 using paired Student *t* test. D, MTT assay was performed with T47D cells transfected with control, non-targeting siRNA or PKC $\eta$  siRNA as described under Materials and Methods. The results are representative of 3 independent experiments. \**P* < 0.01 using paired Student *t* test. E, MTT assay was performed with DCIS cells transfected with control non-targeting siRNA or PKC $\eta$ siRNA as described under Materials and Methods.

Figure 7.



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#### **CHAPTER IV**

#### SUMMARY

The development of effective therapeutics for breast cancer warrants a comprehensive understanding of the signaling pathways that are deregulated in breast cancer. PKCs have served as attractive targets for cancer therapy for decades owing to their crucial roles in several cellular processes (1, 2). However, the selective targeting of PKCs has been difficult due to the diverse functional responses of individual PKC isozymes and their complex signaling. PKC $\eta$  is a novel PKC isozyme that is overexpressed in breast cancer (3) and has been implicated in chemotherapeutic resistance (4-7). Thus far, there has been limited understanding of the regulation of PKC $\eta$  in breast cancer.

Findings from our study reveal that the regulation of PKCη is unique. While PKCs serve as receptors for tumor promoting phorbol esters which are potent activators of PKCs (2), persistent activation of PKCs leads to their downregulation and subsequent degradation (8, 9). We have shown that in contrast to other PKC isozymes, PKCη is the only isozyme that resists phorbol ester-induced downregulation and is upregulated by several structurally and functionally distinct PKC activators.

Our results further suggest that PKCn is upregulated at the post-transciptional level, and the PKC activator-induced upregulation of PKC<sub>1</sub> correlates with its phosphorylation status. Since, PKCs can undergo transphosphorylation by PDK1 or by other members of the PKC family (9, 10); we speculated the role of these kinases in the regulation of PKCy. We found that PKCy is transphosphorylated by PDK1 and novel PKCs, especially PKC but not by conventional PKCs. Moreover, PDK1 and nPKCs had distinct effects on PKCy regulation. While transphosphorylation of PKCn by novel PKCs was responsible for activator-induced upregulation of PKC<sub>1</sub>, PDK1 affected PKC<sub>1</sub> basally and had no effect on the upregulation of PKC<sub>1</sub> by activators. While we have shown that PKC<sub>2</sub> is involved in PKC<sub>1</sub> upregulation, the mechanism of their interaction remains to be understood. Since both PKCn and PKCE localize to the Golgi (11, 12), it is possible that their Golgi translocation drives their interaction. Besides PKC isozymes, other kinases and chaperone proteins have also been implicated in the regulation of novel PKCs (13, 14). Future studies should help discern the role of these proteins in the regulation of PKCy. Moreover, potential autophosphorylation sites were identified in the structure of PKCn (15); hence, it is plausible that upon activation by PKC activators, PKCn can mediate autophosphorylation culminating in its upregulation.

We also made a novel observation that inhibition of PDK1 or nPKCs led to PKCn downregulation via two different mechanisms. While inhibition/knockdown of PDK1 caused PKCn downregulation via the proteasomal pathway, the downregulation of PKCn caused by the depletion of PKCc or by nPKC inhibitors was independent of the proteasome-mediated pathway.

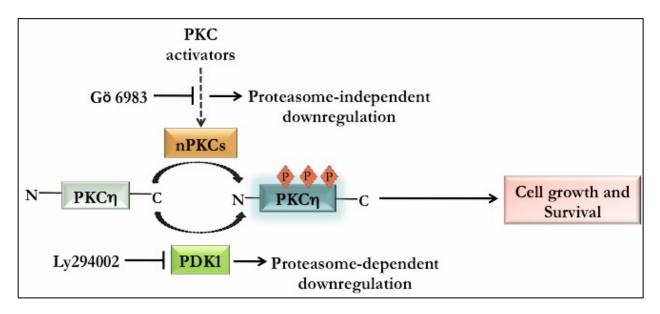
Upon examining the functional consequences of PKC $\eta$  downregulation in breast cancer cells, we found that PKC $\eta$  knockdown led to a significant decrease in the growth and survival of breast cancer cells. We further demonstrated that the levels of PKC $\eta$  increased with the aggressiveness

of breast cancer in the progressive MCF10A series. This progressive increase in protein levels with increased malignancy was not observed with the other PKC isozymes. Taken together, these results implicate PKC $\eta$  in the regulation of growth and survival of breast cancer cells. It would thus be worthwhile to identify novel targets of PKC $\eta$  which mediate its role in breast cancer.

We have shown that PKC $\eta$  levels are regulated by PDK1 and PKC pathways, both of which are critical for breast cancer development and progression (16-18). It has been previously reported that PKC $\eta$  plays a crucial role in the regulation of tight junctions (19). Loss of integrity in the tight junction structure leads to invasion and eventually cancer metastasis (20). These reports coupled with our observation that PKC $\eta$  levels correlate with breast cancer aggressiveneness implicates PKC $\eta$  in breast cancer progression. This suggests the possible use of PKC $\eta$  as a prognostic biomarker for breast cancer. Consistent with our *in vitro* findings, another study reported that invasive tumors associated with significant lymph node metastases maintained high levels of PKC $\eta$  thereby implicating PKC $\eta$  in distal invasion (3). Contrary to this, decreased PKC $\eta$  expression was observed in invasive breast tumor tissues compared to the surrounding normal epithelium suggesting that PKC $\eta$  is decreased during breast cancer progression (3). Thus, the role of PKC $\eta$  in progression of breast cancer cell growth, future studies focused on cell migration and invasion should help discern the role of PKC $\eta$  in breast cancer progression.

While our work has focused on the post-transcriptional mechanism of PKC $\eta$  regulation, the transcriptional control of PKC $\eta$  could also contribute to its role in cancer. The promoter region of PKC $\eta$  contains multiple binding sites for transcription factors which have been implicated in breast cancer proliferation and progression (21-23). Understanding the interplay of these transcription factors and PKC $\eta$  in breast cancer could yield interesting results.

Based on our findings, we propose a hypothetical model to account for the unique regulation of PKC $\eta$  (Figure 1). Phosphorylation of PKC $\eta$  by both PDK1 and nPKCs protect it from downregulation. Ly294002, a PI3K inhibitor, inhibits phosphorylation of PKC $\eta$  by PDK1 and leads to its downregulation via a proteasome-dependent pathway whereas Gö 6983, a general PKC inhibitor, inhibits nPKC-mediated phosphorylation of PKC $\eta$  making it susceptible to downregulation via a proteasome-independent pathway. We have further demonstrated that the regulation of PKC $\eta$  by PDK1 and PKC $\epsilon$  promotes breast cancer cell growth and survival. The unique regulation of PKC $\eta$  suggests that this pathway could be selectively targeted for breast cancer.



**Figure 1. Hypothetical model.** *PKC* $\eta$  is regulated by *PDK1* and *PKC* $\varepsilon$  which maintain *PKC* $\eta$  in a stable form thereby protecting it from degradation. Inhibition of *PDK1* by *Ly294002* leads to *PKC* $\eta$  downregulation via the proteasomal pathway while Gö 6983-mediated inhibition of *PKC* leads to *PKC* $\eta$  downregulation which is proteasome-independent. The upregulation of *PKC* $\eta$  by *PDK1* and *PKC* $\varepsilon$  contributes to the growth and survival of breast cancer cells.

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