

Protein Kinase C δ in Apoptosis: A Brief Overview

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Abstract Protein kinase C-delta (PKC δ), a member of the lipid-regulated serine/threonine PKC family, has been implicated in a wide range of important cellular processes. In the past decade, the critical role of PKC δ in the regulation of both intrinsic and extrinsic apoptosis pathways has been widely explored. In most cases, over-expression or activation of PKC δ results in the induction of apoptosis. The phosphorylations and multiple cell organelle translocations of PKC δ initiate apoptosis by targeting multiple downstream effectors. During apoptosis, PKC δ is proteolytically cleaved by caspase-3 to generate a constitutively activated catalytic fragment, which amplifies apoptosis cascades in nucleus and mitochondria. However, PKC δ also exerts its anti-apoptotic and pro-survival roles in some cases. Therefore, the complicated role of PKC δ in apoptosis appears to be stimulus and cell type dependent. This review is mainly focused on how PKC δ gets activated in diverse ways in response to apoptotic signals and how PKC δ targets different downstream regulators to sponsor or restrain apoptosis induction.

Keywords Protein kinase C-delta · Apoptosis · Signaling molecules

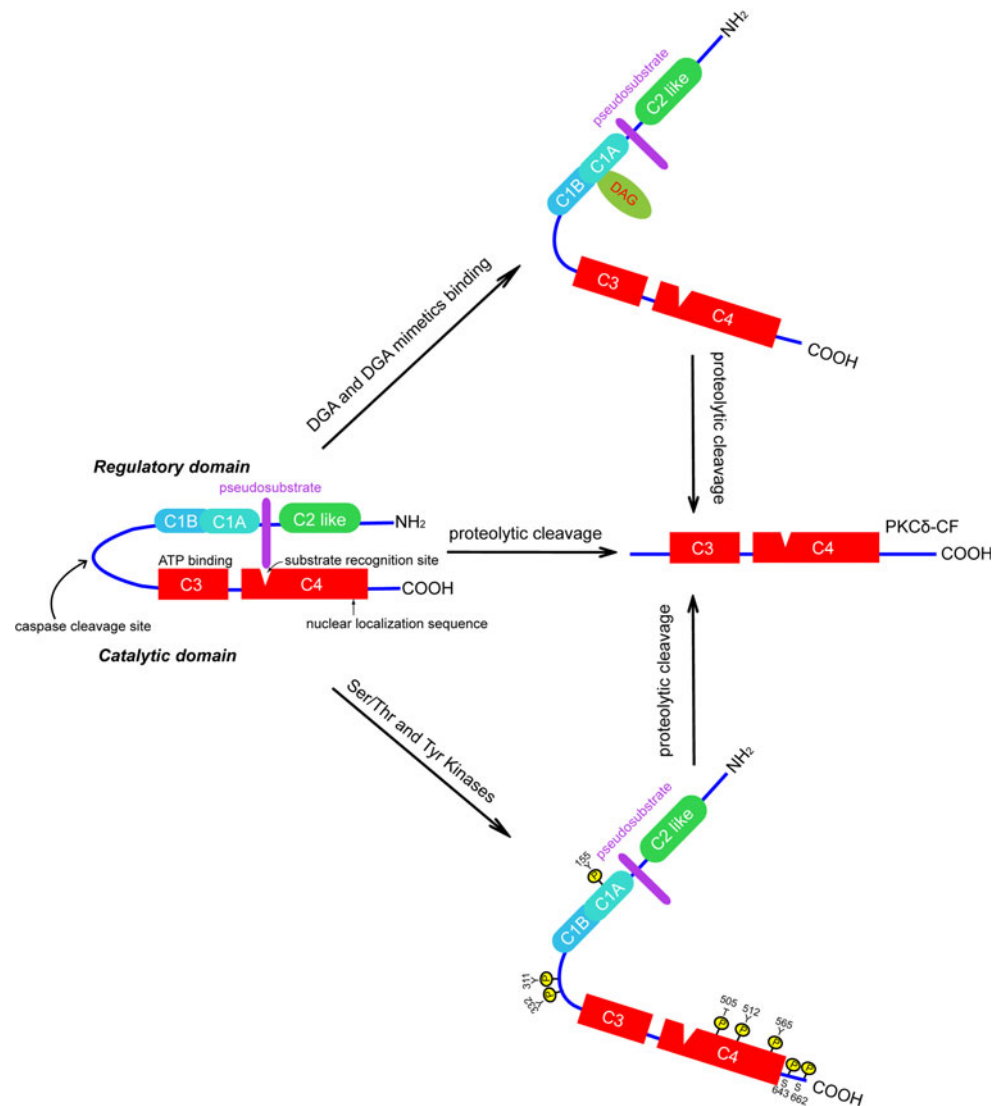
Introduction

Protein kinase C (PKC) is a family of serine/threonine protein kinase which plays key roles in cell proliferation and apoptosis. Over 26,000 research articles have been published on PKCs in the past decade. According to their domain structures and regulation mechanisms, a dozen subspecies in PKC family are classified into three subgroups: conventional PKCs (cPKC), novel PKCs (nPKC), and atypical PKCs (Bertram and Ley 2011). Protein kinase C-delta (PKC δ) is the first identified member of the nPKC subfamily, which is calcium-insensitive but can be activated by diacylglycerol (DAG) or phorbol esters (Kikkawa et al. 2002). Unlike the other cell type-specific members of nPKC, PKC δ is ubiquitously expressed in mammalian tissues, including epidermis, placenta, uterus, brain, lung, hematopoietic system, and kidney (Leibersperger et al. 1991). PKC δ is composed of the N-terminal regulatory and the C-terminal catalytic domains, which are connected by a short link region (Fig. 1). The regulatory domain contains a C1 region and a C2-like region. The former region includes two cysteine-rich sequences (C1A and C1B) that are able to bind DAG and phorbol esters to trigger the activation of PKC δ . Mechanistically, DAG binding changes the configuration of PKC δ and hence exposes the substrate binding region, allowing the downstream signal transduction of PKC δ (Newton 2009). The C2-like region structurally resembles the calcium binding C2 motif of cPKC isoforms yet lacks the amino acids necessary for Ca²⁺ coordination. Consequently, the region is unable to trigger PKC δ activation in response to the increase of Ca²⁺ concentration. There is a pseudosubstrate motif between the C2-like and C1 regions, and this motif is believed to occupy the substrate recognition site in the catalytic domain. Therefore, the kinase is maintained in an inactive form until the

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Fig. 1 Diagram of the activation mechanisms of PKC δ . PKC δ binds to DAG and its mimetics or is phosphorylated by Ser/Thr and Tyr kinases, which changes the conformation and exposes the substrate binding site of PKC δ to get activated. PKC δ is proteolytically cleaved by caspase-3, which releases the catalytic fragment, a constitutively active form



conformational change is induced. The catalytic domain of PKC δ contains two conserved regions, C3 and C4, which are essential for the kinase activity and the binding of adenosine-5'-triphosphate (ATP)/substrate. The catalytic domain tails with a turn motif and a hydrophobic motif, which are important for the catalytic competence and binding interactions between PKC δ and its partners (Kikkawa et al. 2002). The hinge region harbors a caspase cleavage site. During apoptosis, caspase-3 proteolytically cleaves PKC δ into a 41-kDa catalytic fragment and a 38-kDa regulatory fragment. This has been confirmed both in vivo and in vitro (Ghayur et al. 1996), and thus the C-terminal catalytic fragment is released from inhibition of the N-terminal regulatory domain (Emoto et al. 1995, 1996).

PKC δ is activated by a variety of apoptosis stimuli such as DNA damaging agents, ultraviolet (UV) radiation, phorbol 12-myristate 13-acetate (PMA) and reactive

oxygen species (ROS) (Anantharam et al. 2002; Chen et al. 1999; Konishi et al. 2001; Majumder et al. 2001; Reyland et al. 1999; Song et al. 2005). In PKC δ null mice, the mitochondrial functions are compromised, which caused more ROS generation and a shift from glucose to lipid metabolism in murine hearts (Mayr et al. 2004a, b), which indicated the role of PKC δ in mitochondria-related apoptosis. And in PKC δ null mice the smooth muscle cells were resistant to apoptosis induced by UV, tumor necrosis factor (TNF) α , or hydrogen peroxide (Leitges et al. 2001), whereas embryonic fibroblasts (MEFs) cells were resistant to UV radiation-induced G₂/M arrest, Cdk1 phosphorylation, and apoptosis (LaGory et al. 2010). Loss of PKC δ also protected salivary glands against γ -irradiation-induced apoptosis in vivo (Humphries et al. 2006). Furthermore, it has been verified that the overexpression of PKC δ catalytic fragment alone was sufficient to induce apoptosis (DeVries et al. 2002; Leverrier et al. 2002; Zhao et al. 2009). These

studies clearly demonstrated the pro-apoptotic role of PKC δ in vivo in response to diverse apoptotic stimuli. In addition, this pro-apoptotic role of PKC δ has also been proved by the apoptosis inhibition functions of dominant-negative PKC δ mutant, chemical inhibitor as well as RNAi against PKC δ in different cell types (Fujii et al. 2000; Gonzalez-Guerrico and Kazanietz 2005; Song et al. 2005). Recently, Kim et al. (2011) identified another alternative splice form of PKC δ which lacks the N-terminal regulatory domain and the ATP binding region and thus functions as a natural inhibitor to reduce PKC δ -induced apoptosis. The activation of PKC δ in prostate cancer cells caused apoptosis via the release of death receptor ligands and the activation of the extrinsic apoptotic cascade (Gonzalez-Guerrico and Kazanietz 2005), which indicated the role of PKC δ in both intrinsic and extrinsic apoptosis pathways. Overall, these studies suggest the pro-apoptosis functions of PKC δ in diverse cell contexts and apoptosis stimuli. Conversely, it was reported that under TNF α induction, PKC δ targeted the nucleus and formed a complex with RelA/p65, which was important for NF κ B activity and the cell survival protection in response to TNF α (Lu et al. 2009). This review aims to provide an overview of PKC δ regarding regulation and function in response to apoptosis stimuli.

PKC δ Activation and Expression Regulation in Response to Apoptosis

PKC δ is a self-inhibited kinase, in which the substrate recognition site in C-terminal catalytic domain is occupied by a pseudosubstrate motif in N-terminal regulatory domain. PKC δ can be activated by multiple mechanisms, including binding of lipid second messenger DAG and its mimetics, phosphorylations, and proteolytic cleavage (Fig. 1). According to the three-dimensional structure of PKC δ C1 domain and phorbol ester complex, the binding of C1 domain with DAG or PMA forms a contiguous hydrophobic surface and promotes PKC δ binding to cell membranes (Thamilselvan et al. 2009; von Burstin et al. 2010; Zhang et al. 1995). In addition, the binding of C1 to DAG or PMA changes the conformation and exposes the catalytic domain of PKC δ , allowing the substrates to bind (Kanthasamy et al. 2003).

Several phosphorylation sites in PKC δ are modulated in cell type and stimulus specific manner, and thus have different contributions on PKC δ activation (Johnson et al. 1996). Three conserved serine/threonine residues have been identified in the C-terminal catalytic domain of PKC δ including Thr-505 in the activation loop, Ser-643 in the turn motif, and Ser-662 in the hydrophobic motif (Konishi et al. 2001; Newton 2001; Steinberg 2004). Ser-643 is an

auto-phosphorylation site and the site-directed mutation of Ser-643 markedly decreased PKC δ activity (Li et al. 1997). This phosphorylation site was activated in response to interferon (IFN) and PMA treatment (Zhao et al. 2004, 2005), as well as H₂O₂-induced apoptosis (Lee et al. 2005). The phosphorylation of Ser-662 is concomitant with Thr-505 phosphorylation (Le Good et al. 1998). However, serum starvation-induced Ser-662 phosphorylation was independently controlled by a pathway involving mammalian TOR (Parekh et al. 1999). Although Thr-505 did not affect the kinase activity of PKC δ in bacteria expressed recombinant protein (Stempka et al. 1997), its phosphorylation is believed to be important for PKC δ activation under PMA and other stimuli (Kambhampati et al. 2003; Li et al. 2005; Liu et al. 2010) and is required for the stability of PKC δ in embryonic stem cells mediated by the 3-phosphoinositide-dependent protein kinase-1 (Balendran et al. 2000). Moreover, the phosphorylation of Ser-662/Thr505 has also been detected in response to H₂O₂- or PMA-induced apoptosis (Konishi et al. 2001; Lee et al. 2005; Sabri et al. 2002).

PKC δ is the most efficiently tyrosine-phosphorylated kinase among the PKC family. Phosphorylations of Tyr-52, Tyr-64, Tyr-155, Tyr-187, Tyr-311, Tyr-332, Tyr-512, Tyr-523, and Tyr-565 have been identified in PKC δ . These phosphorylations are associated with tyrosine kinases such as Src, Fyn, Lyn, Abl, PYk2, and Lck (Kikkawa et al. 2002). The tyrosine phosphorylation context regulates the catalytic activity of PKC δ . For example, the tyrosine phosphorylations of PKC δ induced by Ras oncogene, transforming growth factor α , or epidermal growth factor in keratinocytes are associated with a reduction of PKC δ catalytic activity (Denning et al. 1993, 1996; Joseloff et al. 2002). Increasing number of studies has showed that the tyrosine phosphorylations are important for PKC δ translocation, activation, and downstream signal transduction (Kikkawa et al. 2002; Kronfeld et al. 2000). Tyr-64 and Tyr-155 phosphorylations in the N-terminal regulatory domain were important for the nuclear translocation and apoptosis induction in salivary epithelial cells (Humphries et al. 2008). Moreover, the translocation of PKC δ into the nucleus required C2 domain tyrosine phosphorylations, which were associated with Src kinase activity induced by G-protein-coupled receptor agonist uridine triphosphate (UTP) (Kajimoto et al. 2010). The etoposide-induced tyrosine phosphorylation of PKC δ also contributed to nuclear translocation and caspase-dependent cleavage of PKC δ . In addition, overexpressing PKC δ mutants in Tyr-64 and Tyr-187 lead to decreased apoptosis in response to etoposide compared to the overexpression of wild type PKC δ (Blass et al. 2002). Mutating Tyr-52, Tyr-155, and Tyr-565 to phenylalanine enhanced etoposide-induced apoptosis in glial cells; in contrast, the mutations of Tyr-64

and Tyr-187 to phenylalanine inhibited caspase-3-dependent PKC δ activation and reduced etoposide-induced apoptosis (Blass et al. 2002). In parallel, the tyrosine phosphorylations of PKC δ identified in ceramide-induced apoptosis also showed different functions. Ceramide, the basic structural unit of the sphingolipids, is an intracellular lipid second messenger (Senchenkov et al. 2001), and its accumulation is related to various apoptosis stimuli (Dbaiibo et al. 1998; Haimovitz-Friedman et al. 1994; Rotolo et al. 2005). Both chemical inhibitor and siRNA knock-down experiments support that PKC δ is important for ceramide-induced apoptosis in Hela cells, in which Tyr-311 and Tyr-332 phosphorylations were observed. However, the function of these phosphorylation sites in apoptosis induction could not be verified by site-directed mutations (Kajimoto et al. 2004; Kikkawa et al. 2002). No uniform pattern and consequence of PKC δ phosphorylations has been established from the published literature, because the catalytic activity of phosphorylated PKC δ is highly cell type and stimulus dependent as described above. One possible reason is that most studies relied on in vitro kinase assays to address the functional changes in PKC δ phosphorylations. It is predictable that more than one tyrosine phosphorylation would be generated simultaneously in vivo in response to stimulus. The phosphorylation context and the resulting conformational change determine the particular activity and function of PKC δ . Overall, it is believed that phosphorylation of the catalytic domain increases the kinase activity, whereas phosphorylation of the regulatory domain is associated with cellular actions of PKC δ (Steinberg 2004).

PKC δ can be activated by caspase-mediated proteolysis. Emoto et al. (1995) reported that PKC δ is proteolytically activated by cysteine protease caspase-1 also called interleukin-1 β converting enzyme in response to ionizing radiation-induced apoptosis. Thereafter, the proteolytic cleavage of PKC δ has been observed in various cell types in response to multiple apoptosis stimuli, including TNF α or Fas ligand and DNA damage agents, such as etoposide, cisplatin, camptothecin and UV, γ -radiation. Following studies showed that PKC δ is an endogenous substrate for caspase-3, and caspase-3 cleaves PKC δ at ³²⁴DILD³²⁷ in mouse, ³²⁴DIPD³²⁷ in rat, and ³²⁶DMQD³²⁹ in human. This process has been well reviewed previously (Brodie and Blumberg 2003; Kanthasamy et al. 2003; Kikkawa et al. 2002). After cleavage, the pseudosubstrate motif in the regulatory domain is released from the substrate recognition site of the catalytic domain, which enables PKC δ to become constitutively activated. This unique mechanism makes the activation of PKC δ irreversible. The conformational changes made by DAG binding and phosphorylation modifications are reversible, which hold PKC δ at a prime status for the auto-inhibition release and

downstream targeting. For example, CD45, a receptor-type tyrosine phosphatase, is shown to be involved in dephosphorylation of PKC δ (Deszo et al. 2001). However, when cells are destined for apoptosis, caspase-3-mediated proteolytic cleavage activates PKC δ in a one-way direction, and this amplified signal is more sufficient for apoptosis induction. This has been verified by the study which showed that overexpression of a caspase-resistant PKC δ mutant (D330A) protected keratinocytes from UV-induced apoptosis (D'Costa and Denning 2005). This is also supported by the observation that overexpression of PKC δ catalytic fragment alone was sufficient to induce apoptosis, and overexpression of PKC δ kinase dead mutants protected cells from apoptosis (DeVries et al. 2002; Zhao et al. 2009). In addition, the regulatory domain of PKC δ is also required for etoposide-induced apoptosis in C6 glioma cells (Blass et al. 2002). In contrast, the proteolytic cleavage of PKC δ also involved caspase-3-independent mechanisms, such as other caspases like caspase-2 which can also cleave PKC δ during apoptosis (Panaretakis et al. 2005). This is also supported by the study which proved the pro-apoptosis role of PKC δ in caspase-3 null MCF-7 cells in response to UV (Zeidan et al. 2008). Our study also showed that the proteolytic cleavage of PKC δ occurred prior to caspase-3 activation in a camptothecin analog-induced apoptosis (Song et al. 2005), indicating the function of PKC δ in an early stage of apoptosis.

Besides the kinase activation regulation, PKC δ expression also fluctuates during apoptosis. Sp protein transcriptionally up-regulates PKC δ , facilitating oxidative stress-induced apoptosis in neuron cells (Jin et al. 2011a). NF κ B P50/p60 forms a complex with p300 and α -synuclein and binds to PKC δ promoter. This complex down-regulated PKC δ and protected dopaminergic neuronal cells against oxidative stress-induced apoptosis (Jin et al. 2011b). After activation by DAG or 12-*O*-tetradecanoylphorbol-13-acetate (TPA), PKC δ was ubiquitinated and targeted to proteasome for degradation in rat fibroblasts (Lu et al. 1998). This negative feedback protects cells from the following apoptosis execution induced by PKC δ activation.

The Early Effect of PKC δ in Apoptosis Induction

Although activated caspase-3 has an amplifying effect on PKC δ proteolysis, in some cases PKC δ -mediated apoptosis does not involve its proteolytic cleavage by caspase-3. This suggests that allosteric activation of PKC δ is also sufficient to trigger apoptosis. For example, caspase-3-dependent cleavage of PKC δ was not required for the cell death in LNCap cells, CHO cells and HaCaT cells treated respectively with phorbol esters, UV and H₂O₂ (Fujii et al. 2000; Fukunaga et al. 2001; Konishi et al. 1997). Our group has

also demonstrated a positive feedback loop between caspase activation and PKC δ activation using that NSC606985, a rarely studied camptothecin analog, in leukemic model. Inhibition of PKC δ activity by chemical inhibitor rottlerin and later on by the overexpression of PKC δ dominant-negative mutant completely blocked NSC606985-induced mitochondrial $\Delta\Psi_m$ loss and caspase-3 activation, while the inhibition of caspase-3 by z-DEVD-fluoromethyl ketone only partially attenuated PKC δ activation and apoptosis (Song et al. 2005; Zhao et al. 2009). It is worthwhile to note that rottlerin, the widely used PKC δ inhibitor, has been shown to have many off-target effects (Davies et al. 2000; Soltoff 2007). So the results from this inhibitor raise the question if PKC δ is truly responsible for those observations, or the off-target effects on other pathways may influence the results. A more specific approach to inhibit PKC δ activity such as overexpression of dominant negative mutant or siRNA knock-down would be a better way to investigate the function of PKC δ . A number of studies showed that PKC δ is able to target mitochondria to initiate apoptosis (Lasfer et al. 2006; Liu et al. 2003a; Majumder et al. 2001). Moreover, the vascular smooth muscle cells isolated from PKC δ null mice were defective in caspase-3 activation in response to oxidative stress-induced apoptosis (Bowles et al. 2007; Kato et al. 2009). All these findings indicated that PKC δ activation could be an early event upstream of mitochondrial $\Delta\Psi_m$ loss and caspase-3 activation during apoptosis, whereas how PKC δ affects mitochondrial membrane potential during apoptosis requires further study. In other words, PKC δ is able to initiate apoptosis signals before caspase-3 activation or in a caspase-3-independent way, which was also supported by the fact that PKC δ increased autocrine release of death receptor ligands to trigger extrinsic apoptotic cascade (Gonzalez-Guerrico and Kazanietz 2005). On the contrary, PKC δ is able to activate caspase-3 and caspase-9 directly. PKC δ -phosphorylated caspase-3 and increased its activity during spontaneous monocyte apoptosis and in monocyte-induced apoptosis (Voss et al. 2005). The role of PKC δ in the activation of caspase-9 was demonstrated in response to etoposide, taxol, and UV radiation (Matassa et al. 2001), possibly via the activation of AKT pathway (Cardone et al. 1998; Martins et al. 1998). Moreover, the phosphorylation of PKC δ may function before the proteolytic cleavage of PKC δ to initiate the apoptotic cascade. The phosphorylations of PKC δ on Tyr-64/187 are regarded to be essential for the cleavage of PKC δ by caspase-3 and the pro-apoptotic effect of PKC δ in response to etoposide treatment (Blass et al. 2002), while the phosphorylations of PKC δ on Tyr-52/64/155 are associated with the anti-apoptotic effect of PKC δ in response to Sindbis virus-induced glioma cell death (Zrachia et al. 2002).

PKC δ in Mitochondria and Apoptosis

Another feature of PKC δ during apoptosis is the multi-subcellular organelle translocations. In response to diverse apoptosis stimuli, PKC δ is localized in almost all the subcellular organelles, including mitochondria, nucleus, cell membrane, Golgi apparatus, endoplasmic reticulum (ER), and recently reported lysosomes. Those subcellular translocalizations of PKC δ are cell type and apoptotic stimulus dependent, which indicates that the downstream targets of PKC δ are distributed among different subcellular organelles for apoptosis induction.

The first well-studied subcellular organelle targeted by PKC δ in apoptosis is mitochondria, which is the apoptosis signal integrator (Brenner and Kroemer 2000). In PMA-induced apoptosis, the mitochondrion translocation of the endogenous and ectopic-expressed PKC δ was found in U937 cells (Majumder et al. 2000) and mouse keratinocyte SP-1 cells (Li et al. 1999). A similar translocation of PKC δ has also been shown in oxidative stress- and DNA damage agents-induced apoptosis (Majumder et al. 2001). Recently, it was reported that the expanded AUUCU repeated intronic RNA within ATXN1, the major pathogenic mechanism of spinocerebellar ataxia type 10 (SCA10), strongly bound to heterogeneous nuclear ribonucleoprotein K (hnRNPK) facilitating massive translocation of PKC δ to mitochondria and activation of caspase-3 in SCA10 cells (White et al. 2010).

Several targets of PKC δ in mitochondria during apoptosis have been reported. PKC δ enhanced ceramide formation in mitochondria in prostate cancer cells during multi anti-cancer drug treatment, which stimulated cytochrome *c* release and caspase-9 activation (Sumitomo et al. 2002). PKC δ also targeted phosphorylated phospholipid scramblase 3, which is a critical regulator of mitochondrial structure and respiration, in UV radiation or PMA treated Hela and HEK293 cells (Liu et al. 2003a, b). More interestingly, it was found that PKC δ directly phosphorylated myeloid cell leukemia protein 1 and promoted its proteolytic degradation during UV-induced apoptosis (Sitailo et al. 2006). In response to DNA damage, PKC δ associated with checkpoint protein Rad9 to target Bcl-2 and facilitated apoptosis (Yoshida et al. 2003). Moreover, the active form of PKC δ stimulated the up-regulation and activation of Bax in response to UV radiation (Sitailo et al. 2004). In addition, PKC δ has been shown to be related to the dephosphorylation of BAD (Murriel et al. 2004). Recently another PKC δ mitochondrial target Drp1, a major mitochondrion fission protein, has been identified in SH-SY5Y neuronal cells. PKC δ phosphorylated Drp1 at Ser 579 and facilitated Drp1 translocation to mitochondria under oxidative stress, thus increasing mitochondrial fragmentation, which is associated with apoptosis (Frank

et al. 2001; Qi et al. 2011). Overall, those studies prove the existence of a positive feedback loop between caspase activation and PKC δ which in turn triggers more caspase activation. Our report showed that the cleavage of PKC δ prior to caspase-3 and block of caspase-3 activity only partially blocked PKC δ activation (Song et al. 2005). This indicated that PKC δ may trigger apoptosis initiating signals in mitochondria prior to caspase-3 activation. In addition, over-expression of kinase inactive mutant PKC δ instead of the wild type failed to target mitochondria and was not able to induce apoptosis in salivary epithelial cells (Matassa et al. 2001). This indicated that the kinase activity of PKC δ is essential for the apoptosis initiation signals in mitochondria.

PKC δ in Nucleus and Apoptosis

The nucleus translocation of PKC δ to amplify apoptosis process has been reported in a wide range of cells in response to various apoptosis stimuli (Blass et al. 2002; DeVries et al. 2002; Scheel-Toellner et al. 1999; Yuan et al. 1998). In particular, the proteolytically cleaved catalytic fragment (PKC δ -CF) has been found to be dominantly localized in nucleus (Blass et al. 2002; DeVries et al. 2002) due to the following mechanisms. First, a nucleus import sequence of PKC δ is identified in the catalytic fragment of PKC δ , which partially explains the dominant localization of PKC δ -CF in nucleus during apoptosis. Furthermore, using site direct mutation DeVries et al. (2002) proved that this nucleus import sequence is necessary for the pro-apoptosis role of PKC δ and only nuclear, but not cytoplasmic, expression of PKC δ dominant-negative mutant inhibits etoposide-induced apoptosis. Second, it was reported that full-length PKC δ also transiently accumulates in the nucleus and is cleaved by activated caspase-3 in response to apoptotic signals (DeVries-Seimon et al. 2007), which has also been verified by the reports that the tyrosine phosphorylation of PKC δ preceded caspase-3 cleavage and was important for PKC δ nuclear accumulation (Blass et al. 2002; Humphries et al. 2008). These indicate that PKC δ -CF is at least partially generated in nucleus during apoptosis.

Accumulating nuclear targets have been identified and most of them function in apoptosis, such as DNA-dependent protein kinase (Bharti et al. 1998), lamin B (Cross et al. 2000), and Rad9 (Yoshida et al. 2003). For example, PKC δ interacted with topoisomerase II α and attenuated DNA damage-induced activation of topoisomerase II α and apoptosis (Yoshida et al. 2006a). It was also shown that PKC δ interacted with and phosphorylated P53 at Ser-15 and Ser-46, which potentiated p53-dependent apoptosis in response to genotoxic stress in MCF-7 and HEK293T cells

as well as nitric oxide-induced apoptosis in dopaminergic cells (Lee et al. 2006; Yoshida et al. 2006b). Ecotropic viral integration site 1 and promyotic leukemic zinc finger, which are associated with DNA damage-induced apoptosis, also have been identified as PKC δ targets (Hew et al. 2011).

Our recent studies demonstrated that PKC δ is involved in proteasome-dependent degradation of nuclear proteins, which contributed to PKC δ -mediated apoptosis. First, we reported that during apoptosis induction of leukemic cells, PKC δ was able to stimulate proteasome-dependent degradation of CCAAT/enhancer-binding protein α (C/EBP α), a key regulator of differentiation and proliferation in various cell types. More importantly, ectopic expression of PKC δ -CF stimulated the ubiquitination of C/EBP α protein, while the chemical inhibition or over-expression of PKC δ dominant-negative mutant significantly suppressed the ubiquitination of C/EBP α protein under apoptosis induction. In addition, the anti-apoptotic function of C/EBP α has also been proved by siRNA silencing and inducible over-expression in leukemic cells (Zhao et al. 2009). More interestingly, we found another nuclear protein, hnRNP K protein, which was also down-regulated by PKC δ in the proteasome-dependent manner (Gao et al. 2009). Although we are still working on whether PKC δ directly phosphorylates C/EBP α and hnRNP K, these studies suggest that PKC δ may affect the ubiquitin–proteasome machinery, which is important for the control of apoptosis induction (Xie 2010).

PKC δ in Other Cell Organelles and Apoptosis

The diverse and varied subcellular localization patterns of PKC δ in apoptosis make PKC δ more intricate. The cell membrane translocation of PKC δ was observed in UV radiation and PMA stimulation in various cell types (Chen et al. 1999; Hendey et al. 2002; Park et al. 2009; von Burstin et al. 2010). Using membrane-targeted PKC δ construct, this peripheral localization of PKC δ has been shown to be required for apoptosis initiation (von Burstin et al. 2010). Recently, a new approach to detect the spatial and temporal PKC δ activation was developed by Kajimoto et al. (2010). Using this Fluorescence resonance energy transfer-based new reporter technology, they observed that phorbol esters triggered fluorescence at the plasma membrane and also in small amounts in the Golgi apparatus and mitochondria in a Src-independent manner (Kajimoto et al. 2010). In parallel, the translocations to ER and Golgi apparatus have also been reported in response to apoptotic signal (Kajimoto et al. 2001; Zrachia et al. 2002). The PKC δ tyrosine phosphorylation and ER translocation were associated with the complex formation between PKC δ and

tyrosine kinase Abl, which was required for ER-stress-mediated apoptosis. Accordingly, the chemical inhibitor rottlerin blocked the translocation of the PKC δ –Abl complex from the ER to the mitochondria and conferred protection against apoptosis, which indicated that the PKC δ –Abl complex is important for the communication between ER and mitochondria in apoptosis response (Qi and Mochly-Rosen 2008). Also, another ER protein P23 (Tmp21) was found to interact with PKC δ and retain PKC δ in the ER. This limited the activation and pro-apoptotic function of PKC δ in LNCaP cells (Wang et al. 2011). Recently, the lysosomal translocation of PKC δ has been reported in camptothecin lactone (CPT)-treated U937 cells. It was shown that PKC δ targeted lysosomal acidic sphingomyelinase to increase ceramide content, inducing the labilization of lysosomal membranes and activating lysosomal pathway of apoptosis under CPT treatment (Parent et al. 2011). Translocation of PKC δ to Golgi apparatus was found under ceramide or IFN γ stimulus (Kajimoto et al. 2004). This translocation was associated with PKC δ tyrosine phosphorylation, but whether it is related to apoptosis induction is still not clear (Kajimoto et al. 2004).

Other PKC δ -Related Downstream Signals During Apoptosis

It has been well studied that STAT1 activation under IFN stimulation is dependent on the signal transduction between PKC δ and c-Jun NH₂-terminal kinase (JNK) (Zhao et al. 2005). In response to apoptosis induction, the JNK/STAT1 pathway has been proven as a functional downstream target of PKC δ contributing to apoptosis. When cells were treated with PMA or etoposide, JNK kinase was activated in a PKC δ -dependent manner. Blocking PKC δ by the chemical inhibitor rottlerin significantly inhibited JNK activation, and suppressing the JNK pathway also reduced PKC δ -related galectin-1-induced T cell apoptosis (Brandt et al. 2010) and arsenic-induced hepatic cell death (Das et al. 2010). JNK was activated by PKC δ possibly through MKK7 (MAPK kinase 7) during DNA damage–response (Yoshida et al. 2002). At the bottom of PKC δ –JNK signal pathway, STAT1 transactivation has also been proven to be important for PKC δ -related apoptosis. Etoposide treatment resulted in PKC δ -dependent phosphorylation of STAT1 on ser-727 in HeLa cells, and PKC δ -induced apoptosis was suppressed in STAT1 deficient U3A cells (DeVries et al. 2004). All this evidence indicates that PKC δ –JNK–STAT1 might be a major signal pathway for apoptosis inducing role of PKC δ .

Directly targeting or not, activated PKC δ also affects other signaling cascades in apoptosis regulation, including PI3-kinase/AKT pathway (Murriel et al. 2004), extracellular

signal-regulated kinase (ERK), and P38 pathway (Efimova et al. 2004; Lee et al. 2002). For example, PKC δ formed a complex with ShcA to induce phosphorylation of ERK in MEF cells in response to H₂O₂-induced apoptosis (Hu et al. 2007). Recently serine/threonine kinase vaccinia-related kinase 1 (VRK1) was identified as a PKC δ target. PKC δ activated VRK1 and P53 in nucleus, thus was involved in DNA damage-induced apoptosis (Park et al. 2011).

Conclusions and Future Perspectives

The mechanisms by which PKC δ regulate apoptosis as illustrated in Fig. 2 still remain elusive. A positive loop between mitochondrial-mediated caspase activation and PKC δ cleavage and activation supported the pro-apoptotic role of PKC δ in cytoplasm. The nucleus may be another major target for PKC δ to amplify apoptosis signal. The nucleus translocation of PKC δ has been proven to be essential for apoptosis induction, and the proteolytically cleaved constitutive active catalytic fragment of PKC δ accumulates in nucleus (DeVries et al. 2002). Therefore, more and more studies are revealing new nuclear targets of PKC δ , including the recently identified C/EBP α and hnRNPK (Gao et al. 2009; Zhao et al. 2009) which function in apoptosis. PKC δ is an early and essential regulator of apoptosis in diverse cell types and under various stimuli. For example, PKC δ functions upstream of the mitochondria as an integrator for various death signals, and the cytoplasm-localized PKC δ may function at the initial stage of apoptosis. Phosphorylations, especially the tyrosine phosphorylations of PKC δ , which usually occur at the beginning of apoptosis, are responsible for its translocations to cell membrane, mitochondria, ER, and lysosome. However, a detailed understanding of the intracellular actions of PKC δ will require the knowledge of their distinct cellular substrates in response to apoptosis.

Although some kinase signals have been proven to activate PKC δ at an early stage of apoptosis, the exact mechanisms are still largely unknown. In order to address this question, we performed quantitative proteomic analysis before PKC δ activation under NSC606985 treatment in U937 cells and found that over 30 proteins are regulated. The down-regulation of NDRG1 was proved to be involved in proteolytic activation of PKC δ during apoptosis induction (Zheng et al. 2009). Yet, it is still difficult to identify the direct effectors which initiate PKC δ activation during apoptosis. Using a structural or functional approach to identify PKC δ complex and the interaction binding sites in PKC δ would be a more practical way. Addressing all the above queries will lead to a thorough understanding of how the complex interactions retain PKC δ in the cytoplasm or translocate PKC δ into other

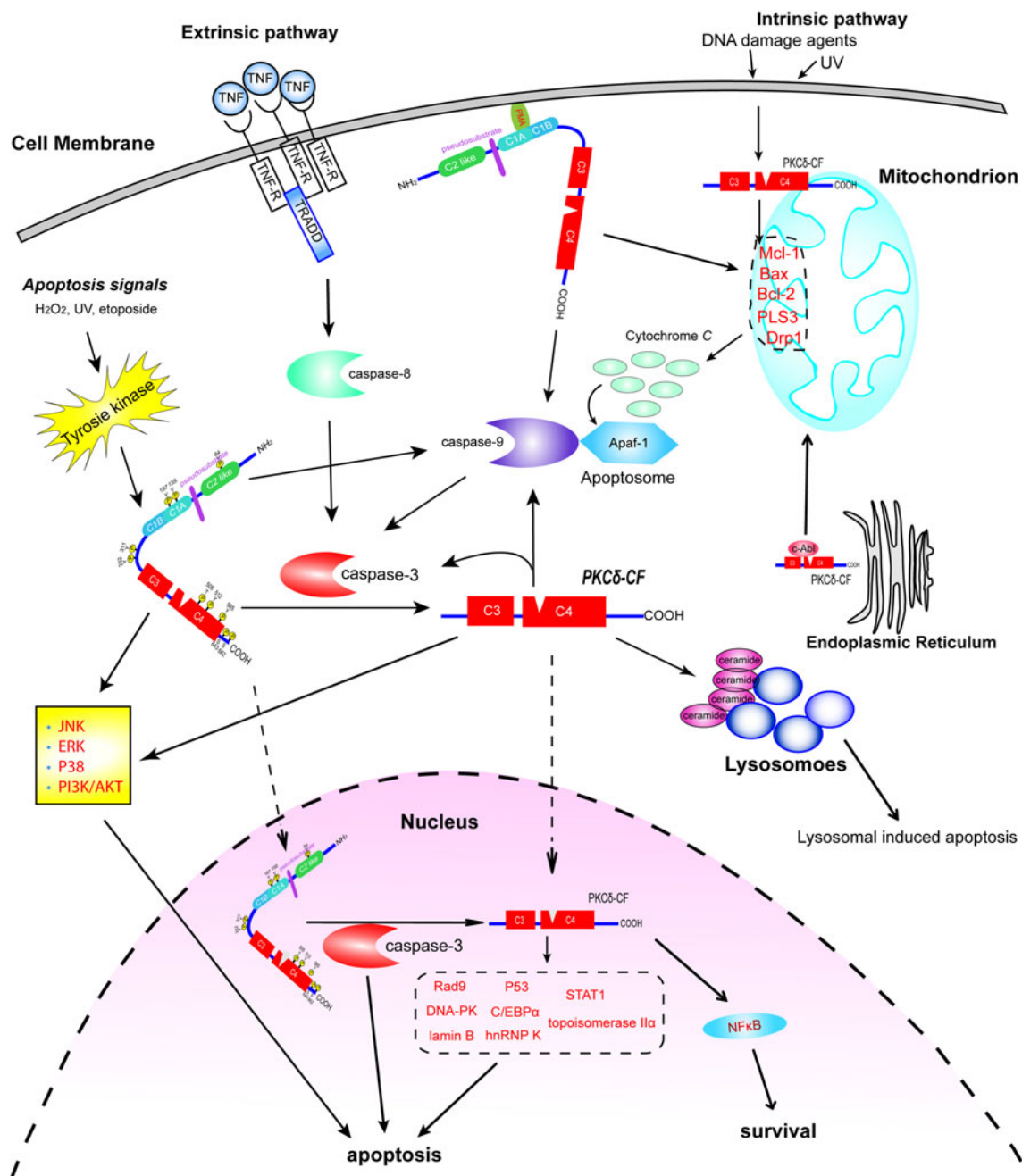


Fig. 2 Major PKC δ signals in response to apoptosis. Death receptor apoptosis signal triggers activation of caspase-8, which in turn prompts caspase-3 activation and then initiates proteolytic cleavage of PKC δ . In parallel, the intrinsic apoptosis signals from mitochondria release Cytochrome *c*, active caspase-9 and Apaf-1 to form apoptosome and then trigger the activation of caspase-3, which initiates the proteolytic cleavage of PKC δ . The PKC δ with PMA binding on cell membrane functions on apoptosome to facilitate apoptosis. The cleaved PKC δ constitutively active fragment (PKC δ -CF) feeds back on caspase-3 and caspase-9 to amplify apoptosis. Moreover, PKC δ -CF translocates into (1) mitochondria to enhance the intrinsic apoptosis signal, (2) endoplasmic reticulum to form complex with c-Abl and communicate with mitochondria to enhance intrinsic

apoptosis signal, (3) lysosomes to increase the accumulation of ceramide and then initiate the lysosomal-induced apoptosis, (4) nucleus to target the downstream effectors and induce apoptosis. On the other hand, the activated PKC δ in nucleus targets NF κ B to induce survival signals. In addition, apoptosis agents such as H₂O₂, UV, or etoposide activate tyrosine kinases which phosphorylate PKC δ , targeting either apoptosome or other kinase such as PI3K or MAP kinase to induce apoptosis. Furthermore, the phosphorylated PKC δ translocates into different cell organelles including nucleus and is proteolytically cleaved by caspase-3. *TNF* tumor necrosis factor, *TNF-R* TNF receptor, *TRADD* TNF-R-associated death domain, *DNA-PK* DNA-dependent protein kinase

organelles and initiate PKC δ activation at the early stages of apoptosis.

The ability to evade apoptosis is a common feature of cancer, and genetic disruptions of the apoptotic pathway are responsible for neoplasia. As an initiator of apoptosis, PKC δ is suspected as a tumor suppressor gene, and some PKC δ -targeted molecules have shown significant apoptosis induction ability in vitro and in vivo (Hampson et al. 2005; Liu et al. 2007; Podar et al. 2007). However, in some cases PKC also enhanced tumorigenesis, evidenced by that PKC δ deficient mice were protected from urethane-induced lung tumor (Symonds et al. 2011). Maybe this is not related to the pro-apoptotic function of PKC δ . Therefore, elucidating the role of PKC δ in tumor development and therapy would be another promising research direction.

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