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# Molecular mechanisms of PKC[delta] in neurotoxin-induced apoptotic death of nigral dopaminergic neurons: relevance to the pathogenesis of Parkinson's disease

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**Molecular mechanisms of PKC $\delta$  in neurotoxin-induced apoptotic death**

**of nigral dopaminergic neurons:**

**Relevance to the pathogenesis of Parkinson's disease**

by

**Yongjie Yang**

A dissertation submitted to the graduate faculty  
in partial fulfillment of the requirements for the degree of

**DOCTOR OF PHILOSOPHY**

Co-majors: Neuroscience; Genetics

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2005

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**ABSTRACT**

We investigated the molecular role of the delta isoform of protein kinase C (PKC $\delta$ ) in toxicity induced by the Parkinsonian toxin MPP<sup>+</sup>. We also examined the role of PKC $\delta$  in apoptotic death induced by the potential Parkinson's disease (PD) risk factor dieldrin in rat mesencephalic dopaminergic neuronal (N27) cells and in the primary mesencephalic neuronal model. Both the protein and mRNA levels of PKC $\delta$  were selectively higher in the dopaminergic neurons in the substantia nigra (SN) region as compared to the cortex, brainstem, and striatum regions of rodent brains. PKC $\delta$  protein co-localized with tyrosine hydroxylase (TH), the rate-limiting enzyme responsible for dopamine synthesis in dopaminergic neurons. siRNA designed against PCK $\delta$  effectively silenced the expression of PKC $\delta$  and reduced dieldrin or MPP<sup>+</sup>-induced apoptotic death of N27 cells and degeneration of primary dopaminergic neurons. Following dieldrin exposure in (N27) cells, we determined that the full-length PKC $\delta$  is first cleaved in the cytoplasm, and the activated PKC $\delta$  catalytic fragment subsequently translocates into the nucleus. The caspase-3 specific inhibitor (Z-DEVD-FMK), the cleavage resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM), as well as the nuclear localization signal (NLS) deletion mutant of PKC $\delta$  (PKC $\delta$ - $\Delta$ NLS) all abolished the nuclear translocation of activated cleaved PKC $\delta$ . The proteolytic activation of full-length PKC $\delta$  and subsequent nuclear translocation of activated cleaved PKC $\delta$  are integral events required for PKC $\delta$ 's pro-apoptotic function in apoptotic death of dopaminergic neuronal cells. Blockade of proteolytic activation of endogenous PKC $\delta$  by PKC $\delta$ -CRM also protected primary mesencephalic dopaminergic neurons from MPP<sup>+</sup>-induced degeneration. Moreover, we demonstrated that activated cleaved PKC $\delta$  mediates Ser14 phosphorylation of histone

H2B followed by its nuclear translocation in apoptotic dopaminergic neuronal cells. Ser14 phosphorylation of H2B and apoptosis can also be directly induced by the catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF), but not by the regulatory fragment of PKC $\delta$  (PKC $\delta$ -RF), PKC $\delta$ -CRM, PKC $\delta$ - $\Delta$ NLS, or the dominant-negative mutant of PKC $\delta$  (PKC $\delta$ -DN). Transfection of PKC $\delta$ -CF also directly induced degeneration of primary mesencephalic dopaminergic neurons while PKC $\delta$ -RF-transfected primary neurons remained intact. In addition, we also demonstrated that the N- and the C-terminals of PKC $\delta$  are in close proximity in the tertiary structure, as demonstrated by fluorescence resonance energy transfer (FRET). By employing the C1 or C2-like domain deletion mutant of PKC $\delta$  (PKC $\delta$ - $\Delta$ C1 or PKC $\delta$ - $\Delta$ C2), we showed that deletion of the C2-like domain, but not the C1 domain, induces strong nuclear localization of PKC $\delta$ . The exogenously expressed catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF) also primarily localizes to the nucleus. Sequence analysis of the C2-like domain reveals a possible leucine-rich nuclear export signal (NES); however, the C2-like domain is not sensitive to the nuclear export inhibitor leptomycin B (LMB), suggesting that this leucine-rich motif is not a functional NES. Moreover, the C2-like domain alone was fused to the N-terminal of a NES mutated form of Rev protein, the RNA binding protein of Equine Infectious Anemia Virus (EIAV), to generate the Rev chimera. Interestingly, the Rev chimera with the C2-like domain is still primarily localized in the nucleus. Thus, the N-terminal C2-like domain apparently regulates the subcellular localization of PKC $\delta$  by masking the C-terminal NLS through the position obstacle in the tertiary structure, but not through NES or interaction with anchoring proteins. Taken together, our studies show that i) the novel PKC isoform family member PKC $\delta$  is highly expressed in nigral dopaminergic neurons, ii) PKC $\delta$  mainly



localizes in the cytoplasm by the position obstacle effect of the C2-like domain to the NLS, iii) neurotoxin exposure induces proteolytic activation of full-length PKC $\delta$  and subsequent nuclear translocation of the PKC $\delta$  cleaved fragment to cause histone H2B phosphorylation and apoptotic cell death, and iv) RNAi mediated suppression of PKC $\delta$  protects dopaminergic neurons against neurotoxic insults.

## CHAPTER I: GENERAL INTRODUCTION

### Dissertation Organization

This dissertation is written in an alternative dissertation format. It contains a general introduction, four research papers, a general conclusion, and an acknowledgement. The list of references cited is included at the end of each chapter. Chapter I, the general introduction, includes research objectives, background and literature review of my research subjects. Chapter II, "Suppression of caspase-3 dependent proteolytic activation of Protein Kinase C  $\delta$  by small interfering RNA (siRNA) prevents MPP<sup>+</sup>-induced dopaminergic degeneration," has been published in *Molecular and Cellular Neuroscience* (**25**: 406-421, 2004). Chapter III, "Proteolytically activated PKC $\delta$  translocates to the nucleus and mediates Ser14 phosphorylation of histone H2b in neurotoxin-induced apoptotic death of dopaminergic neuronal cells," Chapter IV, "Nuclear localization of PKC $\delta$  is regulated by proximity of N-terminal C2-like domain to the C-terminal nuclear localization signal (NLS)," and Chapter V, "Selectively high expression of oxidative-stress sensitive kinase Protein Kinase C delta (PKC $\delta$ ) contributes to the vulnerability of nigral dopaminergic neurons to the MPP<sup>+</sup>-induced degeneration," will be submitted for publication in *Cell Death and Differentiation*, the *Proceedings of National Academy of Sciences*, and the *Journal of Neuroscience*, respectively. Chapter VI contains the general conclusions.

This dissertation contains the experimental results obtained by the author during his graduate study under the supervision of his major professor, Dr. Anumantha G. Kanthasamy.

## Research Objectives

Mechanisms of selective degeneration of nigral dopaminergic neurons in Parkinson's disease (PD) remain unsolved despite the many advances made during the past three decades. Environmental chemical exposure and genetic mutations have both been implicated in the pathogenesis of PD. Mutations in alpha-synuclein, Parkin and DJ genes are some key genetic defects associated with PD. Findings from *in vitro* and *in vivo* models of PD suggest that environmental neurotoxins-induced oxidative stress is one of the initial events that trigger the mitochondrial intrinsic apoptotic pathway in nigral dopaminergic neurons and apoptotic death (Beal, 2002; Dauer and Przedborski, 2003; Jenner, 2003; Olanow and Tatton, 1999). The deleterious nature of the metabolism of free cytosolic dopamine, the specific neurotransmitter employed by the dopaminergic neurons, potentially increases oxidative stress in dopaminergic neurons. The expression levels of several inherent factors involved in the regulation of free cytosolic dopamine levels have been implicated in the vulnerability of dopaminergic neurons (Hirsch et al., 1997; Uhl, 1998). Recent identification of genetic mutations of PTEN induced kinase 1 (PINK1) (Valente et al., 2004) and leucine-rich repeat kinase 2 (LRRK2) (Zimprich et al., 2004) in familial PD patients suggests that kinase might play an important role in the pathogenesis of PD. Our laboratory previously observed that neurotoxin exposure induces oxidative stress and activation of caspase-3 (Anantharam et al., 2002; Kanthasamy et al., 2003; Kitazawa et al., 2003; Yang et al., 2004). The activated caspase-3 further mediates proteolytic activation of protein kinase C delta (PKC $\delta$ ) and promotes apoptotic death of rat pheochromocytoma (PC12) (Anantharam et al., 2002) and rat mesencephalic dopaminergic neuronal (N27) cells (Kaul et al., 2003; Kitazawa et al., 2003;

Yang et al., 2004). However, the expression level of PKC $\delta$  in nigral dopaminergic neurons and its detailed mechanisms in the apoptotic death of dopaminergic neuronal cells, including the localization change of activated PKC $\delta$ , downstream events following the activation of PKC $\delta$ , and the regulation of the nuclear localization of PKC $\delta$ , have not been investigated.

The major objectives of this dissertation are: 1) to determine the protein and RNA level of PKC $\delta$ , as well as other PKC isoforms in nigral dopaminergic neurons of rodent brains; 2) to investigate the localization change of the activated cleaved fragments of PKC $\delta$  and downstream events in the nucleus following the proteolytic activation of PKC $\delta$ ; 3) to investigate the regulatory role of the N-terminal regulatory fragment in the nuclear localization of full-length PKC $\delta$ ; and 4) to develop small interfering (siRNA) and small hairpin RNA (shRNA) against PKC $\delta$  as a novel neuroprotective strategy to prevent dopaminergic neurons from neurotoxin-induced degeneration. Taken together, these studies will provide detailed mechanisms for PKC $\delta$ 's pro-apoptotic functions in the neurotoxin-induced degeneration of dopaminergic neurons and may provide useful insights about the role of kinase in the pathogenesis of Parkinson's disease.

### **Background and literature review**

This section provides background information related to the studies described in the dissertation: (I) Parkinson's disease and its pathogenesis; (II) Vulnerability of Substantia nigra pars compacta (SNc) dopaminergic neurons in Parkinson's disease; (III) Apoptosis in Parkinson's disease; (IV) Involvement of Serine/Threonine protein kinases in the apoptotic

signaling and neurodegenerative diseases; (V) Proteolytic activation and nuclear translocation of serine/threonine protein kinases in apoptosis; (VI) RNA interference (RNAi) and its neuroprotective application in neurodegenerative diseases.

## **I. Parkinson's disease and its pathogenesis**

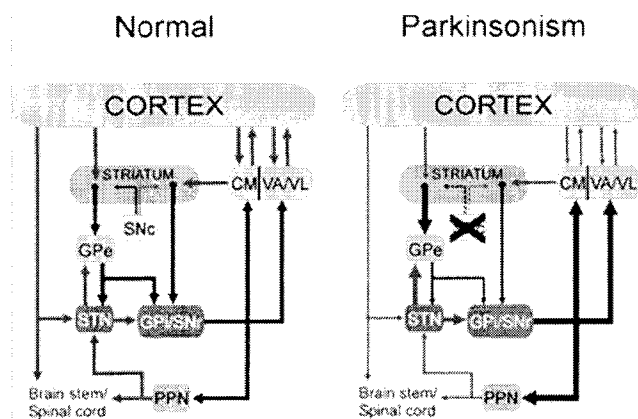
### **I-1: Parkinson's disease**

The clinical features of Parkinson's disease (PD) were first characterized by James Parkinson in his monograph, "An essay on the shaking palsy" in 1817 (Parkinson, 2002). Currently, Parkinson's disease is one of the most devastating neurodegenerative diseases among elders worldwide. In the U.S., about 2,000,000 individuals have been diagnosed with PD (Shastry, 2001). The incidence rate of PD is estimated at 0.3% among the general population and about 1-2% among the population over 65 in industrialized countries (de Rijk et al., 2000; Rajput, 1992). The prevalence of the disease increases up to 4-5% by the age of 85 (Giasson and Lee, 2001). The higher incidence rate in the elder population implies that aging itself contributes to the pathogenesis of PD. On the other hand, Parkinson's disease also occurs in young people. Rare young-onset PD (YOPD), developing between 21 and 40 years, or juvenile Parkinsonism (JP), with an onset age below 21 years, both have been reported (Paviour et al., 2004).

The major clinical symptoms of PD are characterized as resting tremor, muscular rigidity, bradykinesia, and postural instability. Although dysfunction involved in movement mainly defines this disorder, various non-motor features are also found, including cognitive and psychiatric changes, sleep disturbances, and autonomic dysfunction (Samii et al., 2004). A resting tremor, uncontrollable involuntary shaking of the hand or foot (less common) with

frequency of 3-5 Hz (Samii et al., 2004), is usually considered the first symptom in most PD patients. Tremor is usually asymmetric at disease onset and worsens with anxiety, contralateral motor activity, and during ambulation. Rigidity is the raised resistance noted during passive joint movement that is uniform throughout the range of motion of that joint. Rigidity usually correlates positively with resting tremor, as more pronounced rigidity is found in the more tremulous limb (Samii et al., 2004). Bradykinesia, the most disabling symptom of early Parkinson's disease, results in difficulty with fine motor tasks, such as closing buttons or handwriting, as well as reduced arm swing during walking (Martinez-Martin et al., 1994). Postural instability refers to the gradual development of poor balance, leading to an increased risk of falls. Postural instability is rarely seen in the early stage of PD.

After decades of effort, the underlying pathological changes in Parkinson's disease have been well characterized. Anatomically, the most affected portion of the brain in PD patients is the basal ganglia (Albin et al., 1989). The basal ganglia is a group of functionally related subcortical nuclei that includes the neostriatum (comprised of the caudate nucleus and the putamen), the ventral striatum, the Globus pallidus (GPe and GPi), the subthalamic nuclei (STN), and the substantia nigra pars reticulata or pars compacta (SNr and SNc). The dopaminergic neurons in the SNc normally project to the GABAergic neurons at the striatum (mainly the caudate nucleus and putamen) to form the nigrostriatal circuit. The nigrostriatal circuit and subsequent neuronal circuit among the striatum, thalamus, brain stem, and cortex are further organized into the corticobasal gangliathalamocortical circuits, which critically control voluntary movement (Alexander, 1990). The basal ganglia-thalamocortical circuitry under normal and PD conditions is shown in Figure 1. One of the output pathways of the striatum is the projection of the striatal neurons to the GPi (referred to as the direct pathway)



**Figure 1. The basal ganglia-thalamocortical circuitry under normal condition and Parkinson's disease (Modified from Wichmann, 2003)**

to inhibit GABA release from the GPi to the thalamus. On the other hand, striatal neurons also project to the GPe (referred to as the indirect pathway) to subsequently stimulate the release of GABA from the GPe to the subthalamic nucleus to inhibit glutamate release from the subthalamic nucleus to the SNr. The dopaminergic neurons projected from the SNc to the striatum normally release dopamine that is bound to the dopamine receptors in the postsynaptic GABAergic neurons. Because of the presence of two populations of striatal neurons that contain functionally distinct dopamine receptors, D1 or D2, dopamine apparently has dual roles in the modulation of the activity of basal ganglia output neurons. Dopamine released from SNc dopaminergic neurons excites GABAergic neurons in the striatum to either stimulate through the D1 receptor (in the direct pathway) or inhibit through the D2 receptor (in the indirect pathway) the release of the inhibitory neurotransmitter, GABA. The balance between direct and indirect pathways precisely controls the output of the basal ganglia and is critical to maintain normal motor function (Wichmann and DeLong, 2003).

In the early 1960s, Parkinson's disease was shown to result largely from the degeneration of dopaminergic neurons in the substantia nigra pars compacta (SNc) of basal ganglia (Albin et al., 1989). Later, many other studies consistently characterized the progressive and selective degeneration of dopaminergic neurons in the SNc and the resulting depletion of dopamine in the striatum in PD patients. The depletion of dopamine in the

striatum leads to increased activity in the indirect pathway and decreased activity in the direct pathway (Wichmann and DeLong, 2003). Both of these changes contribute to increased activity in the GPi, which results in the increased inhibition of subsequent thalamocortical and midbrain tegmental neurons and thus, the hypokinetic features of the disease (Kandel et al., 2000). The symptoms usually appear when the loss of dopaminergic neurons in the SNc reaches about 80% (Albin et al., 1989). In addition to the selective degeneration of the dopaminergic neurons in the SNc, formation of Lewy bodies, the intracellular inclusions of abnormal protein aggregation, is another pathological hallmark of Parkinson's disease (Hardy, 2003). Lewy bodies are widely found in many regions of the brain, particularly in the dopaminergic neurons of the SNc, the hypothalamus, the hippocampus, and the autonomic neurons of the esophagus and gastrointestinal tract and occasionally in the cortex (Dauer and Przedborski, 2003). Although the detailed mechanisms are still under intense investigation, the production of excessive misfolded proteins and the compromised ubiquitin-proteasome system are considered to play major roles in the formation of Lewy bodies (Dauer and Przedborski, 2003; Huang et al., 2004). Notably, the formation of the Lewy body is not unique in PD; in fact, Lewy bodies are also commonly found in the postmortem brains of Alzheimer's and several types of dementia patients (Dickson, 2002; Hardy, 2003; McKeith et al., 2003), suggesting that the abnormal protein aggregation in neurons is ubiquitously involved in the pathogenesis of various neurodegenerative diseases.

## **I-2: Pathogenesis of Parkinson's disease**

Unlike the well-characterized pathological changes in PD, the pathogenesis of PD is still largely unclear, though great progress has been made in the past thirty years from studies



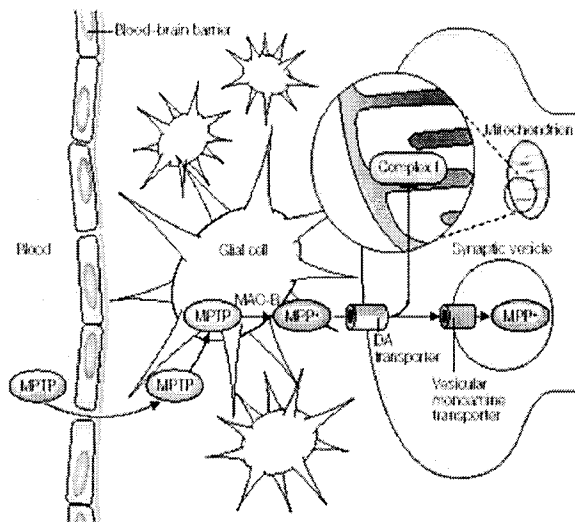
of MPTP-induced Parkinsonism and the genetic mutations identified in familial PD patients. Because the incidence rate of PD is higher in the elder population, aging itself has long been considered to play a role in the pathogenesis of PD. In the central nervous system, dopaminergic neurons are mainly distributed in the midbrain, particularly in the SNc region. At birth, the SNc contains approximately 400,000 dopaminergic neurons. As age increases, the number of dopaminergic neurons in the SNc declines, since dopaminergic neurons in the SNc normally degenerate at a rate of 2,400 neurons per year (Marsden, 1990). However, the number of remaining dopaminergic neurons in the SNc prevents the occurrence of PD symptoms when the degeneration process is not abnormally accelerated. Thus, normal aging is certainly associated with PD and is considered one of the risk factors for PD but does not cause this disorder alone (Samii et al., 2004).

### **I-2-1: Environmental factors in the pathogenesis of PD**

The pathogenesis of PD was not understood until the early 1980s. In 1983, Langston and colleagues reported a series of patients who developed acute Parkinsonism after accidental exposure to 1-methyl-4-phenyl-1,2,5,6-tetrahydropyridine (MPTP), a toxic byproduct in the clandestine synthesis of a pethidine analogue (Langston et al., 1984). These patients also showed significant reduction in dopaminergic neuron activity in the basal ganglia, as normally seen in PD patients. Because MPTP-induced Parkinsonism in humans faithfully replicates the pathological features seen in PD patients, mechanisms of MPTP-induced dopaminergic neuron degeneration are under intense investigation. Numerous *in vitro* cell and *in vivo* animal models (including primate) have been created to study the mechanisms of MPTP-induced Parkinsonism (Przedborski and Vila, 2003). All these models

show that dopaminergic neurons are severely degenerated following MPTP exposure and hypokinetic symptoms develop in animals (Speciale, 2002; Vila and Przedborski, 2003).

MPTP itself is non-toxic but can cross the brain-blood barrier to enter the brain when administered to humans and mammals. In the brain, MPTP is converted into 1-methyl-4-



**Figure 2. The MPTP model of Parkinson's disease (Modified from Vila, 2003)**

phenyl-2,3-dihydropyridinium (MPDP<sup>+</sup>) by monoamine oxidase (MAO-B) in astrocytes (Markey et al., 1984). The MPDP<sup>+</sup> is unstable and spontaneously oxidized to 1-methyl-4-phenylpyridinium (MPP<sup>+</sup>) (Dauer and Przedborski, 2003). The MPP<sup>+</sup> is released from astrocytes and selectively taken into dopaminergic neurons in the SNc through dopamine transporter (DAT) due to its similar structure to dopamine (Mayer et al., 1986; Uhl et al., 1985).

Once inside the dopaminergic neuron, MPP<sup>+</sup> is concentrated within the mitochondria by a mechanism that relies on the mitochondrial transmembrane potential, though it can also be sequestered into synaptosomal vesicles by vesicular monoamine transporter 2 (VMAT2) (Liu et al., 1992). MPP<sup>+</sup> impairs oxidative phosphorylation by inhibiting the multi-enzyme complex I of the mitochondrial electron transport chain, which rapidly results in the low production of ATP in the neuron (Greenamyre et al., 2001; Ramsay et al., 1986; Vila and Przedborski, 2003). The decrease in ATP dramatically affects many processes in the neuron. Meanwhile, the MPP<sup>+</sup>-induced inhibition of the complex I also induces oxidative stress by hampering the flow of electrons through complex I, which further triggers the mitochondria-

dependent apoptotic pathway (Cassarino et al., 1997; Kaul et al., 2003; Viswanath et al., 2001).  $MPP^+$  can also directly interact with cytosolic enzymes (especially with those carrying negative charges) through its positive charges to interfere with their normal functions (Klaidman et al., 1993). Furthermore, perturbations in  $Ca^{2+}$  homeostasis are also observed within hours of MPTP administration in mice (Jackson-Lewis et al., 1995). After these initial events, multiple apoptotic responses are induced in the SNc dopaminergic neurons, including up-regulation of the Bcl-2 family protein Bax (Vila et al., 2001), activation of caspase-9 and -3 (Hartmann et al., 2000; Viswanath et al., 2001), and DNA oxidation-induced activation of pro-apoptotic c-Jun N-terminal kinase (JNK) (Saporito et al., 2000; Xia et al., 2001), which eventually promotes the apoptotic death of SNc dopaminergic neurons.

Although studies of  $MPP^+$ -induced SNc dopaminergic neuronal degeneration in animal models (including primate) have significantly contributed to our knowledge about the pathogenesis of PD, humans are rarely exposed to  $MPP^+$  (or MPTP), which are not found in the environment. In addition, the  $MPP^+$ -induced dopaminergic neuronal degeneration in primates and humans has some features that differ from those observed in PD patients. The most significant pathological difference is that formation of the Lewy body, one of the hallmarks in PD pathology, was not found in MPTP-treated animals (Forno et al., 1993). Nevertheless, the discovery that MPTP causes acute Parkinsonism in humans brings attention to other environmental chemicals possibly involved in the pathogenesis of PD. Because of the observation that  $MPP^+$  strongly inhibits the complex I of mitochondria and induces the elevation of ROS, other complex I inhibitors become candidates of potential risk factors for PD. Interestingly, almost all these complex I inhibitors are also extensively used as herbicides or pesticides, like rotenone, paraquat, and diquat (Jenner, 2001). Animals exposed

to these chemicals all show SNc dopaminergic neuron degeneration and develop PD-like symptoms (Betarbet et al., 2000; Giasson and Lee, 2000; Jenner, 2001; McCormack et al., 2002). In rotenone-exposed rats, formation of the Lewy body in the SNc is also induced (Betarbet et al., 2000). Various case-control studies (Tanner and Ben-Shlomo, 1999; Tanner et al., 1989) also strongly suggest an association between exposure to pesticides and the development of PD. Currently, several other pesticides are also under investigation for their potential role in the pathogenesis of PD. One, dieldrin, is classified as one of the most persistent bioaccumulative and toxic (PBT) chemicals by the US EPA. It is not clear as to whether dieldrin also inhibits mitochondria complex I; however, several studies have indicated that dieldrin exposure is positively associated with the increased incidence of PD. The most supportive piece of evidence is that a significant level of dieldrin was detected in the postmortem brains of PD patients, whereas dieldrin was not found in age-matched control brains (Corrigan et al., 1996; Fleming et al., 1994). In addition, dieldrin exposure depletes dopamine in brains of ducks, rats and ring doves (Heinz et al., 1980; Wagner and Greene, 1978). Furthermore, previous studies from our laboratory and others also showed that dopaminergic cells are more sensitive to dieldrin-induced toxicity (Kitazawa et al., 2001; Sanchez-Ramos et al., 1998). The molecular/cellular mechanisms of dieldrin-induced dopaminergic neuronal degeneration are being investigated in our laboratory.

Besides pesticides, other chemicals are also suggested to be risk factors for PD. Heavy metals, like manganese, copper, iron, lead, and aluminum, have been reported to have a positive association with PD incidence in various etiological studies (Gorell et al., 1997; Kuhn et al., 1998; Paik et al., 1999). Interestingly, smoking, caffeine, and alcohol (not including wine) seem to protect against development of PD, based on case-control studies

(Gorell et al., 1999; Hellenbrand et al., 1996a; Hellenbrand et al., 1996b; Morens et al., 1995). The wide distribution of chemicals, the extensive interaction between different chemicals in the environment, and the exposure of humans to various sources of chemicals make tracking human exposure to environmental chemicals difficult. Furthermore, recognizing the risk of environmental chemicals and their distinct contributions to the pathogenesis of PD remain a challenge.

### I-2-2: Genetic mutations in the pathogenesis of PD

Initially, genetic predisposition in the pathogenesis of PD was not fully recognized because most cases of PD are sporadic. An epidemiology study of 20,000 monozygote (MZ) and dizygote (DZ) twins showed that the concordance of PD incidence is similar between

Gene	Chromosome locus	Gene product	Mode of inheritance
PARK1	4q21.3	$\alpha$ -synuclein	Dominant
PARK2	6q25.2-q27	Parkin	Recessive
PARK3	2q13	Unknown	Dominant
PARK4	4q15	Unknown	Dominant
PARK5	4q14	UCHL1 <sup>a</sup>	Dominant
PARK6	1p35-p36	PINK1 <sup>b</sup>	Recessive
PARK7	1p36	DJ-1	Recessive
PARK8	12p11.2-q13.1	LRRK2 <sup>c</sup>	Dominant
PARK10	1p32	Unknown	Dominant

a. Ubiquitin C-terminal hydrolase L1; b. PTEN-induced kinase 1; c. Leucine-rich repeat kinase 2

**Table 1. Genes associated with familial Parkinson's disease patients**

genes in familial PD patients implicates a direct pathogenic role of genetic predisposition in PD (Huang et al., 2004). The genes found mutated in familial PD patients (Table 1) include  $\alpha$ -synuclein, parkin, ubiquitin carboxyl-terminal hydrolase 1 (UCHL1), DJ-1, PTEN-induced kinase 1 (PINK1), leucine-rich repeat kinase 2 (LRRK2), and several others that have been mapped but not yet cloned (Dawson and Dawson, 2003; Shen, 2004). Among these genes,  $\alpha$ -

MZ and DZ twins, suggesting that genetic predisposition does not play a major role in the pathogenesis of PD (Tanner et al., 1999). However, recent identification of a number of genetic mutations in various

synuclein, parkin, and ubiquitin carboxyl-terminal hydrolase 1 (UCHL1) are mainly involved in protein aggregation and the ubiquitin-proteasome system. Other genes, like DJ-1 and PTEN-induced kinase 1 (PINK1), appear to be related to the oxidative stress response. The discovery of genetic mutations in these genes indicates a strong connection between the protein degradation system and oxidative stress in the pathogenesis of PD.

The first gene implicated in the pathogenesis of PD was  $\alpha$ -synuclein. It was first identified in a large Italian-American family with autosomal dominant early-onset PD. The missense mutation A53T was found in exon 4 of the gene (Golbe et al., 1990). This mutation was also found in affected members of three Greek families with PD (Polymeropoulos et al., 1997). Since then, different mutations in  $\alpha$ -synuclein genes have been identified in different families with PD, including A30P and E46K mutations (Kruger et al., 1998; Zarranz et al., 2004), and triplication of the  $\alpha$ -synuclein gene (Singleton et al., 2003). Cellular studies reveal that  $\alpha$ -synuclein is concentrated at pre-synaptic terminals, and is an important component of the Lewy body, the major PD pathological hallmark (Spillantini et al., 1997). Although tremendous efforts have been made to characterize  $\alpha$ -synuclein's function, its exact physiological function remains unclear (Lotharius and Brundin, 2002). Recent studies with  $\alpha$ -synuclein knock-out mice suggest that  $\alpha$ -synuclein plays a role in synaptic vesicle cycling (Abeliovich et al., 2000). Cultured hippocampal neurons from these mice were found to have fewer synaptic vesicles than control mice, particularly in the reserve pool (Cabin et al., 2002). These mice also showed defects in synaptic transmission after prolonged, high-frequency stimulation. Other studies suggest that  $\alpha$ -synuclein may function like a chaperone-

like protein (Recchia et al., 2004) or regulate gene expression (Baptista et al., 2003; Lindersson et al., 2004).

Yet, the pathogenic function of  $\alpha$ -synuclein in PD is much better established. Full-length  $\alpha$ -synuclein (140aa) normally is soluble in the cell, but at high concentrations, it can form protofibrils that are intermediate species in the fibrillization process from monomer to fibril (Lotharius and Brundin, 2002). The protofibrils further form the fibrils present in Lewy bodies in a nucleation-dependent manner. The A53T and A30P mutations identified in familial PD patients both increase the tendency for  $\alpha$ -synuclein to form protofibrils (Conway et al., 2000a; Conway et al., 2000b); however, the A30P mutation inhibits the further formation of fibrils (Conway et al., 2000c). Along with evidence from other studies, the protofibrils are considered to be deleterious species and are highly toxic to the neurons (Bucciantini et al., 2002). Notably, various post-translational modifications, including phosphorylation (Fujiwara et al., 2002; Lee et al., 2004; Okochi et al., 2000), glycosylation (Munch et al., 2000), oxidation (Przedborski et al., 2001), nitration (Hodara et al., 2004; Souza et al., 2000), and ubiquitination (Shimura et al., 2001), have all been found in  $\alpha$ -synuclein. In particular,  $\alpha$ -synuclein deposited in the Lewy body is found to be ubiquitinated (Tofaris et al., 2003), suggesting these post-translational modifications are involved in the  $\alpha$ -synuclein protofibril and fibril formation. Indeed, oxidative dimer formation has been demonstrated to be the critical rate-limiting step for  $\alpha$ -synuclein fibrillogenesis in Parkinson's disease (Krishnan et al., 2003). Although the mechanisms by which  $\alpha$ -synuclein-formed protofibrils lead to the degeneration of dopaminergic neurons are not clear, some evidence suggests that the desensitization of dopamine transporter (DAT) is inhibited when  $\alpha$ -

synuclein becomes aggregated, resulting in massive uptake of dopamine from the synaptic cleft into the dopaminergic neurons and high production of oxidative species (Sidhu et al., 2004). The  $\alpha$ -synuclein-formed protofibrils were also reported to permeabilize the synaptic vesicle, causing the increase in free dopamine in the cytosol and elevation of reactive oxygen species (Schulz et al., 2000). In contrast to the toxic effect of protofibrils,  $\alpha$ -synuclein-formed fibrils are considered to be neuroprotective and neutralize the toxic effect of protofibrils by forming inclusion bodies (Lotharius and Brundin, 2002).

Besides  $\alpha$ -synuclein, parkin and UCHL1 are two other genes mutated in familial PD patients. Genetic mutations of parkin are mainly identified in juvenile Parkinsonism and other early-onset PD patients (Lucking et al., 1998). Structurally, parkin is characterized as one of the members of ubiquitin E3 ligase, which attaches short ubiquitin peptide chains to proteins and tags them for degradation through the proteasome pathway. Although mutations in parkin are rarely found in sporadic PD patients, parkin is also found in Lewy bodies in sporadic PD patients, implicating its pathogenic role in both familial and sporadic PD (Vila and Przedborski, 2004). The direct link between loss of parkin function and dopaminergic neuron degeneration has not been established. Mutated parkin loses its E3 ligase activity, and thus is speculated to impair the neuron's ability to degrade the misfolded proteins, contributing to the abnormal protein aggregation. The E3 ligase activity of parkin was shown to modulate the sensitivity of cells to both proteasome inhibitor- and mutant  $\alpha$ -synuclein-dependent cell death (Vila and Przedborski, 2004). Several studies have shown the functional interaction between  $\alpha$ -synuclein and parkin. One report even showed that a 22-KDa glycosylated form of  $\alpha$ -synuclein is a substrate of parkin (Shimura et al., 2001). Other than



glycosylated  $\alpha$ -synuclein, several other substrates of parkin have also been identified, including cyclin E, synphilin-1, and parkin-associated endothelin receptor-like receptor (Chung et al., 2001; Imai et al., 2001; Zhang et al., 2000); however, none of these substrates shows enriched expression in dopaminergic neurons or plays a particularly important role in dopaminergic neurons. It remains unknown how the loss of parkin function selectively leads to the degeneration of the SNc dopaminergic neurons. UCHL1 is another enzyme involved in the proteasome system. This enzyme catalyzes the hydrolysis of C-terminal ubiquityl ester to release ubiquitin from degraded protein and recycle it in the proteasome system. Current studies on UCHL1's pathogenic role in PD are inconclusive (Vila and Przedborski, 2004). The I93M mutation identified in PD patients decreases the activity of UCHL1; however, UCHL1 knock-out mice do not display dopaminergic neuronal degeneration, suggesting that the loss of UCHL1 function can be compensated for *in vivo* (Saigoh et al., 1999). Recently, UCHL1 was demonstrated to also have ubiquitin ligase activity upon dimerization, which might be related to its pathogenic role in PD (Liu et al., 2002).

A number of other genes are being examined as genetic risk factors in PD, including genes involved in dopamine synthesis and metabolism, neurotrophic factors, genes involved in energy supply and oxidative stress response, genes involved in detoxification of metabolites, and genes involved in the maturation of dopaminergic neurons during development (Huang et al., 2004). It is highly likely that multiple mechanisms are present for the pathogenesis of PD as a result of the combinational effect of different genetic mutations and exposure to environmental chemicals. This complicates the development of a universal strategy to delay or cure PD, but could provide more targets for development of drugs which

specifically and effectively prevent degeneration of dopaminergic neurons involving different mechanisms and delay the further development of symptoms in PD patients.

## **II. Vulnerability of substantia nigra pars compacta (SNc) dopaminergic neurons in Parkinson's disease**

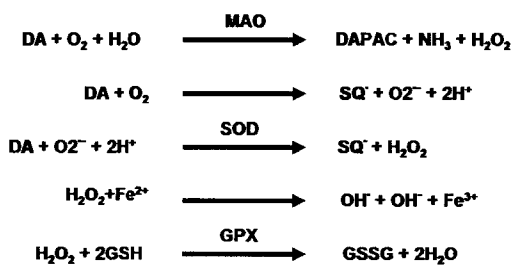
In Parkinson's disease, dopaminergic neurons are most severely degenerated, though the degeneration of noradrenergic neurons (locus coeruleus), serotonergic neurons (raphe), and cholinergic neurons (nucleus basalis of meynert, dorsal motor nucleus of vagus, and cerebral cortex) is also observed (Dauer and Przedborski, 2003). In particular, the dopaminergic neurons in the SNc region are selectively degenerated, though dopaminergic neurons are predominantly localized not only in the SNc but also in the ventral tegmental area (VTA) and the retrorubral field of the midbrain (Korotkova et al., 2004; Riddle and Pollock, 2003). Within the SNc region, the degeneration of dopaminergic neurons is also not uniform. Dopaminergic neurons localized in the caudal, ventral, and lateral regions are more vulnerable than those in the rostral, dorsal, and medial regions (Gonzalez-Hernandez et al., 2004; Hirsch et al., 1997). It is clear that some groups of the SNc dopaminergic neurons are more vulnerable to the same level of environmental insults or same degree of comprise from genetic mutations. Different inherent factors in dopaminergic neurons have been implicated in selective vulnerability.

### **II-1: Dopamine metabolism and vulnerability of dopaminergic neurons**

Dopamine, a catecholamine, is the specific neurotransmitter synthesized in and released from dopaminergic neurons. At the pre-synaptic terminal projected from

dopaminergic neurons, dopamine is synthesized from two steps of enzymatic reaction. Tyrosine is first converted to L-3,4-dihydroxyphenylalanine (L-dopa) by tyrosine hydroxylase (TH) and then to dopamine by aromatic amino acid decarboxylase (AADC) (Kandel et al., 2000). Synthesized dopamine is usually sequestered into vesicles for storage by vesicle membrane associated transporter 2 (VMAT2) and released to the synaptic cleft upon stimulation. The released dopamine is either bound by dopamine receptors residing on the membrane of post-synaptic neurons or reuptaken by dopamine transporter (DAT) on the pre-synaptic membrane.

Dopamine (DA) itself has been shown to be one of the inherent factors that contributes to the susceptibility of dopaminergic neurons in PD (Carlsson and Fornstedt,



**Figure 3. Dopamine metabolism and generation of reactive oxygen species (ROS)**

1991; Hirsch et al., 1997). The metabolism of dopamine and generation of reactive oxygen species is illustrated in Figure 3. Free cytosolic dopamine can auto-oxidize at normal pH into toxic dopamine-quinone

species (SQ<sup>·</sup>), superoxide radicals (O<sub>2</sub><sup>·-</sup>), and hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) (Graham, 1978; Lotharius and Brundin, 2002). Dopamine-quinone species can directly mediate modification of α-synuclein, which promotes its protofibril formation (Conway et al., 2001). Superoxide radicals are further converted into hydrogen peroxide by superoxide dismutase (SOD). Alternatively, dopamine is deaminated by monoamine oxidase (MAO) into 3, 4-dihydroxyphenylacetic acid (DOPAC) and hydrogen peroxide (Makler et al., 1981). Although hydrogen peroxide itself is innocuous and is usually converted into water while glutathione (GSH) is oxidized to glutathione disulfide (GSSG) by glutathione peroxidase, it can also be

broken down into cytotoxic hydroxyl radicals in a reaction involving  $\text{Fe}^{2+}$  (Halliwell, 1992). More vulnerable dopaminergic neurons have lower expression of glutathione peroxidase than neurons preserved in PD (Damier et al., 1993), which suggests that more cytotoxic hydroxyl radicals are generated in those neurons. All these reactive oxygen species directly cause lipid peroxidation and protein or DNA oxidation, which in turn leads to the loss of normal enzyme function or membrane integrity. Because of the deleterious nature of the metabolism of dopamine, SNc dopaminergic neurons are more exposed to oxidative stress. Indeed, several studies have demonstrated that oxidative stress is more severe in the SNc region of PD brains, as indicated by lipid peroxidation and protein or DNA oxidation (Dexter et al., 1989; Floor and Wetzel, 1998; Jenner, 1998).

The deleterious nature of the metabolism of dopamine necessitates tight control of the free dopamine level in the cytosol. The cytosolic level of dopamine depends on its synthesis and two transport processes mediated by DAT or VMAT2, respectively. Tyrosine hydroxylase (TH) is the key enzyme that catalyzes the rate-limiting reaction for catecholamine biosynthesis, including dopamine (Ramsey and Fitzpatrick, 2000). The activity of TH is regulated by its serine phosphorylation status and feedback inhibition of synthesized catecholamines in competition with tetrahydrobiopterin, the cofactor for TH (Nagatsu, 1995). The phosphorylation of different serine residues (Ser19, Ser31, and Ser40) on TH has been shown to increase its activity (Dunkley et al., 2004). Various Serine/Threonine kinases, including cAMP-dependent protein kinase A (PKA) (Lovenberg et al., 1975), cGMP-dependent protein kinase G (PKG) (Roskoski et al., 1987), protein kinase C (PKC) (Albert et al., 1984),  $\text{Ca}^{2+}$ -calmodulin dependent protein kinase II (CaMKII) (Vulliet et al., 1984), extracellular signal-related kinase (ERK1/2) (Sutherland et al., 1993),

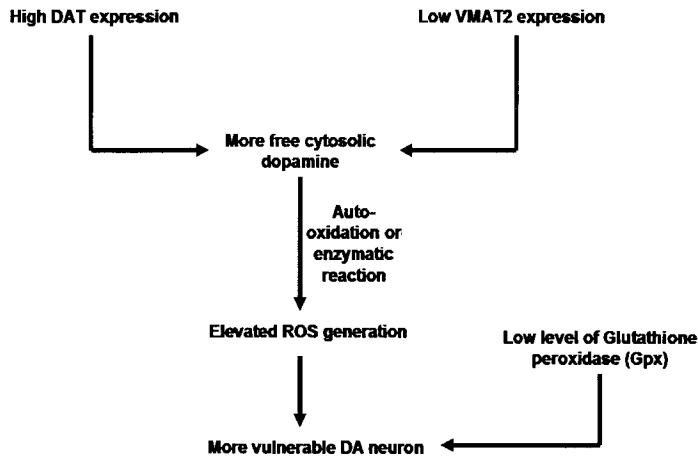
and the recently identified cyclin-dependent protein kinase 5 (Cdk5) (Moy and Tsai, 2004) are responsible for mediating the phosphorylation of different serine residues on TH. However, none of these kinases were shown to selectively phosphorylate TH to increase its activity and subsequent dopamine synthesis in different groups of dopaminergic neurons in the brain. It is also unknown whether TH activity is dramatically changed during the pathogenesis of PD. Moreover, previous studies have shown that no expression change in TH was found in postmortem brains of age-matched control subjects and PD patients. Studies on the differentiation of dopaminergic neurons in rodent brain development also show that TH expression is uniform in different groups of dopaminergic neurons and constant from the time TH expression is induced through adulthood (Simon et al., 2003). In contrast, DAT and VMAT2, two transporters involved in the uptake of dopamine from the synaptic cleft into the neuron and in sequestration of free dopamine from the cytosol into the vesicle, respectively, show significantly different expression patterns in different groups of dopaminergic neurons.

DAT is only expressed in the dopaminergic neurons. It localizes on the plasma membrane to uptake released dopamine, thus regulating the intensity and duration of dopaminergic neurotransmission at the synapse. The expression pattern of DAT in different dopaminergic neurons is closely related to the neuronal vulnerability in PD. Immunostaining revealed that DAT has the highest expression in the caudal, ventral, and lateral regions of the SNc in monkey brains and postmortem brains of PD patients (Gonzalez-Hernandez et al., 2004; Hitri et al., 1994). Likewise, dopaminergic neurons in these regions have the most severe loss in PD. The intensity of DAT staining decreases dramatically in the dorsal region of SNc and the VTA region. A similar pattern was also shown by *in situ* hybridization in rat (Sanghera et al., 1997; Uhl, 1998). More DAT in the plasma membrane could uptake more

dopamine and cause increased production of cytotoxic metabolites of dopamine. In addition to its uptake of dopamine into the dopaminergic neurons, DAT can also selectively uptake some toxic chemicals into dopaminergic neurons, like MPP<sup>+</sup>, 6-hydroxydopamine (6-OHDA), isoquinoline derivatives, and  $\beta$ -carboline derivatives because of their structural similarity to dopamine (Storch et al., 2004). Since humans are widely exposed to environmental chemicals, more DAT on the plasma membrane of dopaminergic neurons facilitates certain neurotoxin entry into dopaminergic neurons, thus increasing their susceptibility to degeneration. The expression of DAT in neurons that lack DAT confers these neurons susceptibility to MPP<sup>+</sup>-induced toxicity (Gonzalez-Hernandez et al., 2004). The effect of DAT on the vulnerability of dopaminergic neurons has also been demonstrated in DAT knock-out or transgenic mice. In DAT heterozygous mice that express about one-half of the normal level of DAT, acute dopaminergic toxicity induced by MPTP is reduced to about one-half of that found in wild-type mice (Gainetdinov et al., 1997). In the DAT overexpressed mice, DAT expression is increased over 130%; however, dopaminergic neurons become more vulnerable and 70% more dopaminergic neuronal loss is observed in comparison to that in wild-type control mice following MPTP treatment (Uhl, 1998).

In contrast to the higher expression of DAT, vesicle membrane associated transporter 2 (VMAT2) has a lower expression level in the more vulnerable dopaminergic neurons. VMAT2 is expressed in the monoaminergic neurons. Immunoelectron microscopy reveals that VMAT2 protein is more abundant in the processes of neurons of the VTA than in those of the SNc (Nirenberg et al., 1996). This was also observed by *in situ* hybridization of VMAT2 (Peter et al., 1995). Because VMAT2 can sequester dopamine into vesicles so that less cytotoxic metabolites of dopamine are produced, higher expression of VMAT2 is

considered to be protective and reduces the susceptibility of dopaminergic neurons to oxidative stress. Like DAT, VMAT2 can also sequestrate not only dopamine but also other



**Figure 4. Regulation of free cytosolic dopamine level and the vulnerability of dopaminergic neurons**

toxic chemicals structurally similar to dopamine, like MPP<sup>+</sup>, into the vesicles. The neuroprotective effect of VMAT2 is supported by studies demonstrating that genetic or pharmacological blockade of VMAT2 makes dopaminergic neurons more vulnerable to

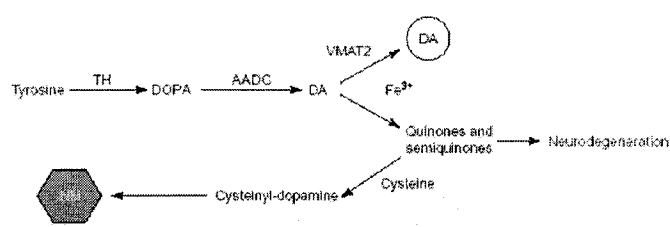
neurotoxins (Gainetdinov et al., 1998; Speciale et al., 1998). The heterozygous mice that express one-half the normal levels of VMAT2 show more than twice as much MPTP-induced dopaminergic neuronal loss than that in wild-type mice (Takahashi et al., 1997). Based on the relationship between the vulnerability of dopaminergic neurons and the expression level of DAT and VMAT2, the ratio between DAT and VMAT2 expression levels may determine the susceptibility of dopaminergic neurons to degeneration (Edwards, 1993; Miller et al., 1999; Uhl, 1998).

## **II-2: Neuromelanin, iron and the vulnerability of dopaminergic neurons**

Dopaminergic neurons are the most highly pigmented cells in the human brain because of the preferential presence of neuromelanin (NM). Neuromelanin is an electron-dense substance that locates in the NM granules characterized as organelles surrounded by a double membrane in the neuronal perikaryon (Zecca et al., 2001). NM is only present in

primates, like the chimpanzee, gibbon and human. The proposed connection between NM and the vulnerability of dopaminergic neurons is based on the observation that melanized dopaminergic neurons are the most severely degenerated, whereas non-melanized dopaminergic neurons are preserved in PD (Hirsch et al., 1997).

Although it is not entirely clear, NM synthesis appears to be related to dopamine oxidation. Employing a chemical approach, a dopamine-NM compound was synthesized by



**Figure 5. Synthesis of Neuromelanin (NM) (Modified from Zecca, 2003)**

the auto-oxidation of dopamine (Double et al., 2002). Alternatively, NM could be derived from quinones or semiquinones, the oxidized metabolite of dopamine with addition

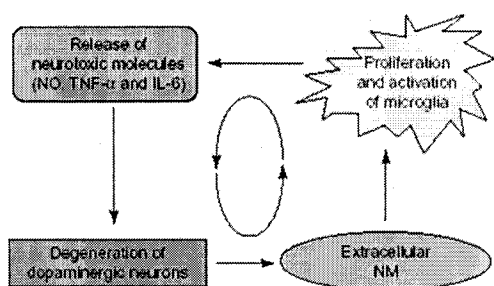
of a thiol group in mammalian brains (Fornstedt et al., 1986). NM synthesis was also experimentally induced in cultured rat substantial nigra neurons exposed to L-dopa (Sulzer et al., 2000). The experimental NM synthesis in rat neurons was blocked by overexpression of VMAT2, suggesting that an excess of cytosolic dopamine indeed contributes to the synthesis of NM (Liang et al., 2004). Although the pigmented dopaminergic neurons are consistently observed to be the most highly degenerated in PD, current knowledge about the effect of NM in the vulnerability of dopaminergic neurons is still contradictory.

Because NM synthesis involves dopamine oxidation, more production of NM leads to the generation of a greater amount of free radicals during the oxidation of dopamine, which increases neuronal susceptibility (Double et al., 2002). Other evidence for its positive correlation with the vulnerability of dopaminergic neurons is that released NM from normally degenerated dopaminergic neurons during aging can stimulate release of the



neurotoxic mediators, including tumor-necrotic factor  $\alpha$  (TNF- $\alpha$ ), interleukin 6 (IL-6), and nitric oxide (NO) from microglia (Wilms et al., 2003). These factors potentially lead to a subsequent aggravation of neurodegeneration. Very recently, NM was shown to inhibit the enzymatic activity of 26S proteasome in human dopaminergic SH-SY5Y cells (Shamoto-Nagai et al., 2004). Since abnormal proteasome activity has been strongly implicated in the pathogenesis of PD, preferential localization of NM in dopaminergic neurons and its inhibition of 26S proteasome activity could significantly contribute to the vulnerability of dopaminergic neurons in PD.

On the other hand, the neuroprotective role of NM has also been suggested. The derivation of NM from quinones reduces the cytosolic level of quinones and prevents their potential damage to the neuron. In addition, NM can bind to toxins like MPP<sup>+</sup> and a variety



**Figure 6. Possible role of NM in the pathogenesis of PD**  
(Modified from Zecca, 2003)

of metals, including Zn, Cu, Mn, Cr, Co, Hg, Pb, Cd, and in particular, Fe (Zecca et al., 1994; Zecca et al., 1996). The accumulation of these metals and toxins in NM is considered to be protective, as the binding effectively inactivates their activity, thus significantly

reducing their damage to the neuron. For example, the binding of NM to iron keeps it inactive and inhibits the production of hydroxyl radicals involving redox-active iron and hydrogen peroxide (Zareba et al., 1995). However, the protective NM can become cytotoxic depending on the cellular level of these metals and toxins, at least in the case of iron, as discussed below. With its binding ability to a variety of metals and toxic chemicals, NM is

speculated to act as a high capacity “waste handling center” to transport metals and toxins to lysosomes for their eventual degradation (Zecca et al., 2003).

Iron is another factor relevant to the vulnerability of dopaminergic neurons. The increase in iron content (30-35%) only in the SNc has consistently been found in both postmortem Parkinsonian brains and in living patients by imaging techniques (Good et al., 1992; Jellinger, 2000; Sofic et al., 1991). The regional increase in iron has also been reported in other neurodegenerative diseases, like Huntington’s and Alzheimer’s disease (Connor et al., 1992; Smith et al., 1997). Very interestingly, the topographical distribution of the increased iron matches well with the degenerated regions in these disorders, suggesting a ubiquitous role of iron in the vulnerability of different neurons in different disorders (Double et al., 2002). Although the mechanisms for the selective increase in iron in specific regions remain unclear, the increase in iron in the SNc is suggested to be partially due to the high amount of NM present in dopaminergic neurons, as iron accumulates in NM granules (Sofic et al., 1991).

Redox-active iron is potentially harmful to cells, as it is actively involved in the generation of hydroxyl radicals from superoxide or hydrogen peroxide. Thus, the selective elevation of iron in the SNc could promote the higher production of the hydroxyl radicals, making neurons more exposed to the oxidative stress. In addition, the effect of iron on the vulnerability of the SNc dopaminergic neurons is related to its cellular level and association with NM. When the cellular iron concentration is not high, NM can almost sequester all the iron into the granules, resulting in less free radical generation and an antioxidant effect; however, when the cellular iron concentration exceeds the threshold that NM can sequester, generation of free radicals is increased with increasing iron concentration (Zareba et al.,

1995). Interestingly, NM also appears to become a pro-oxidant in the presence of high iron concentrations, resulting in a measurably increased production of hydroxyl radicals measured with electron spin resonance (Pilas et al., 1988). Because of the dual effect of NM, when iron is selectively elevated in the SNc region due to unknown mechanisms, higher levels of cellular iron could be involved in the greater production of free radicals not only by itself but also by its modification of NM from neuroprotective to cytotoxic, resulting in the increased vulnerability of dopaminergic neurons. Still, many questions related to the effect of NM and iron on the vulnerability of SNc dopaminergic neurons remain unanswered. For example, are NM structure and properties modified in Parkinsonian brains (Lopiano et al., 2000)? How exactly does iron switch NM from anti-oxidant to pro-oxidant? What are the mechanisms responsible for the selective elevation of iron in the SNc? The development of new experimental tools and a model system are needed to answer these questions.

### **II-3: Calbindin D28K and the vulnerability of dopaminergic neurons**

Calbindin-D28K (CB) is one of the  $\text{Ca}^{2+}$  binding proteins expressed in neurophils of the SNc and other regions of the brain (Andressen et al., 1993). The association between CB and the vulnerability of dopaminergic neurons is suggested from the observation that CB-rich dopaminergic neurons are much better preserved than CB-poor dopaminergic neurons in the SNc region in PD (Damier et al., 1999a, b). Based on the immunostaining pattern of CB, the SNc of the PD brain is subdivided into a CB-rich nigra matrix region and five CB-poor nigrosomes embedded in the matrix (Damier et al., 1999a). The examination of dopaminergic neuron loss by TH staining in these brains correspondingly reveals that the loss of dopaminergic neurons in the nigrosomes is significantly higher than the loss of dopaminergic

neurons in the matrix. Even within the five nigrosomes, the degree of dopaminergic neuron loss is not uniform. The mechanisms of CB's selectively high expression in some groups of dopaminergic neurons are unknown; however, neurotrophic factors have been suggested to increase CB expression in neurons and further reduce the vulnerability of these neurons to degeneration induced by various insults (Alexi and Hefti, 1996; Cheng and Mattson, 1991; Prehn et al., 1994). The up-regulation of CB and its protective role is also shown in the cadmium-adapted U937 cells. Up-regulation of CB by cadmium was suggested to maintain intracellular  $Ca^{2+}$  homeostasis and confer resistance to  $Ca^{2+}$  rise-induced apoptosis in U937 cells (Jeon et al., 2004). Although the protective role of CB has been characterized *in vitro*, the CB knock-out mice did not differ significantly in the MPTP-induced loss of dopaminergic neurons in comparison to the CB wild-type mice (Liang et al., 1996). It is still debatable as to whether the high expression of CB is directly related to the protective effect or is only a phenomenon observed simultaneously as other molecules are performing the real protective actions.

These studies indicate that the expression levels of molecules involved in the regulation of free cytosolic dopamine and dopamine-induced oxidative stress are closely associated with the vulnerability of dopaminergic neurons in PD. It is very likely that expression levels of other molecules sensitive to oxidative stress also contribute to the vulnerability of dopaminergic neurons. In addition to the oxidative stress, proteasome dysfunction, activation of microglia and inflammation, and glutamate excitatory toxicity are also implicated in the pathogenesis of PD (Mattson, 2000; Vila and Przedborski, 2003). The expression levels of molecules involved in these systems, for example, selectively high expression of a cytotoxic substrate for proteasome, could potentially contribute to the

vulnerability of dopaminergic neurons. Studies investigating the vulnerability of dopaminergic neurons will provide important insights into the distinct pathogenic mechanisms of PD and help to identify selective targets for the development of neuroprotective drugs.

### **III. Apoptosis in Parkinson's disease**

Apoptosis is a genetically regulated form of cell death that critically controls embryonic development and maintains tissue homeostasis in adults (Meier et al., 2000). The machinery regulating apoptosis is evolutionarily conserved from lower organisms, like *C. elegans* and *Drosophila*, to higher mammals, like mice and humans (Aravind et al., 2001). Dysfunctional regulation of apoptosis in development and tissue homeostasis has been implicated in many human diseases, including cancer, neurodegenerative diseases, and autoimmune disease, etc. (Nijhawan et al., 2000; Yuan and Yankner, 2000). For the past twenty years, many genes involved in the regulation and execution of apoptosis have been identified, and the biochemical mechanisms of apoptosis have been well characterized.

#### **III-1: Signal transduction in apoptosis**

Apoptotic signaling was first identified in studies of programmed cell death in *C. elegans*. In the early 1990s, three apoptosis related genes, CED-3, CED-4, and CED-9, were first cloned by H.R. Horvitz and colleagues from *C. elegans* (Metzstein et al., 1998). Since then, major groups of regulators and executioners of apoptosis have been cloned across different species, including ligands and death receptors, adaptors, cysteinyl aspartate-specific proteases (caspases, including initiator caspases and effector caspases), B cell leukemia (Bcl)

family proteins, non-caspase protease, etc. (Strasser et al., 2000). These regulators and executioners are coordinately involved in three major apoptotic signaling pathways: the extrinsic (receptor-mediated) or intrinsic (mitochondria-mediated) pathways and the caspase-independent pathway (see Figure 7) (Orrenius et al., 2003).

The extrinsic pathway mainly mediates apoptotic signals from the extracellular environment. The ligands, like Fas or TNF-related apoptosis-inducing ligand (TRAIL), bind to the death receptor and form the death-inducible signaling complex (DISC), resulting in the activation of pro-caspase-8, one of the initiator caspases (Chinnaiyan et al., 1995; Medema et al., 1997). The pro-caspase-8 directly activates pro-caspase-3 by cleavage, which subsequently cleaves target proteins in the cell, leading to cell death. The intrinsic apoptotic pathway is triggered by damage inside the cell and is mainly mitochondria centered (Wang, 2001). Specific damage sensors located on different organelles detect the damage caused by either the external agents or internal dysfunction of physiological processes in the cells. Such damage includes toxins-induced loss of mitochondrial membrane integrity or elevation of reactive oxidative species, DNA-damaging agents or irradiation-induced DNA damage in the nucleus, abnormal protein folding or perturbations of calcium homeostasis in the endoplasmic reticulum (ER), etc. (Ferri and Kroemer, 2001). After the detection of damage by organelle-specific sensors, apoptotic signals are transmitted to the mitochondria and trigger the intrinsic pathway. The initial and most important steps in the intrinsic pathways are the release of cytochrome C. Cytochrome C normally resides in the inner membrane space of the mitochondria and is involved in oxidation phosphorylation, but becomes an apoptosome recruiting molecule in apoptosis (Li et al., 1997). Although not entirely clear, several models have been proposed to explain the release of cytochrome C from

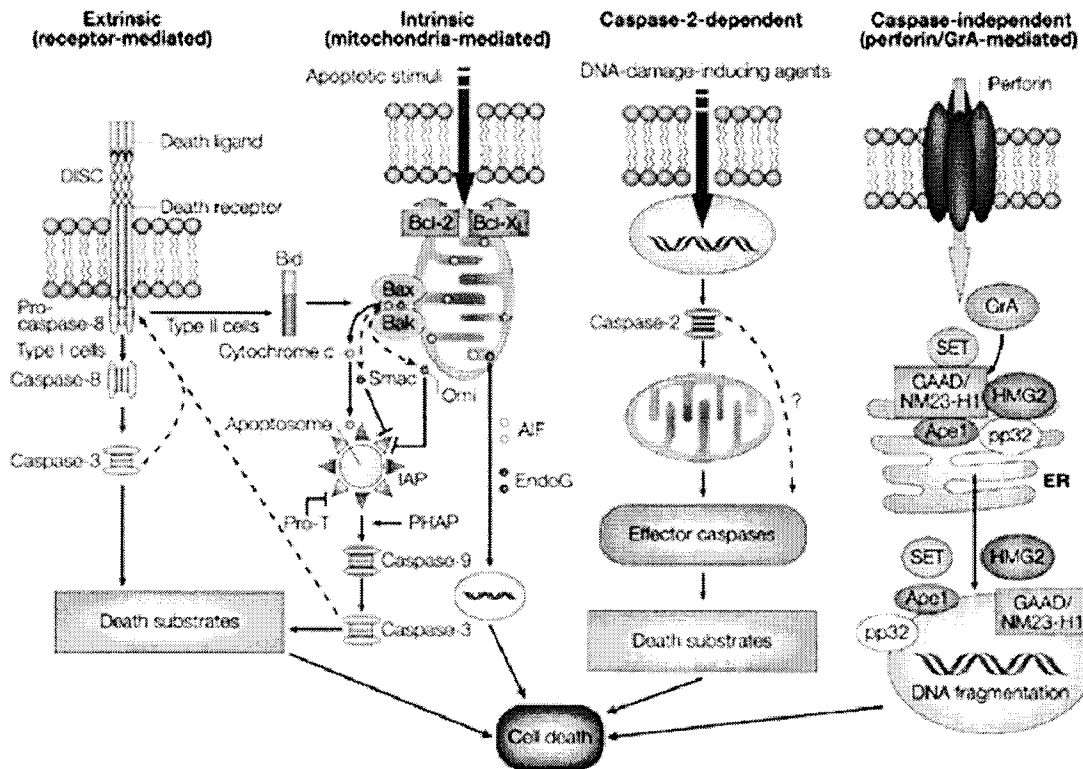
mitochondria. Among these models, oligomerization of pro-apoptotic and anti-apoptotic members in the Bcl-2 family and their translocation to the outer membrane of mitochondria play critical regulatory roles (Vander Heiden and Thompson, 1999). The released cytochrome C recruits apoptosis protease activating factor 1 (Apaf-1) and pro-caspase-9 to form apoptosome, causing the activation of pro-caspase-9 and subsequent activation of pro-caspase-3 by activated caspase-9 mediated cleavage (Li et al., 1997).

Besides Bcl-2 family proteins, many other apoptosis regulators and regulatory roles in this pathway have also been characterized, including inhibitor of apoptosis proteins (IAP) as inhibitors of caspases (Srinivasula et al., 2001), and second mitochondrial activator of caspases (Smac) and Omi as negative regulators of IAPs (Du et al., 2000; Hegde et al., 2002), pro-thymosin- $\alpha$  (Pro-T) and the tumor suppressor putative HLA-DR-associated protein (PHAP) as regulators of apoptosome (Jiang et al., 2003). Moreover, caspase-independent mechanisms are also present in the intrinsic pathway. At least two proteins, apoptosis inducing factor (AIF) (Susin et al., 1996) and endonuclease G (EndoG) (Li et al., 2001) are released from mitochondria and translocate to the nucleus, inducing the appearance of chromatin condensation and DNA fragmentation, hallmarks of apoptosis.

The extrinsic and intrinsic apoptotic pathways are connected. In the extrinsic pathway, as an alternative to caspase-8 mediated activation of caspase-3, caspase-8 can cleave Bid and induce its oligomerization with anti-apoptotic Bcl-2/xl followed by its translocation to the mitochondria, allowing oligomerization and insertion of pro-apoptotic Bax/Bak into the mitochondrial outer membrane to induce pore formation at the mitochondria and subsequent release of cytochrome C (Schmitz et al., 1999). Moreover, extensive cross-talks are present among different organelle-specific apoptotic pathways,

which allow different organelles to coordinately respond to apoptotic signals (Ferri and Kroemer, 2001). Caspase-3 activation is the central step in both the extrinsic and intrinsic apoptotic pathways. Activated caspase-3 cleaves various substrates that contain the DXXD tetrapeptide motif (Grutter, 2000; Nicholson and Thornberry, 1997). Cleavage of these substrates leads to the release of activated DNase (Enari et al., 1998), inactivation of enzymes for cell survival (Itoh and Horio, 2001), collapse of nuclear envelope structure (Buendia et al., 1999), and amplification of apoptotic signals (Leverrier et al., 2002), which globally accelerates the death process.

In addition to the extrinsic and intrinsic pathways that exert caspase-3 as the major



**Figure 7. Major signal transduction pathways in apoptosis (Modified from Orrenius, 2003)**

executioner, the noncaspase protease-mediated apoptotic pathway has also been described in



some cells. Noncaspase proteases characterized so far include cathepsins, calpains, and granzymes (Johnson, 2000). The Granzyme A (GrA)-mediated apoptotic pathway in the target cells, as employed by cytotoxic T lymphocytes (CTLs) and natural killer cells to defend against viruses and parasitic agents, has been well characterized (Beresford et al., 2001; Fan et al., 2003). In this pathway, serine protease Granzyme A and the membrane pore formation protein perforin are secreted from CTLs or natural killer cells and enter into target cells through the perforin formed membrane pore (Liu et al., 1995). After entering the target cells, Granzyme A starts to cleave the inhibitor of GrA-activated DNase (IGAAD) protein complex that normally inhibits the endonuclease involved in the formation of single-stranded DNA nicks in the target cells. The GrA-mediated cleavage of the IGAAD complex releases GrA-activated DNase (GAAD), which further translocates to the nucleus and induces DNA strand break (Beresford et al., 2001; Fan et al., 2003).

### **III-2: Apoptosis of nigral dopaminergic neurons in Parkinson's disease**

Apoptosis is not only a physiologically important process in neurogenesis; the aberrations in apoptosis control also contribute to the pathogenesis of a variety of neurological disorders, including Parkinson's disease (Mattson, 2000; Yuan and Yankner, 2000). To demonstrate that dopaminergic neurons undergo apoptosis in PD, the apoptotic hallmarks were detected in postmortem brains of PD patients. By using the TdT-mediated dUTP digoxigenin nick end labeling (TUNEL) technique, apoptotic dopaminergic neurons were found in some Parkinsonian brains (Mochizuki et al., 1996). Subsequent studies, using other apoptotic characteristics, either succeeded or failed to detect apoptotic dopaminergic neurons in postmortem PD brain samples (Vila and Przedborski, 2003). In addition to the

apoptotic hallmarks, expression changes in key regulators or activation of key executioners in apoptotic pathways have also been observed. For example, a higher expression level of Bax, one of the pro-apoptotic Bcl-2 family proteins, was found in the SNc dopaminergic neurons of postmortem PD brains as compared to control brains (Hartmann et al., 2001a); increased activity of both initiator caspases, caspase-8, -9, and the effector caspase, caspase-3, have been observed in postmortem PD brains (Hartmann et al., 2000; Hartmann et al., 2001b). Because most SNc dopaminergic neurons in postmortem PD brains are usually degenerated at the time of pathological evaluation, the direct detection of apoptotic dopaminergic neurons in the postmortem PD brains is difficult and hard to reproduce.

Numerous *in vivo* and *in vitro* models have been developed to investigate the mechanisms of MPP<sup>+</sup>-induced degeneration of dopaminergic neurons after MPP<sup>+</sup> was found to cause degeneration of the SNc dopaminergic neurons and to induce acute Parkinsonism in humans. The establishment of these models also facilitates the investigation of the involvement of apoptosis in SNc dopaminergic neuron degeneration. In MPTP-administered mice, alteration of energy metabolism, generation of reactive oxygen species (Zarranz et al.), and perturbations in Ca<sup>2+</sup> homeostasis were observed and suggested as upstream events to trigger various downstream apoptotic pathways (Vila and Przedborski, 2003). In this model, the pro-apoptotic Bax is strongly up-regulated (Vila et al., 2001), whereas anti-apoptotic Bcl-2 is down-regulated (Sharma and Ebadi, 2003). The recruitment of the intrinsic apoptotic pathway and subsequent activation of caspase-9 and caspase-3 are also characterized (Viswanath et al., 2001). In addition to the intrinsic apoptotic pathway, the extrinsic apoptotic pathway is also recruited in the degeneration of SNc dopaminergic neurons, as caspase-8 is activated in MPTP-administered mice (Hartmann et al., 2001b; Viswanath et al.,

2001). The activation of both intrinsic and extrinsic apoptotic pathways is also observed in PD models developed using other neurotoxins or genes involved in familial PD, suggesting apoptosis is a fundamental mode of cell death in the degeneration of SNc dopaminergic neurons in PD (Lev et al., 2003; Tatton et al., 2003).

#### **IV. Involvement of serine/threonine protein kinases in apoptotic signaling and neurodegenerative diseases**

Serine/threonine phosphorylation of a wide range of apoptotic components, including major apoptotic regulators (Bcl-2 family proteins), executioners (caspases), organelle-specific stress sensors, various effectors downstream of caspase activation, and apoptosis-involved transcriptional factors, have been found in different systems. The serine/threonine phosphorylation of apoptotic components dramatically modulates their pro- or anti-apoptotic property to either promote or inhibit the apoptotic process (Cross et al., 2000b).

##### **IV-1: Survival and apoptotic serine/threonine kinases in the apoptotic signaling**

Many upstream serine/threonine protein kinases responsible for phosphorylation have been identified and categorized as either survival or apoptotic kinases based upon the effect of phosphorylation on these apoptotic components. Survival kinases mainly include protein kinase B (PKB, also known as Akt), full-length P21-activated protein kinase 2 (PAK-2), extracellular signal-related kinase (ERK), pp90 ribosome S6 kinase (Rsk), and  $\alpha$ ,  $\beta$ I,  $\epsilon$  isoforms of protein kinase C (PKC $\alpha$ , PKC $\beta$ I, PKC $\epsilon$ ). PKB, PAK-2, ERK, and Rsk all can phosphorylate Bad, one of the pro-apoptotic members in the Bcl-2 family, causing its binding to chaperone protein 14-3-3 and blocking its translocation to mitochondria and induction of

cytochrome C release (Bonni et al., 1999; Scheid and Duronio, 1998; Yuan and Yankner, 2000). ERK and Rsk also phosphorylate transcription factor cAMP response element binding protein (CREB) to further induce expression of survival genes (Bonni et al., 1999; Yuan and Yankner, 2000). In addition, PKB can phosphorylate caspase-9 to reduce its activity (Cardone et al., 1998). It also can phosphorylate Forkhead transcription factor (FKHRL) to inhibit transcription of death-inducing genes like Fas ligand (Brunet et al., 1999). Besides the mitochondrial apoptotic pathway, phosphorylation of the elongation factor  $2\alpha$  (eIF2 $\alpha$ ) by ER-resident type I transmembrane protein kinase (PERK) in the ER, in response to the accumulation of unfolded proteins in the ER, shuts down the translation before the degradation of all unfolded proteins and protects cells against unfolded proteins-induced apoptosis (Ferri and Kroemer, 2001; Kadowaki et al., 2004).

Apoptotic kinases promoting apoptosis mainly include C-Jun N-terminal kinases (JNKs), p38 mitogen-activated protein (MAP) kinase, apoptosis signal-regulating kinase 1 (ASK1), mammalian sterile 20-like kinase (Mst), and  $\delta$ ,  $\theta$  isoforms of protein kinase C (PKC $\delta$ , PKC $\theta$ ). In particular, JNK/p38 MAP kinase and ASK1 all belong to the MAP kinase family and are major kinases involved in the stress-induced apoptotic signaling (Davis, 2000; Matsuzawa and Ichijo, 2005). ASK1 is one of the very upstream kinases in the MAP kinase family that mediates activation of JNK and p38 after its activation by oxidative stress, the extracellular death signal TNF or Fas ligand, or ER stress (Matsukawa et al., 2004; Takeda et al., 2003). JNK is involved in both the mitochondrial-mediated intrinsic and death-receptor-mediated extrinsic apoptotic pathways. In the intrinsic pathway, activation of JNK is required for stress-induced release of cytochrome C, but the exact mechanism is not yet clear (Tournier et al., 2000). However, both Bcl-2 and Bcl-x1, two anti-apoptotic members in the

Bcl-2 family, have been found to be phosphorylated by JNK *in vitro*, and the phosphorylation inhibits their anti-apoptotic property (Maundrell et al., 1997; Yamamoto et al., 1999), which might be one of the mechanisms for JNK's function in the induction of stress-induced release of cytochrome C. JNK's involvement in the extrinsic pathway is linked to the ER unfolded protein-induced apoptotic signaling. Unfolded proteins in the ER bind to the ER chaperone Bip/Grp78, resulting in the dissociation of Bip to the Ire1- $\alpha$ , a transmembrane ER serine/threonine kinase, and its auto-activation (Katayama et al., 1999). The activation of Ire1- $\alpha$  recruits the cytosolic adapter protein TRAF2, leading to activation of the upstream kinase ASK1 and subsequent activation of JNK (Urano et al., 2000). MAP kinase p38 is usually activated along with JNK and also mediates stress-induced apoptotic signaling (Takeda et al., 2003).

Mst kinase is in another apoptotic kinase family. The pro-apoptotic function of Mst is related to the JNK/p38 MAP pathway, as different genetic analyses have suggested that Mst acts upstream of JNK/p38 MAP kinase to directly activate JNK/p38 MAP kinase (de Souza and Lindsay, 2004). In addition, Mst can also be proteolytically activated by activated caspase-3 and translocate to the nucleus, mediating phosphorylation of histone H2B and facilitating chromatin condensation (Cheung et al., 2003; Lee et al., 2001; Lee and Yonehara, 2002). The pro-apoptotic function of apoptotic kinases has been extensively demonstrated by genetic analysis in cells or knock-out mice; however, biochemical mechanisms of these apoptotic kinases in apoptotic signaling have not been well characterized, largely due to the failure to identify their specific substrates in the apoptotic signaling pathways. So far, only several transcription factors, AP-1, p53, and NF- $\kappa$ B and possibly members of the Bcl-2 family, have been suggested to be the substrates for these apoptotic kinases (Cross et al.,

2000b; Ferri and Kroemer, 2001). More efforts are needed to identify substrates and to better elucidate the regulation of apoptotic kinases in the signal transduction of apoptosis.

#### IV-2: Activation of protein kinase C delta (PKC $\delta$ ) and its function in apoptosis

Protein kinase C delta (PKC $\delta$ ) is one of the novel PKC members. So far, more than 11 isoforms have been categorized in the PKC family and subdivided into three major subfamilies, i.e., conventional PKC ( $\alpha$ ,  $\beta$ I,  $\beta$ II,  $\gamma$ ), novel PKC ( $\delta$ ,  $\epsilon$ ,  $\eta$ ,  $\theta$ ), and atypical PKC ( $\tau/\lambda$ ,  $\zeta$ ) (Newton, 2003; Spitaler and Cantrell, 2004). A conserved structural property of the PKC family, PKC $\delta$  contains N-terminal regulatory and C-terminal catalytic fragments that are connected by a hinge region harboring the caspase-3 recognition and cleavage motif

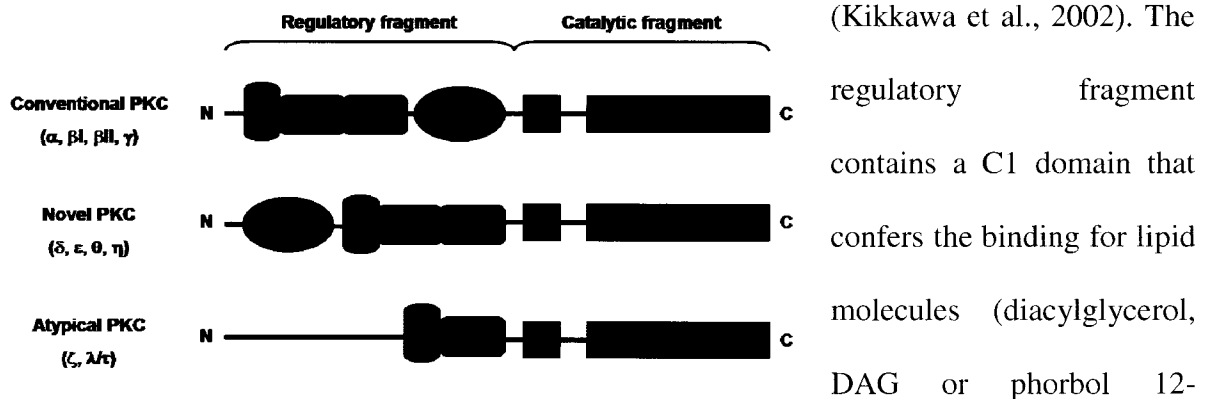


Figure 8. Classification and primary structure of PKC isoforms

myristate 13-acetate, PMA) and a C2-like domain that lacks the Ca<sup>2+</sup> binding capacity. The regulatory fragment also contains a pseudosubstrate that binds to the catalytic site in the tertiary structure and keeps the kinase inactivated. PKC $\delta$  is ubiquitously expressed in most tissues and cell types (Leibersperger et al., 1991; Wetsel et al., 1992). In murine tissue, a high expression level of PKC $\delta$  was found in the epidermis, placenta, uterus, brain, lung, and kidney (Leibersperger et al., 1991). In the central nervous system, PKC $\delta$  is highly expressed

in the thalamus, septal nuclei, and purkinje cells in the posterior cerebellum (Barmack et al., 2000; Naik et al., 2000); however, the expression of PKC $\delta$  in the SNc dopaminergic neurons has not been investigated.

Diverse functions of PKC $\delta$  have been described in different cells. The function of PKC $\delta$  appears to be closely related to its activation mechanism (Gschwendt, 1999; Kikkawa et al., 2002). Three mechanisms for the activation of PKC $\delta$  have been suggested: the first is membrane translocation. The translocated PKC $\delta$  either binds to the phosphatidylserine (PS) on the plasma membrane or diacylglycerol (DAG) generated from phosphatidylinositol 4,5 - bisphosphate (PIP<sub>2</sub>) by phospholipase C (PLC) or the exogenously added lipid molecule PMA. The binding of lipid molecules changes the conformation of PKC $\delta$ , releasing the

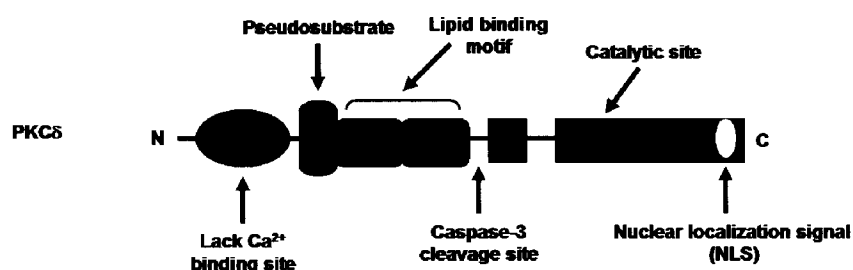


Figure 9. Functional domains of PKC $\delta$

pseudosubstrate from the catalytic site and activating the kinase (Nishizuka, 1992;

Toker, 1998). The lipid-mediated activation of PKC $\delta$  is mostly involved in its normal physiological function as downstream effector of the G-protein coupled receptor (GPCR) or other receptors (Nishizuka, 1992). The second mechanism of activation of PKC $\delta$  is proteolytic cleavage. Caspase-3-mediated proteolytic cleavage of PKC $\delta$  removes the pseudosubstrate along with the whole regulatory domain to persistently activate the kinase (Emoto et al., 1996; Emoto et al., 1995). The proteolytic activation of PKC $\delta$  mainly responds to apoptotic stimuli and promotes the cell death process (Brodie and Blumberg, 2003). The

third mechanism of activation of PKC $\delta$  is phosphorylation. Both serine/threonine and tyrosine phosphorylation activate PKC $\delta$  (Blass et al., 2002; Konishi et al., 2001; Toker, 1998). The activation loop at the terminal of the catalytic domain contains threonine 505 and serine 643 and 662 (Newton, 2003). The phosphorylation of these serine/threonines possibly by 3-phosphoinositide-dependent kinase 1 (PDK-1) facilitates the conformational change for the removal of pseudosubstrate from the catalytic site and is sufficient for activation of the kinase (Hodgkinson and Sale, 2002; Le Good et al., 1998). Extensive tyrosine phosphorylation has been found at various tyrosine sites (Blass et al., 2002; Konishi et al., 2001). The effect of tyrosine phosphorylation on the activity of PKC $\delta$  depends on the individual tyrosine sites; in particular, Y311 and Y332 phosphorylated PKC $\delta$  recovered from H<sub>2</sub>O<sub>2</sub>-treated cells has been found to be constitutively active and independent of DAG (Konishi et al., 1997; Konishi et al., 2001).

The involvement of PKC $\delta$  in apoptosis has been well demonstrated in different cells (Brodie and Blumberg, 2003). In most of cases, PKC $\delta$  is pro-apoptotic, though some studies suggest that it is anti-apoptotic. Depending on the apoptotic stimuli and cell types, PKC $\delta$  can translocate to the mitochondria, nucleus, endoplasmic reticulum (ER), golgi, as well as the plasma membrane in apoptotic cells (Brodie and Blumberg, 2003). Translocation of PKC $\delta$  to the mitochondria was shown to facilitate the mitochondrial pore formation, promote cytochrome C release, and induce the redistribution of Bcl-2 family proteins (Majumder et al., 2000; Murriel et al., 2004; Sitailo et al., 2004). The translocation of PKC $\delta$  to the nucleus was linked to nuclear events that either regulate the mitochondrial apoptotic pathway or facilitate the collapse of nuclear structure in apoptotic cells (Cross et al., 2000a; DeVries et al., 2002).



A potential feedback mechanism between PKC $\delta$  and caspase-3 at either the nucleic or mitochondrial level has been suggested to amplify apoptotic signals by increasing caspase-3 activity (DeVries et al., 2002; Leitges et al., 2001; Leverrier et al., 2002). Although PKC $\delta$  has been found to undergo caspase-3-dependent proteolytic activation and promote neurotoxin-induced apoptotic death of dopaminergic neuronal cells (Kaul et al., 2003; Kitazawa et al., 2003), the detailed mechanisms, including the localization change of activated PKC $\delta$  and downstream events following the activation of PKC $\delta$ , have not been investigated in dopaminergic neuronal cells.

#### **IV-3: Involvement of serine/threonine kinases in neurodegenerative diseases**

Abnormality of serine/threonine protein kinases is also implicated in the neurodegenerative diseases (Wagey and Krieger, 1998). In Parkinson's disease, recent studies have identified mutations in the PTEN-induced kinase 1 (PINK1) or leucine-rich repeat kinase 2 (LRRK2) from familial PD patients. Both PINK1 and LRRK2 appear to be involved in Ras/MAP kinase signaling, as suggested by preliminary studies (Shen, 2004). A mutation in PKC $\gamma$  was also shown to cause Parkinsonian syndrome in the rat (Craig et al., 2001). In MPTP-administered mice, JNK was activated and promoted the apoptotic death of dopaminergic neurons (Saporito et al., 2000; Xia et al., 2001). Moreover, casein kinase-1 and -2 (CK-1 and -2) were found to phosphorylate  $\alpha$ -synuclein which was mutated in familial PD patients (Lee et al., 2004; Okochi et al., 2000). The phosphorylation regulates  $\alpha$ -synuclein and synphilin-1 interaction and inclusion body formation (Lee et al., 2004). In Alzheimer's disease, several kinases, like glycogen synthase kinase-3 (GSK3) and cyclin-dependent

kinase 5 (Cdk5), cause hyperphosphorylation of the microtubule associated protein Tau (Jope and Johnson, 2004; Stoothoff and Johnson, 2005). Hyperphosphorylation of Tau prevents the normal assembly of Tau with microtubules and the orderly polymerization of microtubules, to promote the formation of intracellular neurofibrillary tangle (NFT) (Stoothoff and Johnson, 2005). GSK3 also facilitates the production of  $\beta$ -amyloid (A $\beta$ ) peptide (Phiel et al., 2003). Activation of GSK3 was also observed in the neurons exposed to A $\beta$ , and inhibition of GSK3 activity protects neurons from A $\beta$ -induced neurotoxicity (Jope and Johnson, 2004). In Huntington's disease, PKC $\delta$  associates with intranuclear inclusions in a transgenic model of Huntington's disease (Zemskov et al., 2003). The extensive involvement of serine/threonine protein kinases in various neurological disorders demonstrates the importance of fully understanding their exact roles, especially their regulation or mediation roles in the pathogenesis of these neurological disorders.

## **V. Proteolytic activation and nuclear translocation of serine/threonine protein kinases in apoptosis**

### **V-1: Proteolytic activation of serine/threonine kinases and their function in apoptosis**

Serine/threonine protein kinases have emerged as one main category of substrates of activated caspase-3. Serine/threonine protein kinases identified as substrates of caspase-3 include focal adhesion kinase (FAK) (Wen et al., 1997), mutated in ataxia telangiectasia kinase (ATM) (Tong et al., 2000), DNA dependent protein kinase catalytic subunit (DNA-PKcs) (Itoh and Horio, 2001), p21-activated protein kinase 2 (PAR2) (Jakobi et al., 2003), LIM-kinase 1 (LIMK1) (Tomiyoshi et al., 2004), first level mitogen-activated kinase 1 (MEKK1) (Cardone et al., 1997), mammalian sterile 20-like (Mst) kinase family (de Souza

and Lindsay, 2004; Lee et al., 2001), Rho associated kinases I ROCKI (Coleman et al., 2001), protein kinase N (PKN) (Takahashi et al., 1998), sterile 20-related kinase (SLK) (Sabourin et al., 2000), hematopoietic progenitor kinase 1 (HPK1) (Chen et al., 1999), and two isoforms of protein kinase C (PKC $\delta$  and PKC $\theta$ ) (Datta et al., 1997; Emoto et al., 1995). Most of these kinases, except for FAK, ATM, and DNA-PKcs, are normally inactivated due to the binding of the auto-inhibitory motif located on the regulatory domain of the catalytic site in their tertiary structure. Therefore, caspase-3-mediated proteolytic cleavage removes the auto-inhibitory domain and leads to the constitutive activation of kinases. However, caspase-3-mediated cleavage inactivates ATM, DNA-PKcs, and FAK activity. Inactivation of ATM and DNA-PKcs abolishes their phosphorylation to the downstream kinase DNA-damage-induced kinases (Chk) and inhibits the phosphorylation of transcriptional factor p53 and its degradation, resulting in down-regulation of anti-apoptotic Bcl-2 and up-regulation of pro-apoptotic proteins, Bax, Noxa, and PUMA (Ferri and Kroemer, 2001). The inactivation of FAK disrupts the integrin-mediated cell attachment to the extracellular matrix or other cells and promotes cell death (Wen et al., 1997).

The proteolytically activated kinases all promote apoptosis as the overexpression of the catalytic domain is sufficient to induce apoptosis, and the dominant-negative form of kinases inhibits their pro-apoptotic function. Some of them, MEKK1, HPK1, Mst, and SLK, are suggested to amplify apoptotic signals by forming nuclear or mitochondrial feedback loops as caspase activity increased along with the proteolytic activation of these kinases (de Souza and Lindsay, 2004; Widmann et al., 1998). Indeed, the JNK pathway has been ubiquitously found to be activated by these kinases after their proteolytic activation in different cell lines (Chen et al., 1999). In addition, proteolytically activated kinases more

often serve as effectors to directly mediate the morphological and biochemical changes in apoptotic cells, which eventually accelerate the apoptotic process. Proteolytic activation of ROCK1, LIMK 1, PAK2, PKN, SLK, MST, HPAK65 is involved in the appearance of different apoptotic morphology and biochemical changes, including formation of membrane blebbing and the apoptotic body, cell and nucleus shrinkage, collapse of the nuclear envelope, chromatin condensation, etc. (Chen et al., 1999; Coleman et al., 2001; Cross et al., 2000a; Rudel and Bokoch, 1997; Sabourin et al., 2000; Tomiyoshi et al., 2004).

The ectopic expression of cleaved active hPAK65 was found to associate with cellular and nuclear shrinkage in apoptosis (Lee et al., 1997). The proteolytic cleavage of SLK releases not only an activated kinase domain, but also an actin-disassembling domain, which efficiently promotes the cytoskeleton fiber disassembly in apoptosis (Sabourin et al., 2000). ROCK1, the Rho-associated kinase, after its proteolytic activation, plays an essential role in membrane blebbing in the apoptotic cells by phosphorylating myosin light chain to induce actomyosin contractility (Coleman et al., 2001; Sebbagh et al., 2001). Proteolytically activated LIMK1 is another kinase involved in the membrane blebbing of apoptotic cells (Tomiyoshi et al., 2004). Activated LIMK1 can stabilize ROCK-induced actomyosin contractile structures and phosphorylate cofilin to inactivate it. As cofilin is an actin-binding protein that stimulates depolymerization of actin filament, its inactivation thus promotes actin filament assembly in the blebbing process of apoptotic cells (Tomiyoshi et al., 2004). PAR2 is another kinase that can be proteolytically activated and contributes to the morphological and cytoskeletal changes in apoptosis (Rudel and Bokoch, 1997), though the exact mechanism is not yet clear. PKC $\delta$ , one of the novel PKC isoforms, can also be proteolytically activated by caspase-3. Activated PKC $\delta$  mediates phosphorylation of lamin B

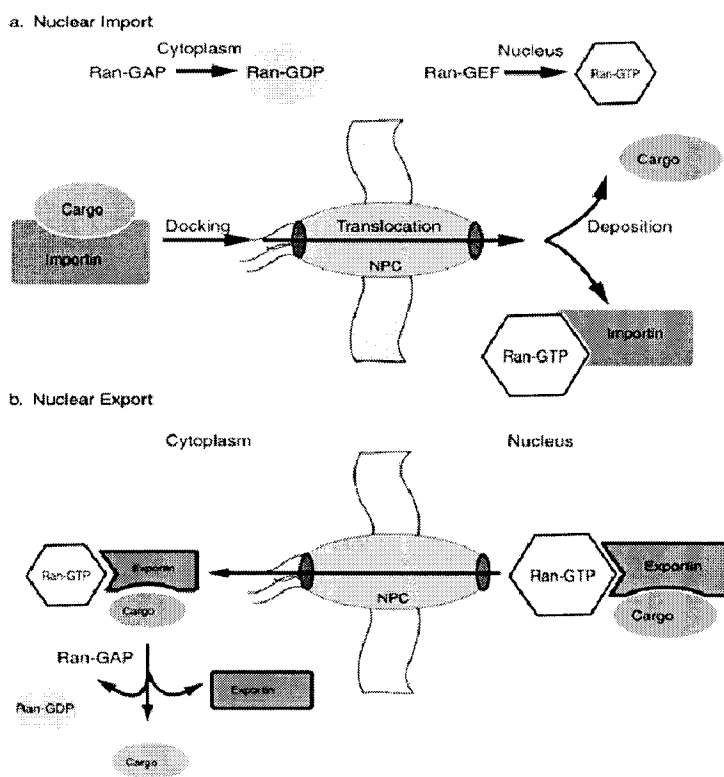
and increases its susceptibility to caspase-3-mediated cleavage, thus facilitating the collapse of the nuclear envelope in apoptotic cells (Cross et al., 2000a). Major biochemical changes in the apoptotic cells include DNA fragmentation and chromatin condensation. The fragmentation of chromatin is due to the action of caspase-activated DNase (CAD) or several other DNases, like endonuclease G (Endo G) and Granzyme A-activated DNase (GAAD) (Orrenius et al., 2003). However, the mechanisms of chromatin condensation are still unclear. It has been suggested that post-translational modification of histones may play an essential role in the condensation of chromatin in apoptosis, as histone phosphorylation has been associated with chromatin condensation in mitosis (Ajiro, 2000; Cheung et al., 2000; Nowak and Corces, 2004). Recently, proteolytically activated Mst1 was shown to translocate to the nucleus and mediate phosphorylation of histone H2B which is associated with chromatin condensation in apoptotic cells (Cheung et al., 2003).

Protein kinases that can be proteolytically activated are normally regulated by other signaling molecules and are involved in other cellular processes. For example, full-length MEKK1 and PAK2 are normally activated by p21 GTP-binding protein Ras or Cdc42/Rac (Knaus and Bokoch, 1998). The activated full-length MEKK1 and PAK2 promote cell survival (Jakobi, 2004). ROCK1 is normally regulated by Rho GTPase and LIMK is activated by Rho-ROCK and Rac/Cdc42-PAK, regulating actin cytoskeleton reorganization (Coleman et al., 2001; Tomiyoshi et al., 2004). However, proteolytic activation of protein kinases in apoptosis and their extensive mediation roles in the apoptotic morphological and biochemical changes suggest that proteolytic cleavage serves as an important switch that converts these kinases from their normal function to pro-apoptotic function. Knowledge of the proteolytic activation of these serine/threonine kinases provides a target for drug

development to specifically inhibit the proteolytic cleavage instead of inhibiting the normal kinase activity, which could block the apoptotic morphological and biochemical changes and rescue the cells from death or delay the death process.

## V-2: Mechanisms of nuclear/cytoplasmic transport

Subcellular localization and trafficking of protein kinases are important, as kinases



**Figure 10. NLS/NES mediated Nuclear import/export (Modified from Kaffman, 1999)**

need to be in close proximity to their activators or substrates for rapid transmission of signals and fulfillment of their effector function (Teruel and Meyer, 2000). The nucleocytoplasmic transport of kinases is particularly important because the cytoplasm and nucleus are two major compartments for all activities in the cell. Although molecules smaller than 40KDa can passively diffuse into the

nucleus, nucleocytoplasmic transport is mainly regulated by the nuclear import and export machinery that includes nuclear localization signal (NLS)/nuclear export signal (NES), importin/exportin, and Ran GTPase (Moroianu, 1999). For nuclear import, proteins bearing the nuclear localization signal (NLS) are bound to the import receptor, importin. The protein-

importin complex is then targeted to the nuclear pore complex (NPC) and translocates into the nucleus. In the nucleus, proteins are dissociated from importin as importin binds to the Ran-GTP. For nuclear export, the export receptor exportin only binds to NES containing proteins in the presence of Ran-GTP. The protein-exportin-Ran-GTP complex is transported out of the nucleus and proteins are disassociated when Ran-GTP undergoes hydrolysis induced by Ran-GTPase activating protein (Ran-GAP) and Ran-binding protein 1 (Kaffman and O'Shea, 1999).

### **V-3: Regulation of nuclear localization of serine/threonine kinases by proteolytic cleavage in apoptosis**

In apoptosis, many kinases undergo NLS or NES dependent transport between the nucleus and the cytoplasm. For example, ERK translocates to the nucleus and phosphorylates transcriptional factor CREB in response to neurotrophic factors induced cell survival (Ajenjo et al., 2004; Yuan and Yankner, 2000). Interestingly, proteolytic cleavage of kinases by caspase-3 closely regulates their nucleocytoplasmic localization, which further regulates their distinct function in apoptosis (Jakobi, 2004). The regulatory role of proteolytic cleavage in kinase subcellular localization and function is based on the observation that full-length PAR2 is predominantly localized in the cytoplasm and is involved in cell survival, whereas the cleaved PAR2p34 translocates to the nucleus and promotes apoptosis (Jakobi et al., 2003; Knaus and Bokoch, 1998). Full-length PAR2 contains an N-terminal regulatory and a C-terminal catalytic domain. Although the regulatory domain contains a functional NES motif and the hinge region contains a functional NLS motif, the nuclear export seems dominant over the nuclear import, and thus full-length PAR2 predominantly localizes in the cytoplasm.

After the cleavage, however, the NES is removed along with the regulatory domain; the nuclear import mediated by the NLS in the hinge region becomes dominant and leads to the nuclear localization of cleaved PAR2p34 (Jakobi et al., 2003). Similar to the PAR2, two functional NES are found in the C-terminal regulatory domain of Mst1 to keep full-length MSt1 in the cytoplasm (Lee and Yonehara, 2002; Ura et al., 2001). The proteolytic cleavage removes both NES along with C-terminal regulatory domain and induces nuclear translocation of cleaved Mst1p36 (Ura et al., 2001). PKC $\delta$  is another kinase that the cleaved catalytic domain translocates to the nucleus (Brodie and Blumberg, 2003). Functional NLS has been found in the C-terminal catalytic domain and no functional NES has been found yet (DeVries et al., 2002). Intriguingly, although it contains only functional NLS, but not functional NES, PKC $\delta$  is primarily localized in the cytoplasm, though a small fraction is localized in the nucleus. It is likely that the NLS in PKC $\delta$  is normally kept, possibly by the N-terminal regulatory domain, in the incompetent status, and the proteolytic cleavage could convert the NLS from incompetent status into competent status by removing the regulatory domain, thus promoting its nuclear translocation.

## **VI. RNA interference (RNAi) and its neuroprotective application in neurodegenerative diseases**

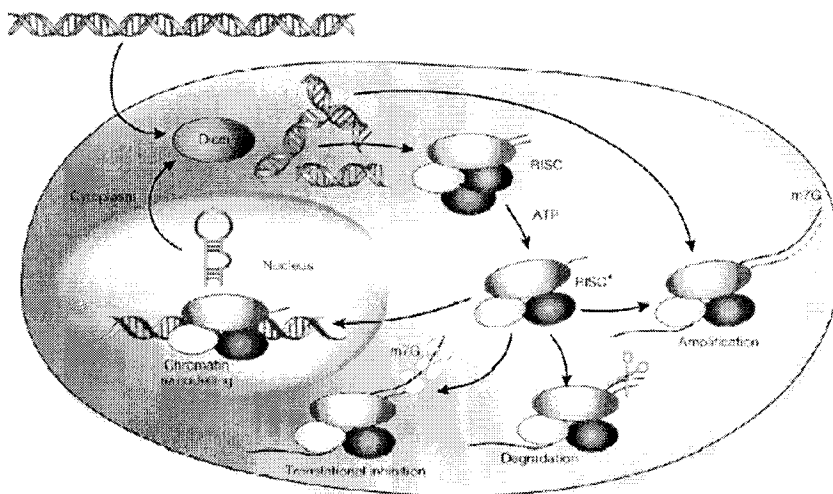
RNA interference (RNAi) is a new form of post-transcriptional gene silencing (PTGS) discovered within the past 10 years. The endogenous process down-regulates gene expression by either inducing the sequence-specific degradation of complementary mRNA or by inhibiting translation, or possibly by promoting DNA methylation or formation of heterochromatin (Hannon, 2002). After its initial discovery in *C. elegans*, the RNAi



phenomenon has been observed in many other systems, including *Arabidopsis* (also called co-suppression or virus induced gene silencing, VIGS), fungi, *Drosophila*, various mammalian cells and animals (Fire et al., 1998; Hammond et al., 2001; Schwarz et al., 2002). Meanwhile, endogenous micro RNA (miRNA) encoding genes are being rapidly and widely identified in different species, including humans, and are implicated in regulation of various physiological processes (Bartel, 2004).

### VI-1: Mechanisms of RNA interference

The machinery and mechanisms of RNAi are being rapidly revealed after the intense studies conducted during the past several years. The mechanisms of RNAi have been conserved across different species, though specific adjustments are present in different species. For example, in *C. elegans* and plants, RNAi is heritable and shows a systematic (spreading throughout the whole organism) nature of silencing; in *Drosophila* and mammals,



**Figure 11. General mechanisms of RNAi (Modified from Hannon, 2002)**

it shows cell-autonomous, non-heritable silencing (Hannon, 2002). All species have a Dicer enzyme that belongs to the RNase III ribonuclease family

and catalyzes the conversion of exogenous long (300-500bp) double-strand RNA (dsRNA) to

21-23bp small interfering RNA (siRNA) (Bernstein et al., 2001). The generated siRNA usually contains 5' phosphates and 2 nt 3' overhangs, as characteristic of RNase III cleavage products (Elbashir et al., 2001b). The double-strand siRNA is then separated by helicase so that only one strand is incorporated into a nuclease complex, RNA induced silencing complex (RISC) (Nykanen et al., 2001; Zamore et al., 2000). This complex, after binding to siRNA, is activated in an ATP dependent manner and leads to the degradation of target mRNA that is complementary to the siRNA (Nykanen et al., 2001; Zamore et al., 2000). In addition to the degradation of target mRNA, the RISC-siRNA complex can also down-regulate gene expression by translational inhibition or by promoting chromatin remodeling, including DNA methylation, heterochromatin formation, and DNA rearrangements (Bartel, 2004; Schramke and Allshire, 2004). In mammals, however, exogenously introduced long dsRNA is recognized as viral RNA by mammalian cellular defense systems, which activates RNA-dependent protein kinase (PKR). Activated PKR subsequently phosphorylates protein synthesis initiation factor EIF-2 $\alpha$  and leads to the inhibition of all protein synthesis in the cells (Gil and Esteban, 2000). Therefore, in mammals, siRNA, instead of dsRNA, is directly used for induction of specific silencing effects (Elbashir et al., 2001a).

The observation that very small amounts of dsRNA can induce strong RNAi effects which spread throughout the organism in plants and *C. elegans* suggests that RNAi in these organisms may have specific mechanisms to amplify and spread RNAi signals (Hannon, 2002). The dsRNA-induced silencing effect in these organisms requires proteins similar in sequence to a tomato RNA-directed RNA polymerase (RdRP) (Schiebel et al., 1998). Genetic studies in *Arabidopsis* and *C. elegans* have identified several mutants that might act as RdRP to produce extra dsRNA using initially generated siRNA as the primer (Dalmay et

al., 2000; Mourrain et al., 2000). The additionally produced dsRNA can be further cleaved by Dicer enzyme to produce more siRNA, thus increasing the silencing effect. It has also been speculated that the RISC-siRNA complex may induce chromatin structure alteration and produce aberrant mRNA, which can also be employed by RdRP to produce extra dsRNA (Hannon, 2002). For systemic RNAi effects, a transitive RNAi phenomenon has been observed in which the silencing signal moved along a particular gene from 3'-5' (in *C. elegans*) or in both directions (in plants) (Baulcombe, 2002a, b). In addition, it has also been speculated in plants that silencing signals could be passed to adjacent cells through cell-cell junctions (movement of RNA and proteins via cell-cell junctions is well characterized), or even further through the vasculature (Hannon, 2002; Voinnet et al., 1998). Indeed, the *sid-1* gene is required for a systemic silencing effect in *C. elegans*. This gene encodes a transmembrane protein that may act as a channel for import of the silencing signal in *C. elegans* (Winston et al., 2002). Interestingly, SID-1 homologues are absent in *Drosophila*, consistent with the lack of systemic spreading of the silencing effect in flies (Hannon, 2002).

## **VI-2: Design of siRNA for mammalian systems**

RNAi provides a powerful tool for characterization of gene function as the loss-of-function phenotype can be quickly linked to a specific gene. Indeed, genome-wide RNAi screening has been carried out in several plants and invertebrates (Dykxhoorn et al., 2003; Hammond et al., 2001). In mammals, though long dsRNA fails to induce specific silencing effects because it triggers cellular defense systems, specific silencing effects have been successfully achieved by an alternative short siRNA strategy (Elbashir et al., 2001a; Mittal, 2004). Although the short siRNA sequence is mainly based on the target mRNA sequence,

the selection of exact target sites on the target mRNA is still difficult and thus not every designed siRNA is effective. Basically, short siRNA (21bp) needs to have a phosphorylation group at the 5' end and 2nt UU overhang at the 3' end, so a typical siRNA would be 5'P-(N19)UU-3', where N is any of four nucleotides (Mittal, 2004).

In addition, several empirical criteria based on the biochemical mechanisms of RNAi have been suggested in the selection of target sites and structural requirements of siRNA sequences (Mittal, 2004; Reynolds et al., 2004). These criteria include: 1) the target sequence has overall low to medium GC content (30-50%) that facilitates its interaction with RISC complex and its unwinding; 2) the internal stability should be lower in the 5' antisense strand but higher in the 5' sense strand to promote the incorporation of antisense but not the sense strand into the RISC complex, i.e., choose A or U instead of G or C at the 3' end of the sense strand that forms weaker hydrogen bonds (Schwarz et al., 2003); 3) no internal repeats or palindromes are present in the siRNA that reduce likelihood of formation of an siRNA dimer; 4) the presence of a U at position 10 of the sense strand that promotes RISC mediated cleavage of mRNA and dissociation of the RISC-siRNA complex. These criteria significantly improve the efficiency of designed siRNA, though all designed siRNAs still need to be tested. Designed siRNA can be either chemically synthesized or generated via *in vitro* transcription (Holle et al., 2004; Yu et al., 2002). For *in vitro* transcription, the DNA template for siRNA is usually linked to a T7 promoter so that both sense and antisense strands can be transcribed *in vitro* by T7 RNA polymerase and annealed to generate the functional double strand siRNA.

Recently, expression of vector-based small hairpin RNA (shRNA) has become preferred, as it can consistently induce a silencing effect for the observation of some late phenotypes and allows establishment of a stable cell line. The design of shRNA is based on

the recent progress made in the natural production and maturation of micro RNA (miRNA) in cells (Bartel, 2004). The miRNA is matured from pri-miRNA transcribed from miRNA

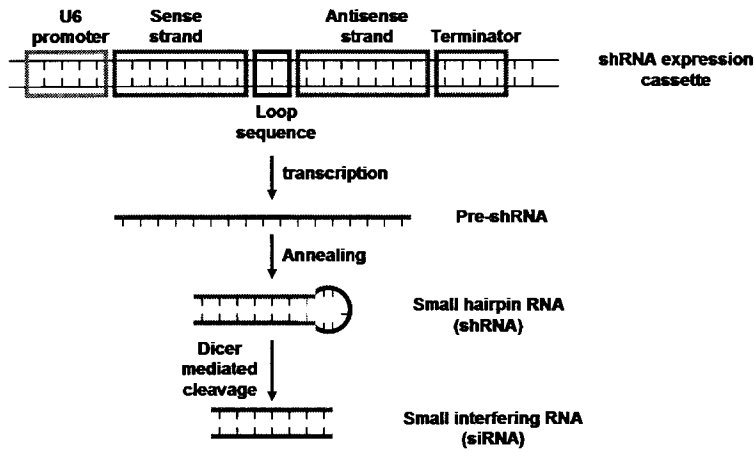


Figure 12. Schematic diagram of shRNA expression cassette and the generation of siRNA from expressed shRNA

genes. The cleavage of pri-miRNA by Drosha RNase III endonuclease in the nucleus releases a 60-70nt stem loop intermediate, known as the miRNA precursor (pre-miRNA) (Lee et al.,

2002; Zeng and Cullen, 2003; Zeng et al., 2003). The stem loop shaped pre-miRNA is then exported out of the nucleus and cleaved by Dicer endonuclease to generate the mature double strand miRNA (Lee et al., 2003). Based on this model, small DNA oligonucleotide that contains sense and antisense strands complementary to the target mRNA and interspaced by loop nucleotides is cloned into an expression vector driven by RNA polymerase III promoter, like small nuclear RNA (snRNA) U6 or H1 RNA (Paddison et al., 2002; Paul et al., 2002; Sui et al., 2002). Similar stem loop structure, like pre-miRNA, would be formed after the DNA oligonucleotide is transcribed in the cell. This expressed stem loop “pre-siRNA” can then be cleaved by Dicer to generate functional siRNA in the cells. This strategy of producing siRNA and induction of a silencing effect has become a choice method, especially for *in vivo* experiments in which delivery of siRNA is usually very inefficient.

### **VI-3: Application of RNAi-mediated neuroprotective strategy in neurodegenerative diseases**

The high efficiency of siRNA in mammalian cells, along with its target specificity and easy handling, has provided a new neuroprotective strategy for neurodegenerative diseases. Because RNAi can specifically down-regulate specific genes, dominant mutated alleles implicated in the pathogenesis of different neurodegenerative diseases are potentially good targets for therapeutic gene silencing (Mittal, 2004). The selective RNAi targeting of only the dominant mutated allele is critical, as the normal allele can still produce proteins for its normal function in the cells. This approach has been recently demonstrated in the selective silencing of mutated ataxia-3, contributing to the polyglutamine (polyQ) toxicity in spinocerebellar ataxia type 3 (SCA3) (Xia et al., 2004). In the polyglutamine disorders, the expansion of the CAG repeat in the genes causes the additional incorporation of glutamine that changes the protein's conformation and promotes the abnormal aggregation. In this study, effective siRNA targeting the CAG repeat was first designed, but down-regulated both the mutant and wild-type genes. Instead, other siRNAs targeting a single nucleotide polymorphism (SNP) located immediately 3' to the CAG repeat, which is in linkage disequilibrium with the disease-causing CAG expansion and segregates with the disease allele in most families, were designed and effectively silenced only the expression of the mutated allele and not the wild type allele (Xia et al., 2004). Similar strategies have also been successfully applied to other dominant disease-causing alleles, including the missense mutation Tau V337M underlying the disorder frontotemporal dementia with Parkinsonism (Miller et al., 2003), the TorsinA gene underlying a form of dystonia, a missense mutation of muscle acetylcholine receptor (AChR)  $\alpha$  subunit S226F that causes the slow channel

congenital myasthenic syndrome (SCCMS) (Gonzalez-Alegre et al., 2003), and a tandem missense mutation of the amyloid precursor protein APP<sup>sw</sup> underlying Alzheimer's disease (Miller et al., 2004). Such technologies show promise for application in other neurodegenerative diseases in which mutated disease-causing dominant alleles are implicated.

For the more common sporadic form of neurodegenerative diseases, progress in the investigation of apoptotic death of neurons will likely lead to identification of cytotoxic proteins that underlie the pathogenesis of diseases as potential targets for RNAi. In our laboratory, we have demonstrated that down-regulation of the oxidative stress sensitive kinase PKC $\delta$  by siRNA effectively protects dopaminergic neurons from MPP<sup>+</sup>-induced toxicity (Yang et al., 2004). The down-regulation of prostate apoptosis response-4 (Par-4) by siRNA protects against cell death in a Cu/Zn superoxide dismutase (Cu/Zn-SOD) transgenic mouse model of Amyotrophic lateral sclerosis (ALS) (Xie et al., 2005). The many enzymes and kinases shown to facilitate the production of free radicals or cell death may be good targets for RNAi. However, because many of these molecules are involved in both physiological and pathological processes, the effect of the down-regulation of these targets on normal physiological process must be considered and be autonomously or artificially compensated for in the cells.

Most of the successful siRNA-mediated neurprotective strategies have been demonstrated in cells by direct transfection of siRNA or introduction of vector expressing shRNA. In some cell lines, chemically synthesized or *in vitro* transcribed siRNA can be easily introduced into the cells by electroporation or lipophilic reagents (Mittal, 2004). However, these approaches are limited by their transient nature, as introduced siRNAs are usually degraded in several days (Dykxhoorn and Lieberman, 2005). Although the

expression of shRNA partially solves this problem by facilitating the establishment of a stable cell line, both the synthetic siRNA and vector-based shRNA often fail to efficiently deliver siRNA into neuronal cells or non-dividing primary neurons due to the very low transfection efficiency in these cells (Mittal, 2004). In addition, an *in vivo* mammalian animal model demonstrating the neuroprotective effect of siRNA is required to really demonstrate that siRNA could be a good therapeutic reagent. Also, new tools for the efficient introduction and long term expression of siRNA in neurons *in vivo* are required.

Numerous viral vectors have been developed from adenovirus, recombinant adeno-associated virus (AAV), retrovirus, and lentivirus to solve the siRNA delivery problem *in vivo* (Brenner and Malech, 2003; Kirik and Bjorklund, 2003; Rubinson et al., 2003). Among these viral vectors, the replication-deficient lentiviral vector is most desirable because lentivirus can infect not only the dividing cells but also the non-dividing cells, and can integrate its genome efficiently into the genome of host cells (Blomer et al., 1997; Kafri et al., 1997; Mittal, 2004; Miyoshi et al., 1997). To deliver the siRNA into the neuron, a shRNA cassette that contains the RNA polymerase III promoter, shRNA template, and RNA polymerase III terminator is first cloned into the replication-deficient lentiviral vector, and then lentivirus is produced by infection of the 293FT cells. The produced lentivirus, after concentration, can be directly injected into the brain to infect certain groups of neurons. Lentiviral vector mediated delivery of shRNA has been successful in mice and inhibits the expression of co-transfected reported plasmids (Lewis et al., 2002; McCaffrey et al., 2002), of the endogenous pro-apoptotic Fas receptor (Song et al., 2003), and of the tyrosine hydroxylase (TH) gene in the brain (Hommel et al., 2003). Recently, inducible lentiviral vectors have also been developed, which provide more flexibility to create animal disease



models and to test the neuroprotective effect of specific siRNA (Wiznerowicz and Trono, 2003). By using the inducible lentiviral vector, in principle, shRNA targeting any genes can be transduced into the mice and inducibly expressed to allow the observation of some late phenotypes (Mittal, 2004). This approach, compared to the large scale ethylnitrosurea (ENU) mutagenesis, is much less laborious and more effective.

**CHAPTER II: SUPPRESSION OF CASPASE-3 DEPENDENT PROTEOLYTIC  
ACTIVATION OF PROTEIN KINASE C $\delta$  BY SMALL INTERFERING RNA (SiRNA)  
PREVENTS MPP<sup>+</sup>-INDUCED DOPAMINERGIC DEGENERATION**

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**ABSTRACT**

The cellular mechanisms underlying the neurodegenerative process in Parkinson's disease are not well understood. Using RNA interference (RNAi), we demonstrate that caspase-3 dependent proteolytic activation of protein kinase C  $\delta$  (PKC $\delta$ ) contributes to the degenerative process in dopaminergic neurons. The Parkinsonian toxin MPP<sup>+</sup> activated caspase-3 and proteolytically cleaved PKC $\delta$  into catalytic and regulatory subunits, resulting in persistent kinase activation in mesencephalic dopaminergic neuronal cells. The caspase-3 inhibitor Z-DEVD-FMK and the caspase-9 inhibitor Z-LEHD-FMK effectively blocked MPP<sup>+</sup>-induced PKC $\delta$  proteolytic activation. To characterize the functional role of PKC $\delta$  activation in MPP<sup>+</sup>-induced dopaminergic cell death, RNAi mediated gene knock-down was performed. Among four siRNAs designed against PKC $\delta$ , two specifically suppressed PKC $\delta$  expression. The application of siRNA abolished the MPP<sup>+</sup>-induced PKC $\delta$  activation, DNA

fragmentation, and TH positive neuronal loss. Together, these results suggest that proteolytic activation of PKC $\delta$  may be a critical downstream event in the degenerative process of Parkinson's disease.

## INTRODUCTION

Understanding the cellular mechanisms involved in the selective loss of nigral dopaminergic neurons in Parkinson's disease (PD) remains a formidable challenge. Apoptosis has recently been recognized as an important mode of cell death in PD, mainly by the identification of key markers of apoptotic cell death including mitochondrial cytochrome c release, caspases activation and DNA fragmentation in PD pathology (Dodel et al., 1998; Hartmann et al., 2000; Mizuno et al., 1998; Viswanath et al., 2001). Major insights into the neurodegenerative process in PD have been gained from the use of the mitochondrial toxin MPTP (1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine), which faithfully replicates the salient Parkinsonian symptoms and pathology (Albanese et al., 1993; Betarbet et al., 2002; Langston et al., 1984). MPTP is converted to its ionic metabolite MPP<sup>+</sup> (1-methyl-4-phenylpyridinium) in the brain, which induces a series of apoptotic signaling events including reactive oxygen species (ROS) generation, mitochondrial dysfunction, cytochrome c release, caspases activation, and DNA fragmentation in cell culture and animal PD models (Cassarino et al., 1997; Cassarino et al., 1999; Hartmann et al., 2000; Lee et al., 2000; Lotharius and O'Malley, 2000; Viswanath et al., 2001; Wu et al., 2003). Furthermore, ROS is one of the major contributors to apoptotic cell death in dopaminergic neurons (Beal, 2002; Ischiropoulos and Beckman, 2003; Lotharius and Brundin, 2002; Olanow and Tatton, 1999). However, little is

known about the molecules and mechanisms that act downstream of caspases during MPP<sup>+</sup>-induced apoptotic cell death in dopaminergic neurons.

Phosphorylation is a major cellular signaling mechanism by which many critical neuronal functions including cell survival, differentiation, and death are regulated. One of the key members of phosphorylation signaling is protein kinase C (PKC) family. It includes 13 isoforms, which are classified mainly into three subgroups based on their dependence upon diacylglycerol (DAG) and Ca<sup>2+</sup> for activation (Dempsey et al., 2000; Gschwendt, 1999; Maher, 2001). The conventional PKC isoforms (PKC  $\alpha$ ,  $\beta$ I,  $\beta$ II, and  $\gamma$ ) require DAG and Ca<sup>2+</sup> for activation, the novel PKC isoforms (PKC  $\delta$ ,  $\epsilon$ ,  $\eta$ ,  $\theta$ , and  $\mu$ ) require only DAG but not Ca<sup>2+</sup> for activation and the atypical PKCs (PKC  $\zeta$ ,  $\lambda$  and  $\iota$ ) require neither Ca<sup>2+</sup> nor DAG for activation. Kinase activation involves autophosphorylation followed by translocation to the cell membrane and other organelles (Brodie and Blumberg, 2003; Gschwendt, 1999; Kikkawa et al., 2002). Recent studies have shown that PKC $\delta$  can be proteolytically activated by caspase-3 during apoptotic cell death in non-neuronal cells (Emoto et al., 1996; Mandil et al., 2001; Meinhardt et al., 1999; Pongracz et al., 1999; Reyland et al., 1999). These studies characterized the function of PKC $\delta$  activation in apoptotic cell death mainly by utilizing the pharmacological inhibitor rottlerin or dominant-negative mutants. The non-specific nature of this pharmacological inhibitor (Davies et al., 2000) and the inherent problems with overexpression (Buchner, 2000; Gschwendt, 1999) warrant use of a more powerful tool to investigate the function of PKC $\delta$  in dopaminergic cell death.

Double-strand RNA (dsRNA)-mediated RNA interference (RNAi) is emerging as a powerful tool to characterize gene function by genetic loss-of-function analysis. This novel

post-transcriptional gene silencing mechanism was first demonstrated with great success in plants, *C. elegans*, *Drosophila* (Barstead, 2001; Carmell et al., 2002; Elbashir et al., 2001a; Hammond et al., 2001; Hasuwa et al., 2002; Morel and Vaucheret, 2000; Shi, 2003; Sorensen et al., 2003; Vaucheret et al., 2001; Vaucheret and Fagard, 2001; Xia et al., 2002) and more recently in cultured mammalian cells as well as in animal models (Carmell et al., 2002; Elbashir et al., 2001a; Hasuwa et al., 2002; Shi, 2003; Sorensen et al., 2003; Xia et al., 2002). Small interfering RNA (siRNA), usually 21 bp, is widely applied in mammalian cell cultures as compared to 300-500 bp dsRNA in non-mammalian systems (Donze and Picard, 2002; Krichevsky and Kosik, 2002; Paddison et al., 2002). Because of its high efficacy, selectivity and ease of application, RNAi is now a preferred method over pharmacological inhibitor studies, the antisense technique, and overexpression analysis (Jen and Gewirtz, 2000; Opalinska and Gewirtz, 2002). In the present study, we demonstrate that proteolytic activation of PKC $\delta$  by caspase-3 facilitates apoptotic cell death in an *in vitro* model of Parkinson's disease and suppression of PKC $\delta$  expression using siRNA rescues dopaminergic neuronal cells from MPP<sup>+</sup>-induced cell death.

## RESULTS

### **MPP<sup>+</sup> exposure induces caspase-3 mediated proteolytic activation of PKC $\delta$**

Activity of the key effector cysteine protease caspase-3 was measured in rat mesencephalic clonal dopaminergic neuronal (N27) cells treated with the Parkinsonian toxin MPP<sup>+</sup> (300  $\mu$ M). Maximal caspase-3 activation of 228% over untreated control cells was observed 36 hr following MPP<sup>+</sup> treatment (Fig 1A). Activation of caspases by MPP<sup>+</sup> was also

confirmed by *in situ* caspase staining (Fig 1B). All the MPP<sup>+</sup>-treated cells showed intense green fluorescence indicative of caspase activation, while untreated cells showed very low levels of caspase activation.

Interestingly, MPP<sup>+</sup> exposure for 36 hr also induced the proteolytic cleavage of native PKC $\delta$  (72-74 kDa) to yield catalytically active (41/38 kDa) fragments (Fig 2A). Co-treatment with the caspase-3-specific inhibitor Z-DEVD-FMK almost significantly reduced MPP<sup>+</sup>-induced proteolytic cleavage of PKC $\delta$ , indicating that caspase-3 mediated the cleavage of PKC $\delta$  (Fig 2A). Densitometric analysis revealed an 81% inhibition of PKC $\delta$  cleavage by Z-DEVD-FMK. Moreover, we sought to determine whether caspase-9, the upstream initiator of the mitochondrial-mediated caspase cascade, contributes to the caspase-3-dependent proteolytic cleavage of PKC $\delta$ . The caspase-9-specific inhibitor Z-LEHD-FMK significantly blocked MPP<sup>+</sup>-induced PKC $\delta$  cleavage (Fig 2B). Thus, caspase-9 might be the upstream initiator caspase that proteolytically activates caspase-3, which subsequently cleaves PKC $\delta$ .

Caspase-3-mediated proteolytic cleavage of PKC $\delta$  results in the permanent dissociation of the regulatory subunit from the catalytic subunit, resulting in the persistently active catalytic fragment. Therefore, we performed immunoprecipitation kinase assays to determine if caspase-3-dependent proteolytic cleavage of PKC $\delta$  increased its kinase activity during MPP<sup>+</sup> treatment. A 36hr exposure to 300  $\mu$ M MPP<sup>+</sup> increased PKC $\delta$  enzymatic activity 239% in comparison to untreated control cells (Fig 2C). Co-treatment with the caspase-3 specific inhibitor Z-DEVD-FMK completely blocked MPP<sup>+</sup>-induced increases in PKC $\delta$  enzyme activity, suggesting that caspase-3 mediated proteolytic activation of PKC $\delta$

contributed to the increases in kinase activity. To further determine whether MPP<sup>+</sup> treatment alters PKC $\delta$  gene expression in dopaminergic neuronal cells, we conducted RT-PCR analysis. As shown Figure 2D, the PKC $\delta$  mRNA level remained unchanged after MPP<sup>+</sup> treatment. PKC $\delta$  translocation was also examined by extraction of membrane and cytosolic fractions and by Western blot analysis. PKC $\delta$  did not translocate to the membrane during MPP<sup>+</sup> treatment (Fig 3A). Cleavage of the other major PKC isoform, PKC $\alpha$  (Fig 3B), was not detected either, suggesting that the PKC $\delta$  isoform is mainly activated by proteolytic cleavage during MPP<sup>+</sup> treatment.

### **Design and generation of siRNAs**

To determine the functional role of proteolytic activation of PKC $\delta$  in apoptotic cell death, genetic loss-of-function analysis was performed using siRNA. Four siRNAs were designed: three targeted different positions within the coding region (siRNA- $\delta$ -1, 2 and 4) and one (siRNA- $\delta$ -3) targeted the 3'UTR of PKC $\delta$  mRNA (Fig 4A). Choice of target sites was based on previous empirical criteria (Elbashir et al., 2001b). A non-specific siRNA (siRNA-NS) was also designed to serve as a negative control. For each siRNA, sense and antisense templates were designed based on each target sequence and partial T7 promoter sequence (Fig 4B). siRNAs were prepared using an *in vitro* transcription method employing Ambion's silencer siRNA construction kit (Ambion, Austin, TX). Synthesized double stranded siRNAs were examined for transcriptional efficacy and purity in the native PAGE gel as shown in Fig 4C. All the siRNAs except siRNA- $\delta$ -3 were transcribed efficiently, as depicted by the single band of expected size. siRNAs were also labeled with Cy3-fluorescent

dye using the Ambion's silencer siRNA labeling kit (Ambion, Austin, TX) to determine the transfection efficiency as well as to identify the siRNA-transfected cells. The transfection efficiency determined by counting the number of Cy3 positive cells at 24 hr post-transfection was about 80%.

### **Selective suppression of PKC $\delta$ expression by siRNA**

We next examined the ability of siRNAs to suppress endogenous PKC $\delta$  expression. N27 cells were transfected with 5-25 nM of siRNA- $\delta$ -1, 2, 3, 4 and siRNA-NS using the *TransIT*-TKO transfection reagent (Mirus, Madison, WI). Cell lysates were extracted at 24 and 48 hrs post transfection and the levels of PKC $\delta$  protein expression were determined by Western blotting. siRNA- $\delta$ -1 and siRNA- $\delta$ -4 significantly suppressed PKC $\delta$  expression in a time- and dose-dependent manner (Fig 5 A&B). Densitometric analysis revealed 12%, 26%, and 66% reduction in endogenous PKC $\delta$  protein expression following transfection with 5 nM, 10 nM, and 25 nM siRNA- $\delta$ -4 for 24 hr, respectively. Unlike siRNA- $\delta$ -4, PKC $\delta$  expression was significantly reduced in siRNA- $\delta$ -1-transfected cells only at 48 hr post-transfection and densitometric analysis revealed 69% reduction following transfection with 25 nM siRNA- $\delta$ -1. On the other hand, PKC $\delta$  expression was not significantly suppressed in siRNA- $\delta$ -2- and siRNA- $\delta$ -3-transfected N27 cells at either 24 hr or 48 hr (data not shown). siRNA-NS had no silencing effect on PKC $\delta$  expression at either 24 hr or 48 hr post-transfection (Fig 5 A&B). Notably, siRNA- $\delta$ -4 and siRNA- $\delta$ -1 did not alter the expression level of the closely related novel PKC isoform PKC $\epsilon$ , indicating their high selectivity for PKC $\delta$  (Fig 5 A&B). Moreover, temporal analysis of PKC $\delta$  expression in cells transfected with siRNA- $\delta$ -4 revealed that the



suppression of PKC $\delta$  expression by siRNA- $\delta$ -4 was maximal at 24 hr post-transfection (Fig 5C). RT-PCR analysis of PKC $\delta$  mRNA also revealed a 50% reduction in PKC $\delta$  mRNA level with siRNA- $\delta$ -4 treatment as compared to siRNA-NS treatment (Fig 5D), indicating that siRNA- $\delta$ -4 effectively degrades PKC $\delta$  transcripts, which subsequently reduces PKC $\delta$  protein expression.

### ***In situ* localization of siRNA and PKC $\delta$ immunohistochemistry**

We next performed siRNA labeling and immunostaining studies to determine if PKC $\delta$  expression was specifically suppressed in siRNA- $\delta$ -4-transfected cells. After transfecting N27 cells with Cy3-labeled siRNA- $\delta$ -4, PKC $\delta$  immunostaining and Hoechst 33342 counterstaining were used to identify PKC $\delta$  protein and nucleus, respectively. PKC $\delta$  immunofluorescence revealed a strong and equal distribution of the kinase in the cytoplasm of normal N27 cells (Fig 6C). In siRNA- $\delta$ -4-transfected cells, Cy3-labeled siRNA accumulated largely in the cytoplasm at the same time PKC $\delta$  protein expression was significantly reduced, indicating that siRNA- $\delta$ -4 transfection indeed suppressed the expression of PKC $\delta$  (Fig 6A). In siRNA-NS transfected cells, merged yellow fluorescence was clearly observed, suggesting that Cy3-labeled siRNA-NS still accumulated but PKC $\delta$  protein expression was not altered at all (Fig 6B). The fluorescence intensity of PKC $\delta$  immunoreactivity was also quantified using Metamorph image analysis software. As shown in Figure 6D, siRNA- $\delta$ -4-transfected cells showed an approximate 71% reduction in PKC $\delta$  expression as compared to control cells, whereas PKC $\delta$  expression was not significantly changed in siRNA-NS-transfected cells compared to controls cells. Furthermore, cellular

morphology and integrity were not changed in siRNA-transfected N27 cells as compared to normal N27 cells, indicating that the cells tolerate siRNA treatment.

### **Suppression of MPP<sup>+</sup>-induced PKC $\delta$ kinase activity and DNA fragmentation by siRNA- $\delta$ -4**

To determine if siRNA- $\delta$ -4 blocks MPP<sup>+</sup>-induced PKC $\delta$  activity, we performed an *in vitro* kinase assay following immunoprecipitation of PKC $\delta$  in control and siRNA- $\delta$ -4-transfected cells after MPP<sup>+</sup> exposure. PKC $\delta$  kinase activity was significantly increased by 215% in cells exposed to MPP<sup>+</sup> (300  $\mu$ M) for 36 hr as compared to untreated control cells (Fig 7A). MPP<sup>+</sup> did not induce PKC $\delta$  activity in siRNA- $\delta$ -4-transfected cells, demonstrating that siRNA- $\delta$ -4 effectively suppressed PKC $\delta$  expression and thereby attenuated MPP<sup>+</sup>-induced proteolytic activation of PKC $\delta$ . To further characterize the functional role of PKC $\delta$  activation in apoptotic cell death, we examined the effect of siRNA- $\delta$ -4 on MPP<sup>+</sup>-induced DNA fragmentation. DNA fragmentation was increased 2-fold in N27 cells following MPP<sup>+</sup> treatment and was almost completely blocked in siRNA- $\delta$ -4 transfected cells (Fig 7B), demonstrating the key proapoptotic function of PKC $\delta$  in MPP<sup>+</sup>-induced dopaminergic cell death.

### **Suppression of PKC $\delta$ expression by siRNA- $\delta$ -4 in primary mesencephalic neuronal cultures**

The efficiency of siRNA- $\delta$ -4 at suppressing PCK $\delta$  expression was further examined in primary dopaminergic neurons. Cy3-labeled siRNAs were transfected into primary

mesencephalic cultures isolated from rat E17 embryos. Tyrosine hydroxylase (TH) and PKC $\delta$  immunostaining were performed 24 hr post-transfection to determine the efficiency of siRNA incorporation in dopaminergic neurons and to measure PKC $\delta$  expression, respectively. As depicted in Figure 8A, Cy3-labeled siRNA- $\delta$ -4 effectively incorporated in TH positive neurons and the siRNAs localized mainly in the cytoplasm. Quantitative analysis of PKC $\delta$  expression, as measured by the fluorescence intensity of PKC $\delta$  immunoreactivity, in siRNA- $\delta$ -4- or siRNA-NS-transfected TH positive neurons revealed a 42% reduction in PKC $\delta$  expression (Fig 8B). Collectively, these results demonstrate that siRNA- $\delta$ -4 efficiently incorporates in primary dopaminergic neurons and suppresses PKC $\delta$  expression.

#### **Neuroprotective effect of siRNA- $\delta$ -4 against MPP<sup>+</sup>-induced dopaminergic toxicity in primary mesencephalic neurons**

We further examined whether or not siRNA- $\delta$ -4 protects against MPP<sup>+</sup>-induced neurotoxicity in nigral dopaminergic neurons. TUNEL staining and nuclei counterstaining with Hoechst 33342 were employed to detect *in situ* DNA fragmentation induced by MPP<sup>+</sup> treatment. TUNEL and TH dual staining is complicated by MPP<sup>+</sup> treatment, which results in significant loss of TH positive cells. However, dopaminergic neurons in primary mesencephalic cultures can be readily identified by their large cell bodies and extensive neuronal processes as compared to other cell types. After selecting a field that contains these neurons, we performed TUNEL imaging. As shown in Figure 9A, Cy3-labeled si-RNA- $\delta$ -4 and siRNA-NS were found in the cytoplasm and around nuclei. TUNEL staining showed that MPP<sup>+</sup> treatment induces apoptosis in siRNA-NS treated cells. The TUNEL positive cells also

showed chromatin condensation, as observed by Hoechst 33342 staining. However, siRNA- $\delta$ -4-transfected neurons showed no TUNEL staining and the nuclei remained intact during MPP<sup>+</sup> treatment. These results indicate that siRNA- $\delta$ -4 prevents MPP<sup>+</sup>-induced DNA fragmentation in primary mesencephalic neurons. To further demonstrate siRNA's protective effect in dopaminergic neurons, the number of TH positive neurons was counted; quantification of TH positive neurons is considered to be a reliable method of determining MPP<sup>+</sup>-induced dopaminergic toxicity in primary mesencephalic cultures (Callier et al., 2002; Choi et al., 1999). Treatment with 10  $\mu$ M MPP<sup>+</sup> for 48 hr substantially decreased the number of dopaminergic neurons by over 87% as compared to untreated control cells (Fig 9B). However, MPP<sup>+</sup>-induced TH<sup>+</sup> neuronal loss was dramatically reduced to 33% in the siRNA- $\delta$ -4-transfected primary neurons, demonstrating a significant neuroprotective effect of siRNA- $\delta$ -4. siRNA-NS-transfected primary neurons were not significantly protected following MPP<sup>+</sup> exposure (Fig 9B). Figure 9C summarizes the actual number of TH positive neurons in each treatment group. Together, these results demonstrate that suppression of PKC $\delta$  expression by siRNA protects against dopaminergic degeneration induced by MPP<sup>+</sup>.

### **Cytotoxicity testing following siRNA- $\delta$ -4 treatment**

In conventional gene silencing methods such as antisense mediated knock-down, cytotoxicity is always a major concern because of the high concentration of antisense oligonucleotides introduced into cells and/or the nucleotide modifications made to the antisense probes. To investigate whether siRNA suppresses gene expression without causing significant toxicity to cells, we monitored lactate dehydrogenase (LDH) release in the

extracellular media as a marker of cytotoxicity (Kanthasamy et al., 1995). As shown in Figure 10, LDH levels in the extracellular medium of either siRNA- $\delta$ -4- or siRNA-NS-transfected cells were not significantly different from untreated control cells, indicating that siRNA treatment is not significantly toxic to mesencephalic neuronal cells.

## DISCUSSION

The present study demonstrates that MPP<sup>+</sup> induces proteolytic activation of PKC $\delta$  in a caspase-3 dependent manner, which subsequently contributes to apoptotic cell death in mesencephalic dopaminergic cells. Notably, siRNA against rat PKC $\delta$  mRNA effectively blocked MPP<sup>+</sup>-induced PKC $\delta$  activation and DNA fragmentation in dopaminergic neuronal cells, suggesting that PKC $\delta$  is an important proapoptotic molecule in dopaminergic degeneration. To our knowledge, this is the first report demonstrating a siRNA based neuroprotective strategy in a cell culture model of Parkinson's disease.

Oxidative stress is considered a key mediator of neurodegenerative processes in Parkinson's disease because of the extreme sensitivity of nigral dopaminergic neurons to oxidative insults (Ischiropoulos and Beckman, 2003; Jenner, 2003; Lotharius and Brundin, 2002). The Parkinsonian neurotoxin MPP<sup>+</sup> induced cell death model serves as an useful model to delineate the cellular mechanisms underlying degenerative process in Parkinson's disease (Kaul et al., 2003; Kaur et al., 2003; Lotharius et al., 1999). Recent studies have demonstrated that reactive oxygen species (ROS) generated from mitochondrial and/or non-mitochondrial sources (Lotharius and O'Malley, 2000) appear to contribute to MPP<sup>+</sup>-induced

neurodegeneration (Kaur et al., 2003; Lee et al., 2000; Lotharius et al., 1999; Wu et al., 2003). MPP<sup>+</sup>-induced ROS generation has been previously shown to promote mitochondrial cytochrome c release, caspase-9 activation and subsequently caspase-3 dependent apoptotic cell death (Jackson-Lewis et al., 1995; Viswanath et al., 2001). However, caspase-8 mediated apoptotic cascade does not seem to be critical to MPP<sup>+</sup>-induced apoptotic cell death (Kaul et al., 2003; Vila and Przedborski, 2003). In this study, we showed that MPP<sup>+</sup> induces activation of caspase-3 within 36 hr of MPP<sup>+</sup> treatment. Our result is in agreement with recent reports which identified caspase-3 as a critical factor in the selective apoptotic cell death of dopaminergic neurons in the MPTP mouse model and in post mortem brains of patients with PD (Dodel et al., 1998; Hartmann et al., 2000). Recently, we showed that ROS scavengers and a caspase-9 inhibitor block MPP<sup>+</sup> induced caspase-3 activation (Kaul et al., 2003). In the present study, we further demonstrate that caspase-9 inhibitor Z-LEHD-FMK significantly inhibit MPP<sup>+</sup> -induced PKC $\delta$  proteolytic cleavage. Taken together, these results suggest that mitochondrial mediated caspase cascade involving cytochrome c release and activation of caspase-9 and caspase-3 may be important upstream events in the proteolytic activation of PKC $\delta$ .

The downstream cellular events initiated by caspase-3 have not been clearly defined in dopaminergic cell death following exposure to MPP<sup>+</sup>. Although the DNA repair enzymes Poly (ADP-ribose) polymerase (PARP) (Earnshaw et al., 1999; Tewari et al., 1995), DNA-PK (Itoh and Horio, 2001), and several nuclear envelope proteins (Martelli et al., 2001) are characterized as substrates of caspase-3 in non-neuronal cells, their contribution to dopaminergic neuronal cell death is unclear. Since phosphorylation is a key regulatory mechanism in apoptotic signaling, we focused our attention on the PKC isoforms in the

present study. The majority of studies have shown that activation of PKC isoforms mainly suppresses apoptosis in a variety of non-neuronal cell types (Brodie and Blumberg, 2003; Dempsey et al., 2000; Gschwendt, 1999; Kikkawa et al., 2002; Maher, 2001). However, accumulating evidence indicates that apoptotic stimuli and oxidative insults induce activation of the novel PKC isoform PKC $\delta$  (Ha et al., 2001; Kikkawa et al., 2002; Majumder et al., 2001; Otieno and Kensler, 2000; Sun et al., 2000) PKC $\delta$  can be activated through at least three different mechanisms: (i) translocation to the plasma membrane, (ii) phosphorylation at tyrosine, serine or threonine, and (iii) caspase-3-mediated proteolytic cleavage (Kikkawa et al., 2002). Our data demonstrate a persistent activation of PKC $\delta$  during MPP<sup>+</sup> treatment resulting from proteolytic cleavage mediated by caspase-3 that leads to permanent dissociation of the catalytic subunit of PKC $\delta$  from the regulatory subunits. The caspase-3 inhibitor Z-DEVD-FMK blocked 81% of PKC $\delta$  cleavage as determined by the densitometric analysis of Western blot data whereas a complete inhibition was observed with Z-DEVD-FMK on PKC $\delta$  activity (Fig 2C). This difference may be due to the residual effect of the cleaved fragments detected in the Western blot or may be due to effectiveness of a newly prepared caspase-3 inhibitor used in the kinase assay. Furthermore, PKC $\delta$  did not translocate to the membrane, indicating that proteolytic activation is the major form of activation of PKC $\delta$  during MPP<sup>+</sup> treatment.

Our findings clearly demonstrate that siRNA inhibits PKC $\delta$  in an isoform specific manner, which has never been possible with the use of pharmacological inhibitors. For example, rottlerin has been widely used as an inhibitor of PKC $\delta$  (Basu et al., 2001; Reyland et al., 1999), but recent reports indicate that rottlerin can inhibit other kinases including MAP

kinases (Davies et al., 2000). The mechanisms of action of siRNA in the present study may be due to translational suppression of PKC $\delta$  because siRNA- $\delta$ -4 effectively inhibited both PKC $\delta$  mRNA (Fig. 5D) and the protein expression (Fig. 5A). Previous studies have shown the suppression of mRNA and protein levels following siRNA treatments (Hannon, 2002; Irie et al., 2002; Nagy et al., 2003). Recently, Kaasinen et al reported that PKC $\delta$  expression was induced following a kainate lesion or in ischemic brain damage (Kaasinen et al., 2002). However, we did not find any significant induction of PKC $\delta$  mRNA expression up to 36 hr of MPP<sup>+</sup> treatment. The induction of PKC $\delta$  expression in kainate and ischemic cell death may be related to the neuronal excitation associated with excitotoxicity. In this regard, neuronal excitation due to glutamate treatment found to increase PKC $\delta$  activation which is independent of cleavage (Ahlemeyer et al., 2002). Blockade of MPP<sup>+</sup>-induced proteolytic activation PKC $\delta$  and DNA fragmentation by siRNA- $\delta$ -4 in N27 cells clearly establishes proapoptotic function for PKC $\delta$  in neuronal apoptosis. Tunnel staining in MPP<sup>+</sup>-treated primary mesencephalic dopaminergic neurons further extends the apoptotic function of PKC $\delta$  in dopaminergic neuronal degeneration. In primary mesencephalic cultures, the effect of siRNA on PKC $\delta$  protein suppression (42%) and dopaminergic neuronal survival (54%) showed a reasonable correlation, further supporting the proapoptotic role of PKC $\delta$  in dopaminergic neuronal cell death.

We also found that siRNA transfected cells were phenotypically similar to control cells, suggesting that siRNA treatments are well tolerated by neuronal cells. Thus, siRNA-mediated knock-down of PKC $\delta$  appears to be an extremely effective method of gene inactivation that does not induce significant toxicity. Because of the high specificity and low



toxicity of siRNAs, the therapeutic application of this technique has recently been explored (Caplen, 2003; O'Neil et al., 2001). Xia et al., 2002 demonstrated as proof of principle that siRNA technology could attenuate neurodegeneration in an animal model of Huntington's disease.

Although the cellular events downstream of PKC $\delta$  responsible for cell death are not well understood, PKC $\delta$  has been shown to regulate a number of molecules that are associated with the cell death process including scrambalase (Frasch et al., 2000), DNA protein kinase (DNA-PK) (Bharti et al., 1998), heat-shock proteins-25/27 (Maizels et al., 1998), lamin B (Cross, 2000 #14), human RAD9 (Yoshida et al., 2003) and the redox sensitive transcription factor NF- $\kappa$ B (Page et al., 2003). Recently, PKC $\delta$  was also shown to translocate to the nucleus upon activation (DeVries et al., 2002). Thus, PKC $\delta$  may exert its proapoptotic function by interacting with the one or more of the downstream effectors. Studies are underway to identify key PKC $\delta$  interacting proteins that might contribute to apoptotic cell death in dopaminergic neurons.

In conclusion, we demonstrated that proteolytic activation of PKC $\delta$  facilitates dopaminergic cell death in cell culture models of PD and selective targeting of the proapoptotic kinase PKC $\delta$  by siRNA could rescue dopaminergic neurons. The proapoptotic function PKC $\delta$  in dopaminergic degeneration may have therapeutic implications in Parkinson's disease.

## MATERIALS AND METHODS

**Reagents**

MPP<sup>+</sup> (1-Methyl-4-phenylpyridinium), protease cocktail, ATP, protein-A-sepharose, and anti- $\beta$ -actin antibody were obtained from Sigma-Aldrich (St. Louis, MO); CaspACE<sup>®</sup> kit was purchased from Promega; Z-DEVD-FMK was obtained from Alexis Biochemicals (San Diego, CA); Z-LEHD-FMK was purchased from BD Biosciences (San Diego, CA). Ac-DEVD-AMC (Acetyl-Asp-Glu-Val-Asp-7-Amino-4-Methyl-Coumarin) and the rabbit polyclonal antibody for tyrosine hydroxylase were obtained from Calbiochem Bioscience, Inc. (King of Prussia, PA); antibodies to PKC $\delta$ , PKC $\alpha$ , and PKC $\epsilon$  were purchased from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA). Anti-rabbit and anti-mouse secondary antibodies and the ECL chemiluminescence kit were purchased from Amersham Pharmacia Biotech. (Piscataway, NJ). Alexa 488 conjugated anti-rabbit antibody and Hoechst 33342 were purchased from Molecular Probes, Inc. (Eugene, OR). The Cell Death Detection ELISA plus Assay Kit was purchased from Roche Molecular Biochemicals (Indianapolis, IN). [ $\gamma$ -<sup>32</sup>P] ATP was purchased from Perkin Elmer Life Science Products (Boston, MA). The Bradford protein assay kit was purchased from Bio-Rad Laboratories (Hercules, CA). RPMI, fetal bovine serum, L-glutamine, penicillin, and streptomycin were purchased from Invitrogen (Gaithersburg, MD). The siRNA silencer construction kit and labeling kit were purchased from Ambion, Inc (Austin, TX). *TransIT*-TKO Reagent was purchased from Mirus (Madison, WI). Oligonucleotides were synthesized and PAGE purified with Integrated DNA Technology (Iowa City, IA). Quantity One 4.2.0 software was purchased from Bio-Rad (Hercules, CA) and Vector NTI software was purchased from InforMax Inc., (Frederick,

MD). TUNEL kit was purchased from Upstate Biotechnology (Lake Placid, NY). cDNA synthesis kit and Taq enzyme were purchased from Invitrogen, Inc., (Carlsbad, CA).

### **Cell culture**

The immortalized rat mesencephalic dopaminergic neuronal cell line (N27) was a kind gift from Dr. Kedar N. Prasad, University of Colorado Health Sciences Center (Denver, CO). N27 cells were grown in RPMI 1640 medium containing 10% fetal bovine serum, 2 mM L-glutamine, 50 units penicillin, and 50 µg/ml streptomycin. Cells were grown in a humidified atmosphere of 5% CO<sub>2</sub> at 37°C as previously described (Anantharam et al., 2002; Kitazawa et al., 2003), and 4-5 days old cells were used for the experiments.

### **Primary mesencephalic neuronal culture**

Primary mesencephalic neuronal cultures were prepared from the ventral mesencephalon of gestational 16-17 day old rat embryos as described in detail elsewhere (Madhavan et al., 2003; Wang et al., 1995). Briefly, dissected tissues were maintained on ice cold calcium free EBSS supplemented with gentomycin (50 mg/ml) and penicillin/streptomycin (200units/ml) and then dissociated in EBSS solution containing trypsin (0.25%) for 15 min. The dissociated cells were plated at equal density ( $0.5 \times 10^6$  cells) in 30 mm diameter tissue culture wells pre-coated with poly-L-lysine (1 mg/ml). Cultures were maintained in a chemically defined, serum-free medium consisting of neurobasal medium fortified with B-27 supplements, L-Glutamine (500 µM), penicillin (100 IU/ml) and streptomycin (100 µg/ml) (Life Technologies). The cells were maintained in a humidified CO<sub>2</sub> incubator (5% CO<sub>2</sub>, 37°C) for 24 hr and then treated with cytosine

arabinoside (10  $\mu\text{M}$ ) for 24 hr to inhibit glial cell proliferation. Half of the culture medium was replaced every 2 days. Approximately 6-7 day old cultures were used for experiments.

### **Treatment paradigm**

Transfected and untransfected N27 cells were treated with 300  $\mu\text{M}$  MPP<sup>+</sup> for 36 to 42 hr at 37°C. Primary neuron was exposed to 10 $\mu\text{M}$  MPP<sup>+</sup> for 48hr. MPP<sup>+</sup> was added to siRNA transfected cells 24 hr post-transfection. In caspase-3 and caspase-9 inhibitor studies, cells were co-treated with Z-DEVD-FMK or Z-LEHD-FMK and MPP<sup>+</sup>. Untreated cells were used as a negative control.

### **Design and preparation of siRNAs**

siRNAs were prepared by an *in vitro* transcription method. Target sites were selected based on previously established empirical criteria (Elbashir et al., 2001b) Initially, four siRNA (siRNA- $\delta$ -1,  $\delta$ -2,  $\delta$ -3, and  $\delta$ -4) target sites specific to rat PKC $\delta$  mRNA (gi: 18959249), as determined by blast analysis, were chosen. One non-specific siRNA (siRNA-NS) was also chosen based on random sequence. For each siRNA, sense and antisense templates were designed based on each target sequence and partial T7 promoter sequence (Donze and Picard, 2002). All template oligonucleotides were chemically synthesized and PAGE purified. *In vitro* transcription, annealing, and purification of siRNA duplexes were performed using the protocol supplied with the silencer siRNA construction kit (Ambion, Inc. Austin, TX). Briefly,  $\sim 2$   $\mu\text{g}$  of each single-strand (ss) transcription template was first annealed with the T7 promoter and filled in by Klenow DNA polymerase to form double-strand transcription templates. For preparation of each siRNA duplex, transcription reactions

were first performed with separated antisense and sense templates using the T7 RNA polymerase provided with the kit and then annealed to form siRNA duplexes. Then the siRNA duplex was treated with DNase and RNase to remove the extra nucleotides of transcribed siRNA to meet the structural 3'UU overhang and 5'phosphate requirement (Elbashir et al., 2001b).

### **siRNA transfection**

N27 Cells (50-70% confluency) and primary mesencephalic neurons were transfected with siRNA duplexes using the protocol supplied with the *TransIT*-TKO Reagent (Mirus Corp, Madison, WI). Briefly, the TKO reagent was first diluted (1:100) into RPMI 1640 medium for about 15 min, and then the siRNA duplex was added to the medium to form a lipid-siRNA complex. Following additional 15 min incubation, transfection was initiated by adding the lipid-siRNA complex to 24-well or 6-well plates. The final concentration of siRNA varied from 5 to 25 nM.

### **Cy3 labeling of siRNAs**

Purified siRNA duplexes were labeled using the silencer siRNA labeling kit (Ambion, Austin, TX). Briefly, ~5  $\mu$ g siRNA duplex was added to the Cy3 labeling reagent and the reaction mixture was then incubated at 37°C in the dark for 1 hr. The unlabeled Cy3 was removed by ethanol precipitation. The labeled siRNAs were then delivered to cells by transfection. Cy3 labeled siRNAs in transfected cells were visualized using a Nikon inverted fluorescence microscope (Model TE-2000U) and pictures were captured with a SPOT digital camera (Diagnostic Instruments, Sterling Heights, MI).

### **Isolation of cytoplasmic fractions**

Cytoplasmic fractions were isolated as described previously (Anantharam et al., 2002). Briefly, after treatment, the N27 cells were harvested with trypsin/EDTA solution and spun at 200 x g for 5 min. Cell pellets were then washed twice with ice-cold PBS (1 mM sodium phosphate, 15 mM NaCl, and pH 7.4) and resuspended in 200  $\mu$ l of hypotonic buffer (10 mM HEPES, pH 7.9, 1.5 mM MgCl<sub>2</sub>, 10 mM KCl, 1 mM DTT, and protease inhibitor cocktail diluted 1:100). Triton-X 100 (final concentration 0.5%) was then added to the homogenization and vortexed vigorously for 15 sec. Cell lysates were centrifuged for 30 min at 14,000 rpm and supernatants were collected. Protein concentrations were determined using a Bradford protein assay kit.

### **Western blotting**

Equal amounts of cytoplasmic protein (10-20 $\mu$ g) were loaded in each lane and separated on a 10% SDS-polyacrylamide gel as described previously (Anantharam et al., 2002). Proteins were then transferred to nitrocellulose membrane by electro-blotting overnight (4°C, 25 V). Non-specific binding sites were blocked by treating the nitrocellulose membranes with 5% non-fat dry milk TBST solution (10 mM Tris, 150 mM NaCl, and 0.1% Tween 20) for 1 hr. The nitrocellulose membranes were then incubated with primary antibodies for 1 hr at RT (anti-PKC $\alpha$ ,  $\delta$  or  $\epsilon$  antibodies, 1:2000). The primary antibody treatment was followed by treatment with secondary HRP-conjugated anti-rabbit or anti-mouse IgG (1:2000) for 1 hr at RT. Secondary antibody-bound proteins were detected using an ECL chemiluminescence kit (Amersham). To confirm equal protein loading, blots were

reprobed with  $\beta$ -actin antibody (1:5000). Gel photographs and densitometric analysis were performed with a Kodak image station (Model 1000R, Rochester, New York).

### **RT-PCR**

After treatment, cells were lysed in 1 ml TRIZOL reagent and total RNA was isolated by chloroform extraction and precipitated by ethanol. First, total RNA was treated with DNase I to remove DNA contamination and then reversely transcribed into first strand cDNA using the SuperScript III first-strand synthesis system (Invitrogen, Inc, Carlsbad, CA) as described in the kit instructions. Quantitative PCR was performed with PKC $\delta$  primers and control GAPDH primers as previously described (Suzuki et al., 2000). The primer sequences used were as follows: rat PKC $\delta$  – forward: 5' gggctacgtttatgcagct 3'; reverse: 5' agcaggtctgggagctcact 3'; rat GAPDH - forward: 5' atgggaagctggatcatcaac 3'; reverse: 5' ttagcccaggatgccctt 3'. The PCR reaction was performed in DNA thermal cycler. The amplified products were visualized on agarose gel impregnated with ethidium bromide and the intensity of amplified products was measured with a Kodak image station.

### **Immunocytochemistry**

Immunostaining of PKC $\delta$  was performed 24 hr post-transfection in untransfected, Cy3-siRNA- $\delta$ -4, and Cy3-siRNA-NS transfected N27 cells. Cells grown on poly L-lysine coated glass cover slips were gently washed with PBS twice, fixed in 4% paraformaldehyde, washed 3 X 7 min with PBS, permeabilized, and blocked with blocking reagent (0.4% BSA, 5% goat serum, and 0.2% Triton-X 100 in PBS) for 20 min. Cells were then incubated with

anti-PKC $\delta$  rabbit polyclonal antibody (1:200 in blocking reagent) overnight at 4°C and then washed 4 X 8 min with PBS. PKC $\delta$  was visualized by incubation with Alexa 488-conjugated goat anti-rabbit secondary antibody (1:200 in PBS) at RT for 90 min. After another 4 X 8 min PBS wash, Hoechst 33342 (final concentration of 10  $\mu$ g/ml in PBS) was added to stain the cell nuclei at RT for 3 min. Finally, cells were washed once in PBS and mounted on a slide with Antifade mounting medium. The cells were observed under a Nikon inverted fluorescence microscope (Model TE-2000U) and pictures were captured with a SPOT digital camera (Diagnostic Instruments, Sterling Heights, MI). For primary neurons, immunostaining of TH was performed using rabbit polyclonal TH antibody (1:200). Quantitative analysis of immuno fluorescence was measured by defining the region of interest (ROI) in Metamorph image analysis software and plotted in Prism software.

### **Immunoprecipitation kinase assay**

PKC $\delta$  enzymatic activity was assayed using an immunoprecipitation kinase assay as previously described (Anantharam et al., 2002). After treatment with MPP<sup>+</sup>, N27 cells were washed twice with PBS and resuspended in 200  $\mu$ l of PKC lysis buffer (25 mM HEPES, pH 7.5, 20 mM  $\beta$ -glycerophosphate, 0.1 mM sodium orthovanadate, 0.1% Triton X 100, 0.3 M NaCl, 1.5 mM MgCl<sub>2</sub>, 0.2 mM EDTA, 0.5 mM DTT, 10 mM NaF, and 4  $\mu$ g/ml each of aprotinin and leupeptin). The cells were homogenized by sonication for 15 sec under ice-cold conditions. The cytoplasmic fractions were collected by centrifuging the cell lysates at 14,000 x g for 30 min. Protein concentrations were determined by Bradford protein assay. Cytoplasmic protein (0.2-0.4 mg) was immunoprecipitated overnight at 4°C using 4  $\mu$ g of



anti-PKC $\delta$  antibody. The immunoprecipitates were then incubated with protein-A-sepharose for 1 hr at 4°C. The protein-A bound antigen-antibody complexes were then washed 3 times with PKC lysis buffer, 3 times with kinase buffer (40 mM Tris, pH 7.4, 20 mM MgCl<sub>2</sub>, 20  $\mu$ M ATP, and 2.5 mM CaCl<sub>2</sub>), and resuspended in 20  $\mu$ l of kinase buffer. Reactions were started by adding 20  $\mu$ l of reaction buffer containing 0.4 mg Histone H1 and 5  $\mu$ Ci of [ $\gamma$ -<sup>32</sup>P] ATP (3,000 Ci/mM) to the immunoprecipitated samples and incubated for 10 min at 30°C. SDS gel loading buffer (2X) was then added to terminate the reaction, the samples were boiled for 5 min, and the products were separated on a 12% SDS-PAGE gel. The phosphorylated H1 histone bands were detected using a Personal Molecular Imager (FX model, Bio-Rad) and quantified using Quantity One 4.2.0 software (Bio-Rad, Hercules, CA).

### **Enzymatic assay for caspase-3**

Caspase-3 activity was measured as previously described (Yoshimura et al., 1998). Briefly, cells were spun down after treatment and the pellets were lysed with Tris buffer (pH 7.4, 50 mM Tris HCl, 1 mM EDTA, and 10 mM EGTA) containing 10  $\mu$ M digitonin for 15 min at 37°C. Lysates were centrifuged at 900 x g for 3 min and the resulting supernatants were incubated with a specific fluorogenic caspase-3 substrate (Ac-DEVD-AMC, 10  $\mu$ M) at 37°C for 1 hr. Cleaved substrate was monitored at excitation  $\lambda$  380 nm and emission  $\lambda$  460 nm using a multiwell fluorescence plate reader (Model: Gemini XS, Molecular Devices, Sunnyvale, CA). Caspase-3 activity was calculated as fluorescence units per mg protein per hour and expressed as percentage of control.

***In situ* analysis of caspase activity**

A cell-permeable fluorescent probe FITC-VAD-FMK was used in this assay. The experimental procedure was performed according to Promega's CaspACE<sup>®</sup> kit, with some minor modifications. N27 cells were grown on poly-L lysine (0.1 mg/ml) coated cover slips for 24 hrs. After exposure to MPP<sup>+</sup>, the cells were treated with 10  $\mu$ M FITC-VAD-FMK for 20 min at 37°C in the dark. Cells were then rinsed once with PBS and fixed with 10% buffered formalin for 30 min at room temperature in the dark. After fixation, the cells were washed twice and observed under a Nikon Diaphot microscope. Pictures were captured with a SPOT digital camera (Diagnostic Instruments, Sterling Heights, MI).

**Quantification assay for DNA fragmentation**

DNA fragmentation was measured using a recently developed Cell Death Detection ELISA plus Assay Kit (Molecular Biochemicals, Indianapolis, IN) (Anantharam et al., 2002; Reyland et al., 1999). Briefly, cells were spun down at 200 x g for 5 min and washed twice with 1X PBS. Cells were then incubated with a lysis buffer (supplied with the kit) at RT. After 30 min, samples were centrifuged and 20  $\mu$ l aliquots of the supernatant were then dispensed into streptavidin-coated 96 well microtiter plates followed by addition of 80  $\mu$ l of HRP-conjugated antibody cocktail, and incubated for 2 hr at RT with mild shaking. After incubation, unbound components were removed by washing with the incubation buffer supplied with the kit. The nucleosomes retained by the antibody cocktail in the immunocomplex were quantified spectrophotometrically with ABTS as an HRP substrate. Measurements were made at 405 nm and 490 nm using a SpectroMax 190 spectrophotometer

(Molecular Devices, Sunnyvale, CA). The difference of absorbance between OD 405 and OD 490 nm was used to measure the actual DNA fragmentation level.

### **TUNEL staining**

Primary neurons were cultured on coverslip in 6-well plates. After siRNA transfection and MPP<sup>+</sup> treatment, cells were washed by 1X PBS and fixed with 4% paraformaldehyde for 15min and permeabilized with 0.2% Triton-X containing 0.2% BSA in PBS for another 15 min. Cells were then incubated in TdT end-labeling cocktail (50 $\mu$ l/coverslip) containing Biotin-dUTP, TdT buffer and TdT for 60 min at RT and reaction was stopped by immersing cells in 1X TB buffer. After the wash, the neurons were incubated in blocking reagent containing avidin-FITC for 30 min at RT and then washed with 1X PBS. Nucleus counterstaining was then performed by incubating cells with Hoechst 33342 for 3 min. Cells were washed with 1X PBS and mounted on slides. The cells were observed and pictures captured as described in the immunocytochemistry section. Quantitative analysis of fluorescence immunoreactivity was measured by defining the region of interests (ROI) in Metamorph software and plotted in Prism software.

### **Lactate Dehydrogenase (LDH) Assay**

LDH activity in the cell-free extracellular supernatant was quantified as an index of cell death (Kanthasamy et al., 1995). We modified the original method to a 96-well format (Kitazawa et al., 2001). Briefly, both untransfected and siRNA transfected N27 cells were plated in 96-well plate and 24 hr after transfection 10  $\mu$ l of the extracellular supernatant was added to 200  $\mu$ l of 0.08 M Tris buffer (pH 7.2) containing 0.2 M NaCl, 0.2 mM NADH, and

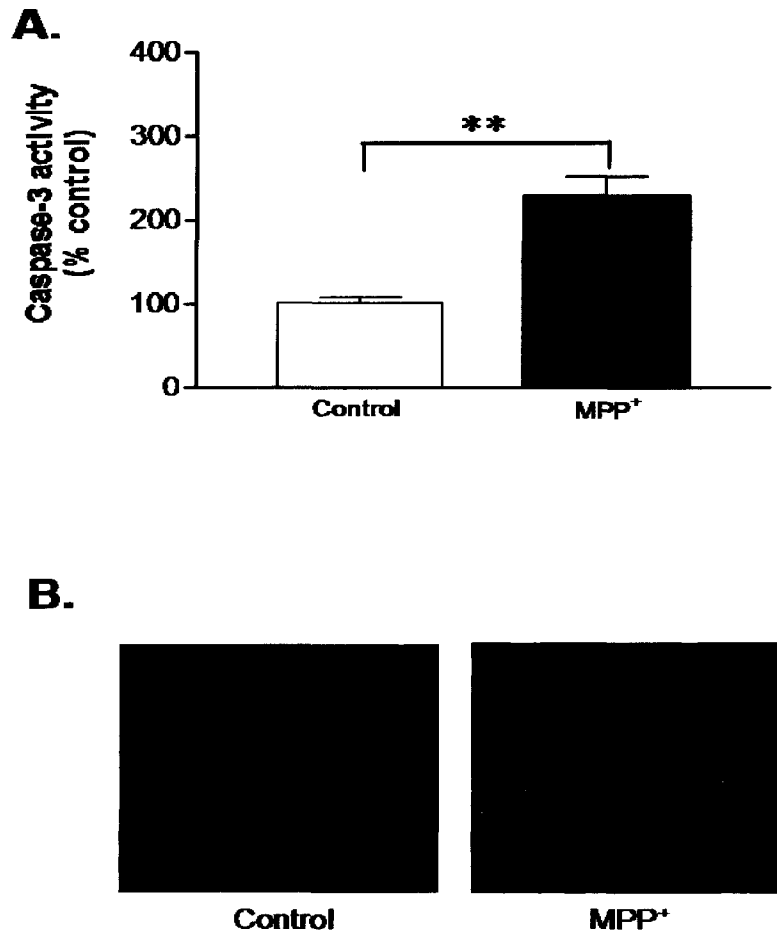
1.6 mM sodium pyruvate. LDH activity was measured continuously by monitoring the decrease in the rate of absorbance at 339 nm using a microplate reader (Molecular Devices, Sunnyvale, CA) and the temperature was maintained at 37°C during reading. Changes in absorbance per minute ( $\delta A/\delta T$ ) were used to calculate LDH activity (U/I), using the following equation:  $U/I = (\delta A/\delta T) \times 9682 \times 0.66$ , where 9682 was a coefficient factor, and 0.66 was a correction factor at 37°C.

### **Data analysis**

Data analysis was performed using Prism 3.0 software (GraphPad Software, San Diego, CA). Data from PKC $\delta$  kinase, DNA fragmentation and LDH assays were first analyzed using one-way ANOVA. Bonferroni's post-test was then performed to compare all groups and differences with  $p < 0.05$  were considered significant. To analyze the caspase-3 enzymatic activity results, the paired t-test was used.

### **ACKNOWLEDGEMENTS**

This study was supported by the National Institute of Health (NIH) grants NS38644 and ES10586.

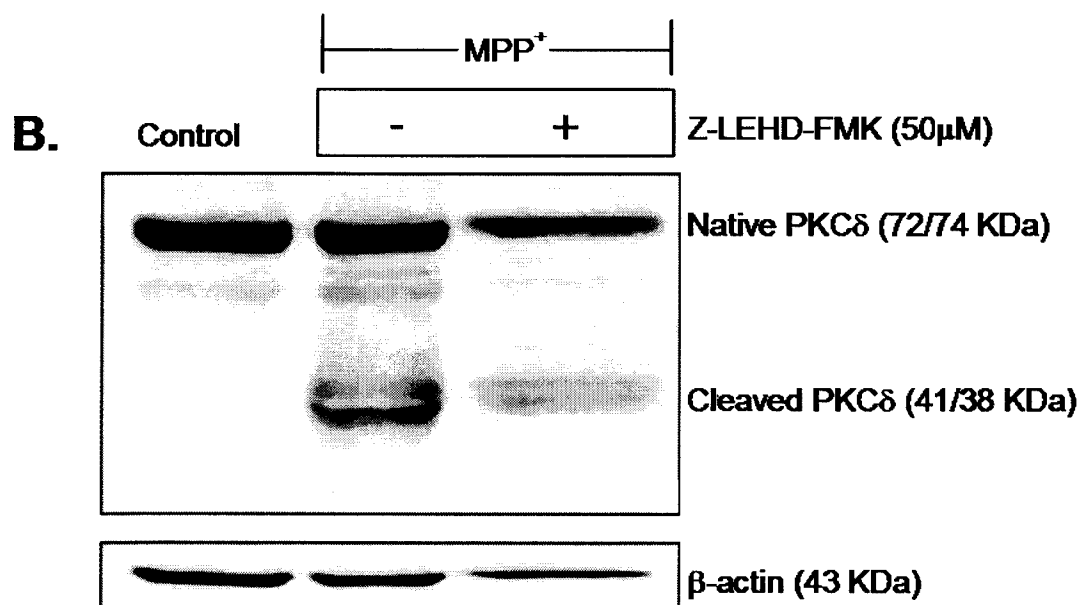
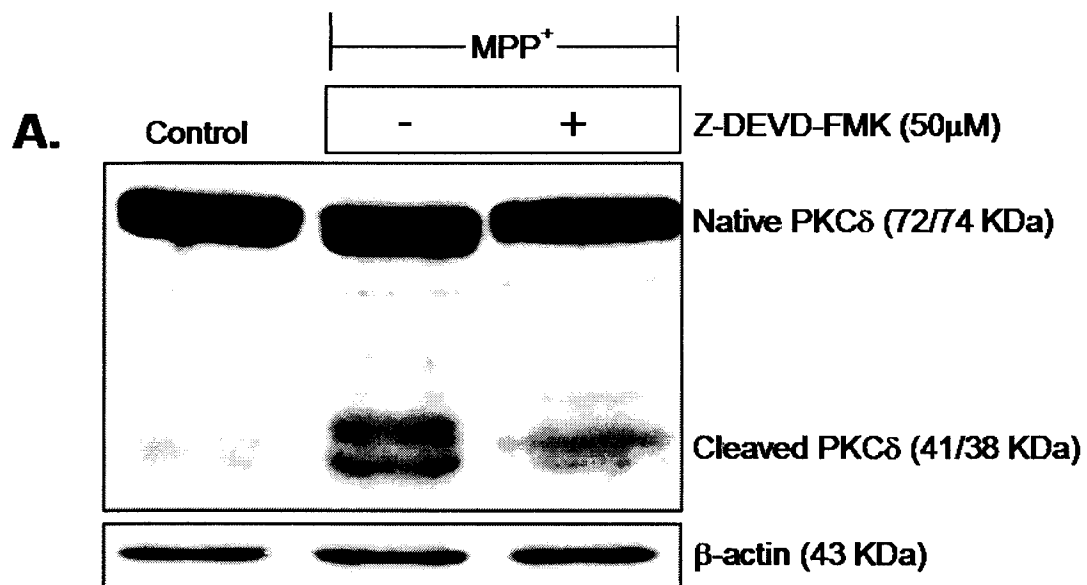


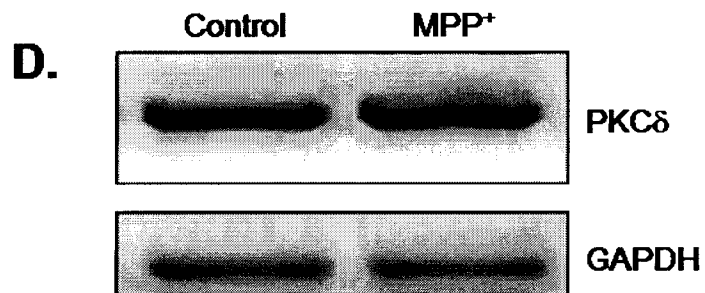
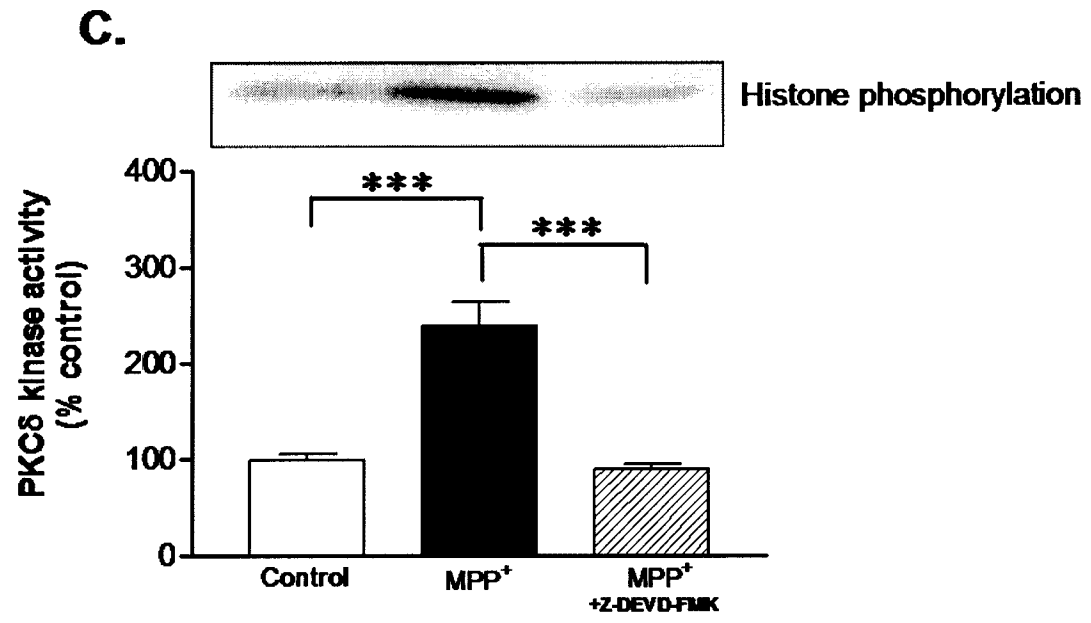
**Figure1: MPP<sup>+</sup> treatment activates caspase-3 in rat mesencephalic dopaminergic neuronal (N27) cells.**

(A) Caspase-3 enzyme activity increases significantly after MPP<sup>+</sup> (300  $\mu$ M) exposure for 36 hr. Caspase-3 activity was assayed using a specific fluorogenic substrate, Ac-DEVD-AMC (10  $\mu$ M), as described in the Methods. The data represent the mean  $\pm$  SEM from two separate experiments in triplicate (\*\*,  $p < 0.01$ ; N=6). (B) MPP<sup>+</sup> (300  $\mu$ M) treatment for 36 hr also induces caspase activation as observed by in situ staining using FITC-VAD-FMK as a substrate.

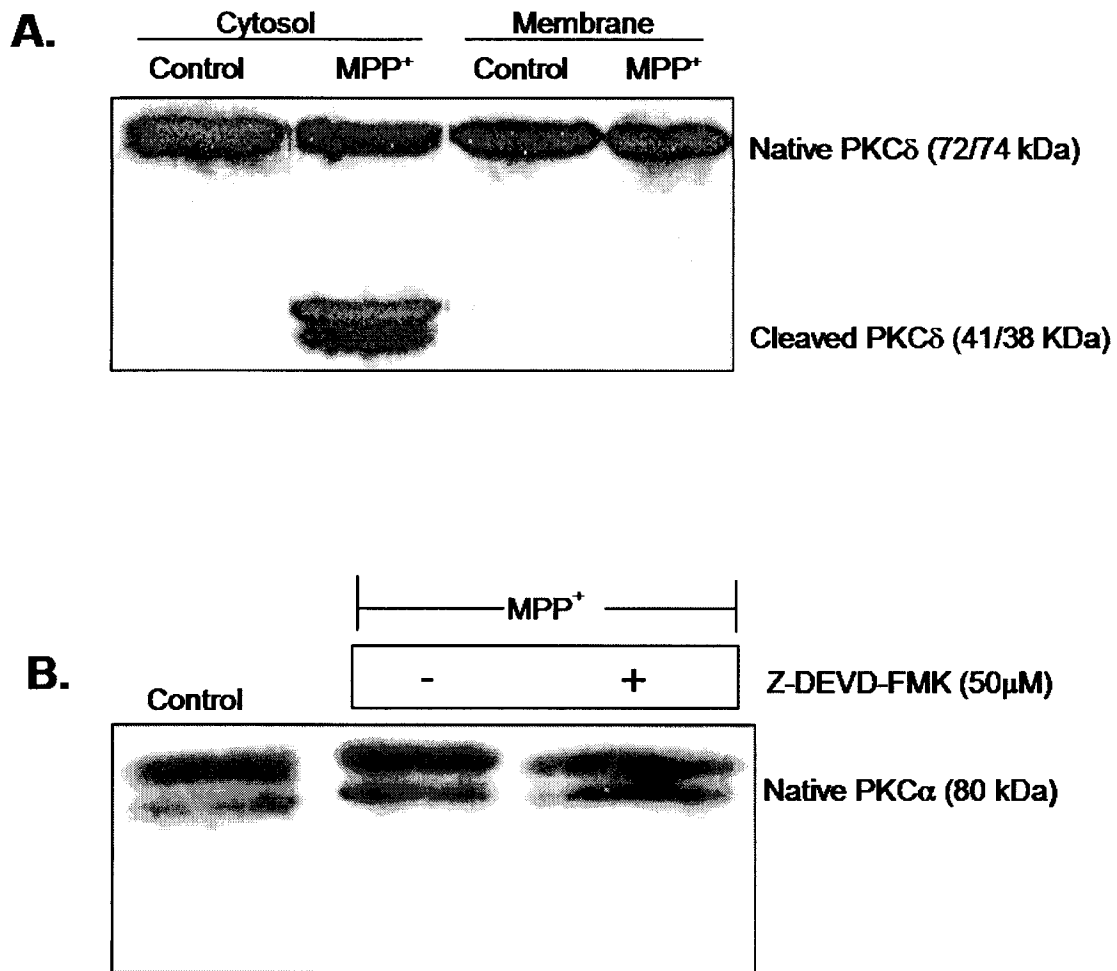
**Figure 2: Caspase-3 and Caspase-9 cascade mediate MPP<sup>+</sup>-induced proteolytic activation of PKC $\delta$  in N27 cells.**

A) Co-treatment with Z-DEVD-FMK (50  $\mu$ M) blocks the MPP<sup>+</sup> (300  $\mu$ M) induced proteolytic cleavage of PKC $\delta$  cleavage (38-41 kDa), (B) Caspase-9 inhibitor Z-LEHD-FMK (50 $\mu$ M) also blocks proteolytic cleavage of PKC $\delta$ , (C) MPP<sup>+</sup> induced PKC $\delta$  kinase activity is suppressed by caspase-3 inhibitor with Z-DEVD-FMK (50  $\mu$ M), and (D) No change in PKC $\delta$  mRNA level during MPP<sup>+</sup> treatment as measured by RT-PCR. Cells were treated with 300  $\mu$ M MPP<sup>+</sup> for 36 hr in the presence or absence of caspase inhibitors. Cells were then lysed and the lysate was used for Western blot analysis and kinase assay. To confirm equal protein loading in Western blot, the membranes were reprobed with  $\beta$ -actin antibody. For RT-PCR analysis, total mRNA was isolated from MPP<sup>+</sup> (300  $\mu$ M for 36 hr) treated cells and then reverse transcription was performed with the use of Superscript III first-strand synthesis system (Invitrogen, Carlsbad, CA). GAPDH was used as internal control. Images are representative from three separate experiments. The kinase assay data represent the mean  $\pm$  SEM from two separate experiments in triplicate (\*\*\*,  $p < 0.001$ ; N=6).









**Figure 3: Specificity of proteolytic activation of PKCδ during MPP<sup>+</sup> treatment**

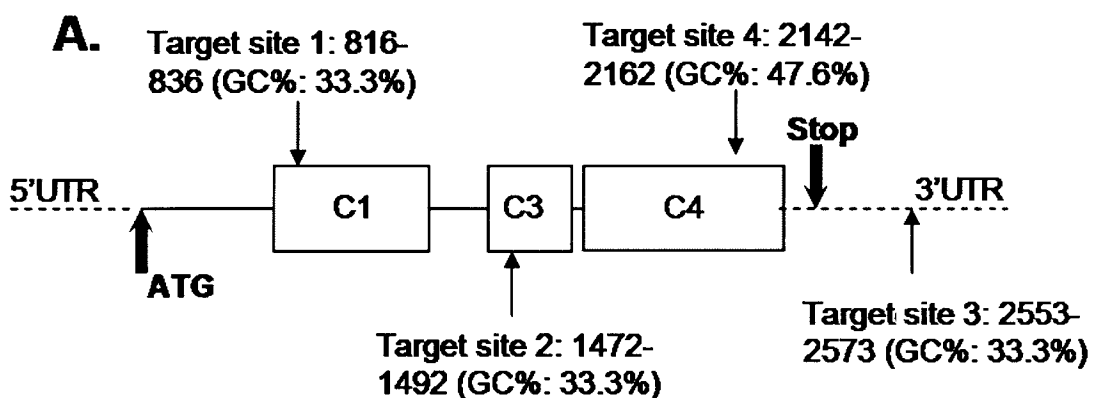
(A) No membrane translocation of PKCδ following MPP<sup>+</sup> treatment. After treatment with 300 μM MPP<sup>+</sup> for 36 hr, cytosol and membrane fractions were separated and used for determining PKCδ translocation. (B) No proteolytic activation of PKCα during MPP<sup>+</sup> treatment. Whole cell lysates were prepared after MPP<sup>+</sup> (300 μM) treatment for determining PKCα cleavage. All experiments were repeated three times and representative images are presented.

**Figure 4: Design and Synthesis of siRNAs against PKC $\delta$ .**

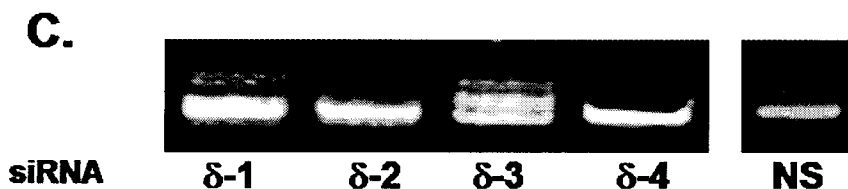
(A) Schematic representation of the primary structure of rat PKC $\delta$  mRNA (gi: 18959249) and four target sites of siRNA. The exact position of each target site was shown in the diagram and GC% was calculated with Vector NTI software (InforMax Inc., Frederick, MD).

(B) Template sequences of siRNA duplexes. A pair of sense and antisense templates was designed to generate siRNA duplexes. The partial T7 promoter sequence (underlined) was also included in each template. All oligonucleotides were synthesized and PAGE purified by Integrated DNA Technology (Iowa City, IA).

(C) In vitro transcription of siRNA. In vitro transcription, annealing, and purification of siRNA duplexes were performed using the protocol supplied with the silencer siRNA kit (Ambion Inc, Austin, TX). The siRNAs were separated on 12% PAGE and visualized by ethidium bromide staining. All siRNAs except siRNA- $\delta$ -3 showed the specific transcription products of expected size.

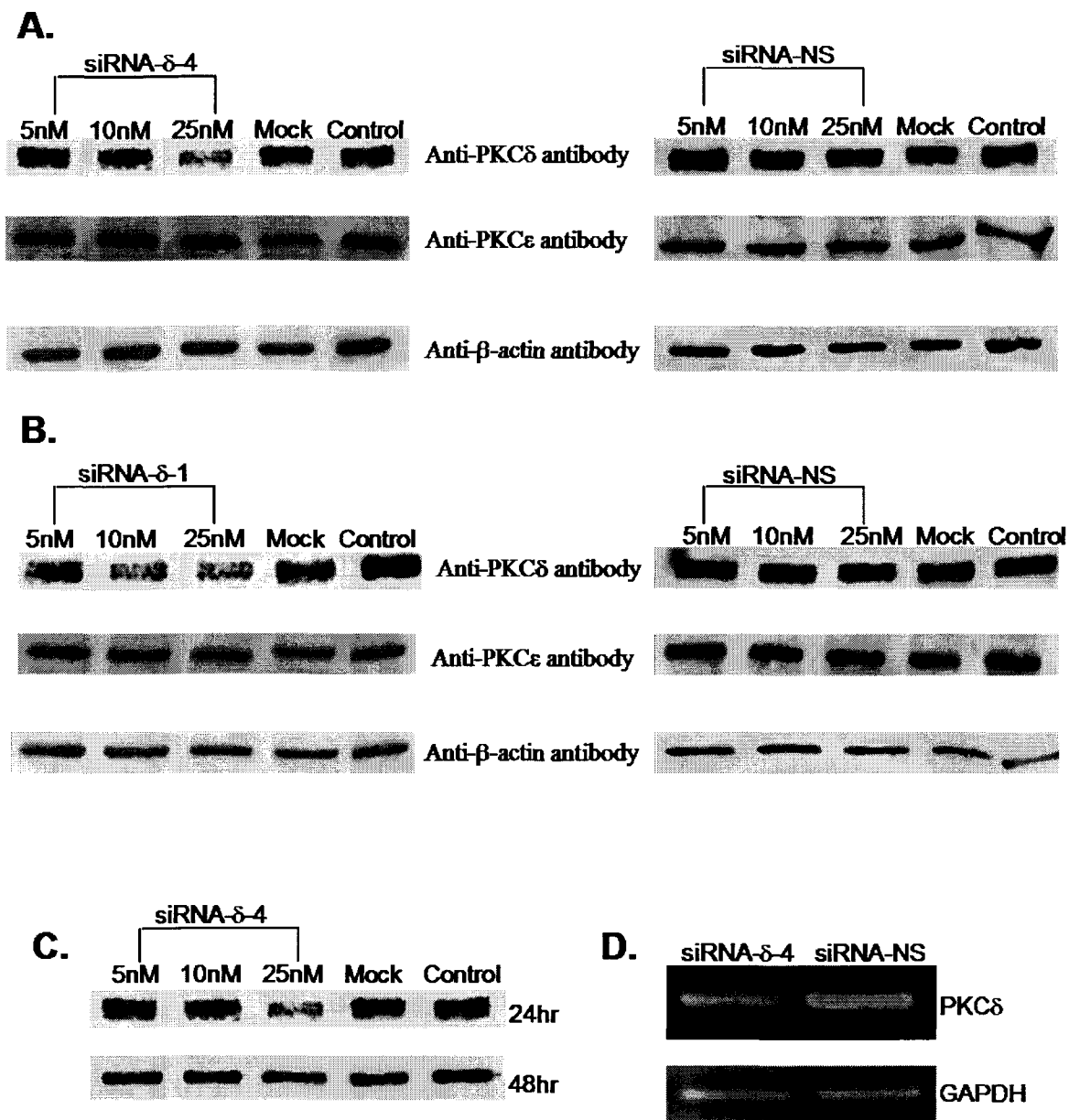


- B.**
- siRNA- $\delta$ -1:**  
 Antisense: 5'-AAGATTCACCTACATCAAGAACCCTGTCTC-3'  
 Sense: 5'-AAGTTCTTGATGTAGTGAATCCCTGTCTC-3'
- siRNA- $\delta$ -2:**  
 Antisense: 5'-AAGGTACTTTGCAATCAAGTACCTGTCTC-3'  
 Sense: 5'-AATACTTGATTGCAAAGTACCCCTGTCTC-3'
- siRNA- $\delta$ -3:**  
 Antisense: 5'-AACATCAGGCTTCACCCCTTTCTGTCTC-3'  
 Sense: 5'-AAAAGGGGTGAAGCCTGATGCCTGTCTC-3'
- siRNA- $\delta$ -4**  
 Antisense: 5'-AACTGTTTGTGAATTTGCCTTCTGTCTC-3'  
 Sense: 5'-AAAAGGCAAATTCACAAACAGCCTGTCTC-3'
- siRNA-NS (non-specific control):**  
 Antisense: 5'-AATTCTCACACTTCGGAGAACCCTGTCTC-3'  
 Sense: 5'-AAGTTCTCCGAAGTGTGAGAACCTGTCTC-3'



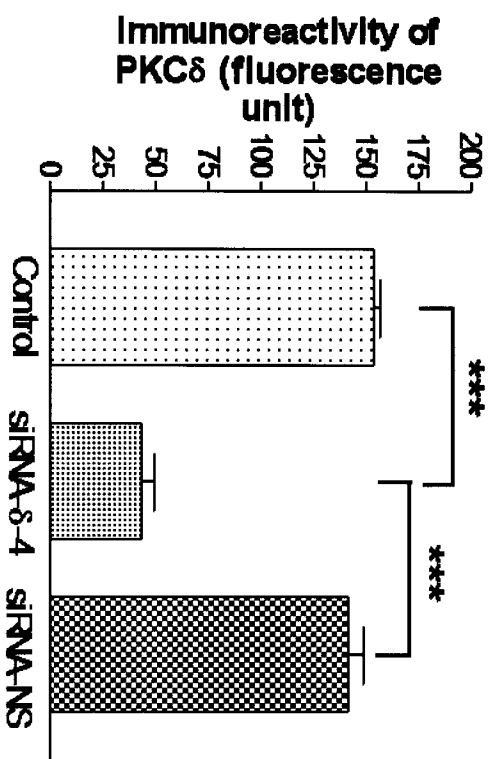
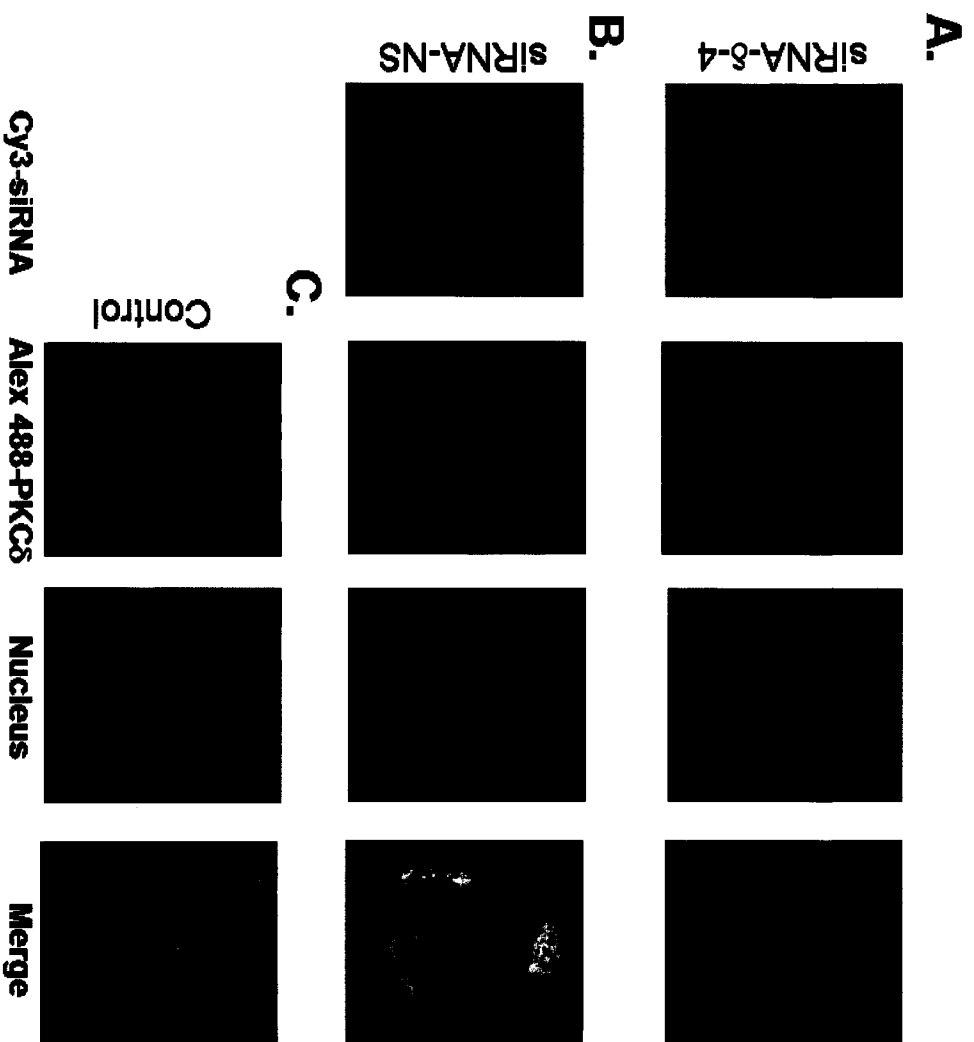
**Figure 5: Suppression of PKC $\delta$  expression in N27 cells transfected with siRNA- $\delta$ -1 and siRNA- $\delta$ -4.**

(A) Isoform specific suppression of PKC $\delta$  expression at 24hr post-transfection with siRNA- $\delta$ -4, (B) Isoform specific suppression of PKC $\delta$  expression at 48hr post-transfection with siRNA- $\delta$ -1, (C) Time course analysis of PKC $\delta$  expression in cells transfected with siRNA- $\delta$ -4. (D) RT-PCR analysis of PKC $\delta$  mRNA expression in siRNA- $\delta$ -4 and siRNA-NS transfected N27 cells. PKC $\delta$  expression in N27 cells transfected with different siRNAs was determined by immunoblotting at 24 hr and 48hr post transfection. Final concentrations of siRNAs varied from 5 nM to 25 nM. To examine the specificity of siRNAs and verify equal protein loading, the membranes were reprobed with PKC $\epsilon$  (90 kDa), one of the closest isoforms of PKC $\delta$ , and  $\beta$ -actin (43 kDa) antibodies, respectively. For RT-PCR analysis, total mRNA was extracted 24 hr after siRNA transfection. All experiments were repeated three times and representative images are presented.



**Figure 6: *In situ* localization of siRNA and immunocytochemistry of PKC $\delta$  in siRNA transfected N27 cells.**

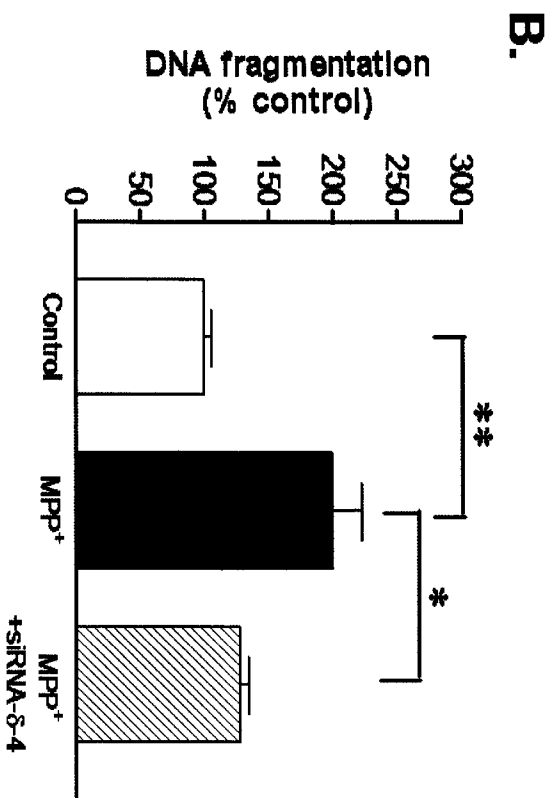
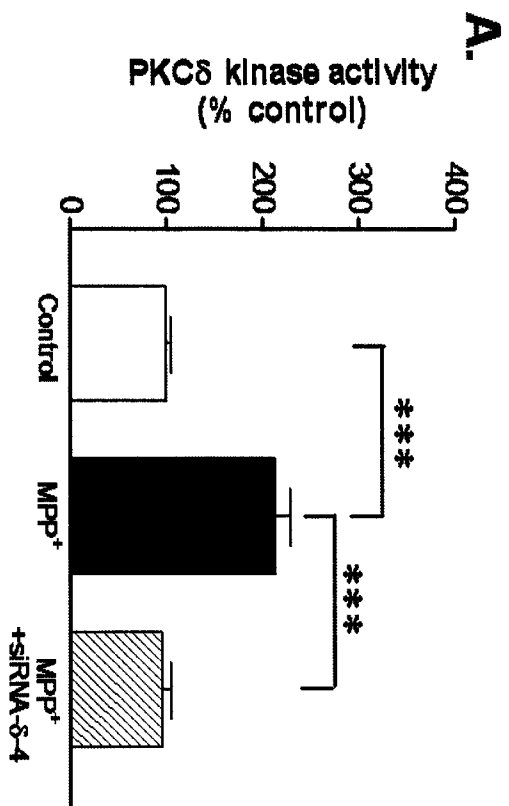
(A) Cells transfected with Cy3-labeled siRNA- $\delta$ -4 (25 nM) showing greatly reduced PKC $\delta$  expression. (B) Cells transfected with Cy3-labeled siRNA-NS (25 nM) showing no change in PKC $\delta$  expression. (C) Untransfected N27 cells showing normal PKC $\delta$  expression. (D) Quantitative analysis of *in situ* suppression of PKC $\delta$  expression by siRNA- $\delta$ -4 in N27 cells. For PKC $\delta$  immunostaining, cells were permeabilized and incubated with PKC $\delta$  antibody 24 hr post-transfection and then visualized with Alexa 488 (green) conjugated anti-rabbit antibody. siRNA was visualized by labeled Cy3 (red) fluorescence. The nuclei were visualized by Hoechst 33342 counterstaining (blue). Cy3-labeled siRNAs were prepared prior to transfection according to the silencer siRNA labeling kit (Ambion Inc, Austin, TX). Cells were observed under a Nikon inverted fluorescence microscope and pictures were captured with a SPOT digital camera (Diagnostic Instruments, Sterling Heights, MI). For *in situ* quantitative analysis of PKC $\delta$  expression, fluorescence immunoreactivity of PKC $\delta$  was measured in each group using Metamorph image software and data plotted in Prism software. Experiments were repeated three times and representative images are presented.



**Figure 7: Ablation of MPP<sup>+</sup>-induced PKC $\delta$  kinase activity and DNA fragmentation by siRNA- $\delta$ -4 in mesencephalic dopaminergic neuronal cells.**

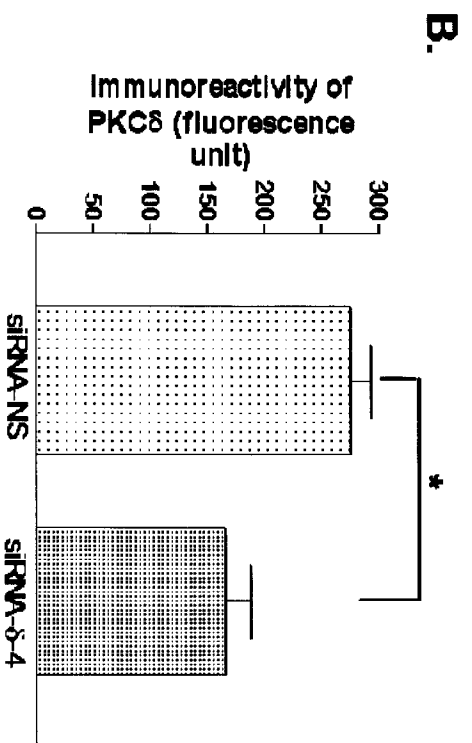
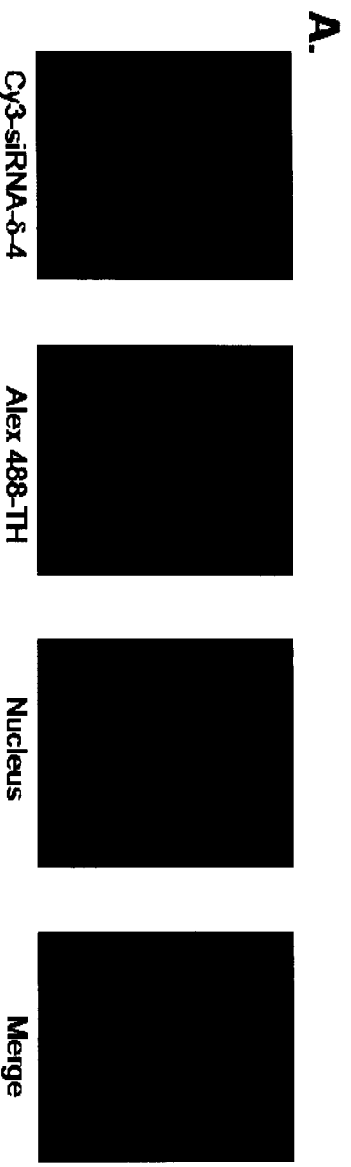
(A) Transfection of siRNA- $\delta$ -4 prior to MPP<sup>+</sup> exposure (300  $\mu$ M for 36 hr) reduces PKC $\delta$  kinase activity to the control level. (B) Transfection of siRNA- $\delta$ -4 almost completely protects cells against MPP<sup>+</sup>-induced DNA fragmentation. Sub-confluent cultures of N27 cells were transfected with siRNA- $\delta$ -4 (25 nM) for 24 hr and the cells were treated with MPP<sup>+</sup> for 42 hr. After exposure to MPP<sup>+</sup>, the N27 cells were harvested, lysed, and analyzed. Untransfected N27 cells not exposed to MPP<sup>+</sup> were used as controls. The data represent the mean  $\pm$  SEM from two separate experiments in triplicate (\*,  $p < 0.05$ ; \*\*,  $p < 0.01$  and \*\*\*,  $p < 0.001$ ; N=6).





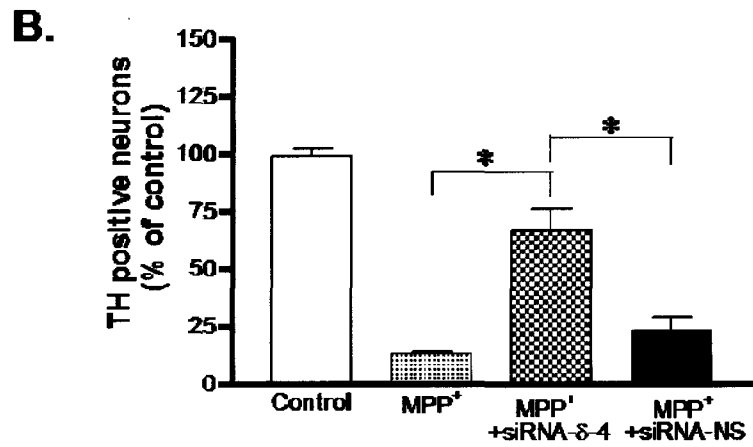
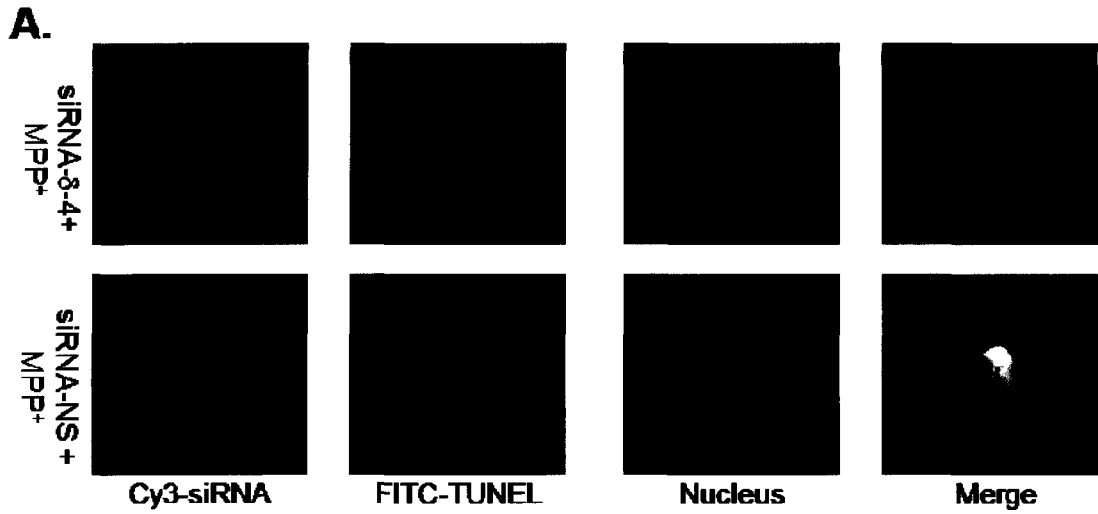
**Figure 8: *In situ* suppression of PKC $\delta$  expression by siRNA- $\delta$ -4 in primary mesencephalic cultures.**

(A) Localization of siRNA- $\delta$ -4 in TH positive neuron. (B) Quantitative analysis of *in situ* suppression of PKC $\delta$  by siRNA- $\delta$ -4 in primary mesencephalic cells. Primary mesencephalic neurons were cultured from E15 rat embryo midbrain and then transfected with Cy3-labelled siRNA (red). PKC $\delta$  or TH immunostaining was performed 24hr post-transfection of siRNA, by using PKC $\delta$  or TH antibodies and then visualized separately with Alexa 488 (green) conjugated anti-rabbit antibody. The nuclei were counterstained by Hoechst 33342 (blue). Stained primary neurons were observed under a Nikon inverted fluorescence microscope and pictures were captured with a SPOT digital camera (Diagnostic Instruments, Sterling Heights, MI). For *in situ* quantitative analysis of PKC $\delta$  expression, fluorescence immunoreactivity of PKC $\delta$  was measured from neurons in each group using Metamorph software and the data plotted in Prism software. The data represent the mean  $\pm$  SEM from two separate experiments in triplicate (\*,  $p < 0.05$ ;  $N=6$ ).



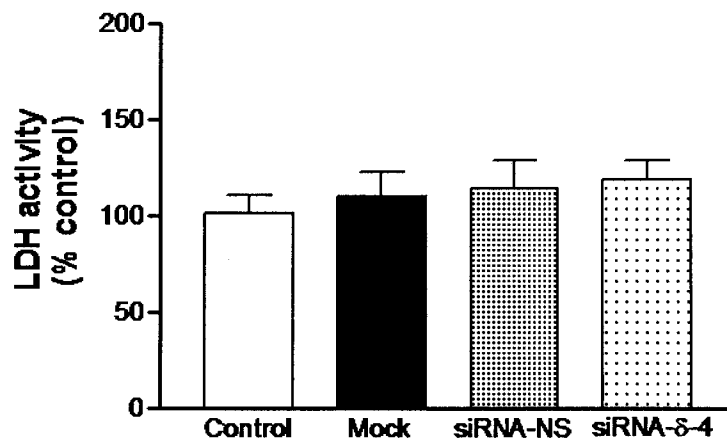
**Figure 9: siRNA- $\delta$ -4 prevents MPP<sup>+</sup>-induced apoptotic death in primary mesencephalic TH positive neurons.**

(A) TUNEL staining in MPP<sup>+</sup> treated rat primary mesencephalic neurons. Primary mesencephalic cultures were transfected with Cy3 labeled siRNAs and then exposed to 10  $\mu$ M MPP<sup>+</sup> for an additional 48 hr. FITC-TUNEL staining and Hoechst 33342 nuclear staining were performed. (B) Quantitative analysis of TH positive neurons following siRNA- $\delta$ -4 transfection and MPP<sup>+</sup> treatment. After siRNAs transfection, cells were exposed to 10  $\mu$ M MPP<sup>+</sup> for 48 hr and then TH positive neurons were identified using anti-TH antibody exposure. Data represent the mean  $\pm$  SEM from two separate experiments in triplicates (\*,  $p < 0.05$ ; N=6). (C) Total number of TH<sup>+</sup> neurons per 5000 mesencephalic primary cells counted in each group.



**C.**

	Control	MPP <sup>+</sup>	siRNA- $\delta$ -4 +MPP <sup>+</sup>	siRNA-NS +MPP <sup>+</sup>
# of TH positive neurons (Mean $\pm$ SEM)	57.0 $\pm$ 10.0	7.3 $\pm$ 0.3	38.0 $\pm$ 5.5	13.3 $\pm$ 3.2



**Figure 10: siRNAs are non-toxic to mesencephalic dopaminergic neuronal cells.**

siRNA-δ-4 and siRNA-NS (25 nM) were transfected into N27 cells. Following the 24 hr transfection, cell free culture medium was collected, and LDH activity was measured spectrophotometrically. Values represent mean  $\pm$  SEM for two separate experiments in triplicate (\*,  $p < 0.05$ ;  $N = 6$ ).

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**CHAPTER III: PROTEOLYTICALLY ACTIVATED PKC $\delta$  TRANSLOCATES TO  
THE NUCLEUS AND MEDIATES SER14 PHOSPHORYLATION OF HISTONE  
H2B IN APOPTOTIC DEATH OF DOPAMINERGIC NEURONAL CELLS**

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**ABSTRACT**

We previously showed that oxidative stress sensitive kinase PKC $\delta$  promotes apoptotic death in dopaminergic neurons following neurotoxin exposures (Kitazawa et al., 2003; Yang et al., 2004). However, its mechanism has not been well understood. In the present study, we determined that the full-length PKC $\delta$  is first cleaved in the cytoplasm and the activated cleaved PKC $\delta$  subsequently translocates into the nucleus. The caspase-3 specific inhibitor Z-DEVD-FMK, the cleavage resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM), as well as the nuclear localization signal (NLS) deletion mutant of PKC $\delta$  (PKC $\delta$ - $\Delta$ NLS) abolishes the nuclear translocation of activated cleaved PKC $\delta$ . Our study showed that proteolytic activation of full-length PKC $\delta$  and subsequent nuclear translocation of activated cleaved PKC $\delta$  are integral events required for PKC $\delta$ 's pro-apoptotic function in apoptosis of dopaminergic neuronal cells. Moreover, we demonstrated that activated cleaved PKC $\delta$ , after its nuclear translocation, mediates Ser14 phosphorylation of histone H2B in apoptotic

dopaminergic neuronal cells. Ser14 phosphorylation of H2B and apoptosis can also be directly induced by the catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF), but not by the regulatory fragment of PKC $\delta$  (PKC $\delta$ -RF), dominant-negative mutant of PKC $\delta$  (PKC $\delta$ -DN), PKC $\delta$ -CRM, or PKC $\delta$ - $\Delta$ NLS. Taken together, our study suggests that proteolytically activated PKC $\delta$  translocates into the nucleus and mediates Ser14 phosphorylation of H2B to promote neurotoxin-induced apoptosis of dopaminergic neuronal cells.

## INTRODUCTION

Mechanisms of selective degeneration of midbrain dopaminergic neurons in Parkinson's disease (PD) remain elusive despite intensive studies into the pathogenesis of PD. Although the recent identification of a number of genetic mutations that cause several groups of familial PD shed light on the understanding of the mechanisms of dopaminergic neuron degeneration (Dawson and Dawson, 2003; Greenamyre and Hastings, 2004; Shen, 2004), exact causes of sporadic PD cases, which account for over 90% of total PD patients, are still not clear. On the other hand, the discovery that mitochondria complex I inhibitor 1-methyl-4-phenyl-1,2,3,6,-tetrahydropyridine (MPTP) induces Parkinsonism in humans (Langston et al., 1984) suggests that exposure to environmental neurotoxins can contribute to dopaminergic neuron degeneration in sporadic PD patients (Dauer and Przedborski, 2003; Langston et al., 1984; Vila and Przedborski, 2003; Wichmann and DeLong, 2003). Mouse and primate models exposed to MPTP or other mitochondria complex I inhibitors have been developed and exhibit degeneration of midbrain dopaminergic neurons and PD-like symptoms (Betarbet et al., 2002; Betarbet et al., 2000; Dauer and Przedborski, 2003; McCormack et al., 2002).

Interestingly, most of these mitochondria complex I inhibitors (paraquat, rotenone) are also commonly used pesticides, which implicates the potential pathogenic role of pesticides in PD (Betarbet et al., 2002; Giasson and Lee, 2000; Greenamyre et al., 2001; Jenner, 2001). As supportive evidence, epidemiological studies have also found that incidence rate of sporadic PD is higher among farming communities (Jenner, 1998; Seidler et al., 1996; Tanner and Langston, 1990).

Dieldrin is an organochlorine pesticide that was widely used decades ago for the control of soil pests. Although it has been banned for about thirty years, the wide exposure of humans to dieldrin still exists through its persistent accumulation in the environment (Kitazawa et al., 2001, 2003). It is not clear as to whether dieldrin also inhibits mitochondria complex I; however, several studies have indicated that dieldrin exposure is positively associated with the increased incidence of PD. In fact, significant levels of dieldrin were detected in postmortem brains of PD patients, whereas no dieldrin was found in age-matched control brains (Corrigan et al., 1998; Fleming et al., 1994). Also, dieldrin exposure depletes dopamine in brains of ducks, ring doves and rats (Heinz et al., 1980; Sharma et al., 1976; Wagner and Greene, 1978). Furthermore, our previous studies also show that dopaminergic cells are highly sensitive to dieldrin induced toxicity (Kitazawa et al., 2001; Kitazawa et al., 2002).

By employing the well-developed MPTP (as well as other neurotoxin) cell and animal models of PD, it has been demonstrated that neurotoxin induced oxidative stress is one of the earliest events that triggers diverse downstream apoptotic pathways and induces the activation of executioner caspases in dopaminergic neurons (Beal, 2002; Greenamyre et al., 2001; Hartmann et al., 2000; Hartmann et al., 2001; Jenner, 2003). Activated executioner

caspsases directly mediate cleavage of a wide range of downstream substrates and lead to cell death. Protein kinases, one of the major signal transducers in the cell, have emerged as one major category of substrates for activated caspsases. Kinases in different families, including Raf-1 and AKT (Widmann et al., 1998b), ATM, MEKK-1 (Widmann et al., 1998a), hPAK2/hPAK65 (Jakobi et al., 2003; Lee et al., 1997), PKC isoform  $\delta$  and  $\theta$  (Datta et al., 1997; Emoto et al., 1995), PKN (Takahashi et al., 1998), ROCK1 (Coleman et al., 2001), SLK (Sabourin et al., 2000), HPK1 (Chen et al., 1999), LIMK1 (Tomiyoshi et al., 2004), and Mst (de Souza and Lindsay, 2004; Huang et al., 2002), have been identified as substrates of activated caspsases. Cleavage of these kinases not only regulates their activity (activation or inactivation), but also induces their relocation inside the cell, which moves kinases proximal to their specific substrates and transduces specific apoptotic signals (Jakobi, 2004; Teruel and Meyer, 2000). The proteolytic cleavage of ATM, for example, inactivates the protein, further impairing the DNA repair mechanism of cells in response to DNA damage (Smith et al., 1999). In other cases, caspsases mediated cleavage activates certain kinases, like Mst, and induces its nuclear translocation to facilitate apoptosis (Cheung et al., 2003; Huang et al., 2002).

Protein kinase C delta (PKC $\delta$ ), a member of the novel PKC family, is one of the kinases identified as a downstream target of caspsase-3 in many different cell types, including dopaminergic neuronal cells, in response to apoptotic stimuli (Anantharam et al., 2002; Brodie and Blumberg, 2003; Kitazawa et al., 2003; Reyland et al., 1999). As a member of the novel PKC family, PKC $\delta$  contains a lipid-sensitive C1 domain and a Ca<sup>2+</sup> binding deficient C2 domain. The binding of lipid molecules (diacylglycerol or 4-phorbol 12-myristate 13-acetate) induces rapid translocation of PKC $\delta$  to the plasma membrane and activates the

kinase through conformational change that removes the pseudosubstrate from the catalytic site (Newton, 2003). The lipid-mediated activation allows PKC $\delta$  to send normal transducing signals from receptors (Nishizuka, 1992). Moreover, the serine/threonine phosphorylation of its activation loop at its C-terminal by PDK-1 also contributes to PKC $\delta$ 's activation (Newton, 2003; Toker, 1998). In apoptotic cells, caspase-3 mediated proteolytic cleavage of PKC $\delta$  removes its regulatory fragment containing the pseudosubstrate and leads to persistent activation of the kinase (Kanthasamy et al., 2003; Kikkawa et al., 2002). The diverse mechanisms for the activation of PKC $\delta$  raise an interesting question as to whether the proteolytic activation of full-length PKC $\delta$  is necessary and specific for its function in apoptosis. Simultaneous with the activation, PKC $\delta$  also relocates to the mitochondria, nucleus, endoplasmic reticulum (ER), golgi, as well as plasma membrane in apoptotic cells (Brodie and Blumberg, 2003). Translocation of PKC $\delta$  to the mitochondria was shown to facilitate the mitochondrial pore formation, promoting cytochrome C release (Majumder et al., 2000) and inducing the redistribution of Bcl-2 family proteins (Murriel et al., 2004; Sitailo et al., 2004). The translocation of PKC $\delta$  to the nucleus was linked to nuclear events that either regulate the mitochondrial apoptotic pathway or facilitate the collapse of nuclear structure in apoptotic cells (Cross et al., 2000; DeVries et al., 2002).

We previously demonstrated that PKC $\delta$  is a downstream target of activated caspase-3 and its proteolytic activation is associated with a wide range of neurotoxins induced apoptosis in dopaminergic neuronal cells (Kaul et al., 2003; Kitazawa et al., 2003; Yang et al., 2004). However, very little is known about the downstream actions of PKC $\delta$  following its proteolytic activation. In the present study, we investigate the downstream events following

proteolytic activation of PKC $\delta$  and determine the correlation between proteolytic cleavage and nuclear translocation of PKC $\delta$  in dopaminergic neuronal cells. Furthermore, we also investigate the function of the activated cleaved PKC $\delta$  in the nucleus of dieldrin induced apoptotic dopaminergic neuronal cells.

## MATERIALS AND METHODS

### Reagents

Anti-cleaved caspase-3 antibody was obtained from Cell Signaling Technology, Inc. (Beverly, MA). Anti-LDH antibody was obtained from Research Diagnostics, Inc. (Flanders, NJ). Anti-lamin B antibody was obtained from Abcam, Inc (Cambridge, MA). Dieldrin, protease cocktail, purified Histone H2B, ATP, protein-A-sepharose, and anti- $\beta$ -actin antibody were obtained from Sigma-Aldrich (St. Louis, MO); Z-DEVD-FMK was obtained from Alexis Biochemicals (San Diego, CA); antibodies to PKC $\delta$  and PARP were purchased from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA). Anti-phospho-Histone H2B (Ser14) antibody was purchased from Upstate Biotechnology (Waltham, MA). TaqMan Rat PKC $\delta$  and 18s ribosome RNA assay kit and PCR master mix was purchased from Applied Biosystems (Foster City, CA). Anti-rabbit and anti-mouse secondary antibodies and the ECL chemiluminescence kit were purchased from Amersham Pharmacia Biotech (Piscataway, NJ). NE-PER<sup>TM</sup> nuclear and cytoplasmic extraction reagent was obtained from Pierce Biotechnology, Inc (Rockford, IL). Alexa 488 conjugated anti-rabbit secondary antibody and Hoechst 33342 were purchased from Molecular Probes, Inc. (Eugene, OR). Cy3 conjugated

anti-mouse secondary antibody was obtained from Jackson Laboratory (Bar Harbor, Maine). The Cell Death Detection ELISA plus Assay Kit was purchased from Roche Molecular Biochemicals (Indianapolis, IN). [ $\gamma$ - $^{32}\text{P}$ ] ATP was purchased from Perkin Elmer Life Science Products (Boston, MA). The Bradford protein assay kit was purchased from Bio-Rad Laboratories (Hercules, CA). *Pfu* DNA polymerase was purchased from Stratagene (La Jolla, CA). SuperScript III first-strand synthesis system, TRIZOL reagent, ViraPower<sup>TM</sup> lentiviral expression system, RPMI, Opti-MEM, fetal bovine serum, L-glutamine, blasticidin, penicillin, and streptomycin were purchased from Invitrogen, Inc. (Carlsbad, CA).

### **Cell culture and treatment**

The immortalized rat mesencephalic dopaminergic neuronal (N27) cell line was a kind gift from Dr. Kedar N. Prasad, University of Colorado Health Sciences Center (Denver, CO) (Adams et al., 1996; Prasad et al., 1998). N27 cells were grown in RPMI 1640 medium containing 10% fetal bovine serum, 2 mM L-glutamine, 50 units penicillin, and 50  $\mu\text{g}/\text{ml}$  streptomycin. Cells were grown in a humidified atmosphere of 5%  $\text{CO}_2$  at 37 $^\circ\text{C}$ . For dieldrin treatment, N27 cells were treated with 60 $\mu\text{M}$  dieldrin in serum-free medium for up to 3hr at 37 $^\circ\text{C}$ . In caspase-3 inhibitor studies, cells were co-treated with 50 -100 $\mu\text{M}$  Z-DEVD-FMK and dieldrin. Untreated cells were used as negative control.

### **Construction of plasmids**

A series of PKC $\delta$ -related constructs was prepared, including PKC $\delta$ -WT (wild type), PKC $\delta$ -CRM (cleavage resistant mutant), PKC $\delta$ - $\Delta\text{NLS}$  (deletion of nuclear localization

signal), PKC $\delta$ -DN (dominant negative mutant), PKC $\delta$ -CF (catalytic fragment), and PKC $\delta$ -RF (regulatory fragment). To prepare PKC $\delta$ -CF, PKC $\delta$ -RF, PKC $\delta$ - $\Delta$ NLS or PKC $\delta$ -WT fragments, 995-2035bp, 14-982bp, 14-1843bp or full-length of mouse PKC $\delta$  (gi: 6755081) cDNA were first amplified from pGFP-PKC $\delta$  (kind gift of Dr. Reyland at University of Colorado) (DeVries et al., 2002) with the following primer pairs, respectively. For PKC $\delta$ -CF, forward primer: 5' caccatgaacaacgggacctatggcaa 3'; reverse primer: 5' aatgtccaggaattgctcaaac 3'; for PKC $\delta$ -RF, forward primer: 5' caccatggcacccttctctgcgc 3'; reverse primer: 5' actcccagagaacttctggctt 3'; for PKC $\delta$ - $\Delta$ NLS, forward primer: 5'caccatggcacccttctctgcgc 3'; reverse primer: 5'ctccaggaggaccagtt 3'; for PKC $\delta$ -WT, forward primer: 5' caccatggcacccttctctgcgc 3'; reverse primer: 5' aatgtccaggaattgctcaaac 3'. To prepare PKC $\delta$ -CRM, full-length mouse PKC $\delta$  cDNA with a point mutation at 993 (A to C) that abolishes the caspase-3 cleavage site of PKC $\delta$  was amplified with pGFP-PKC $\delta$ <sup>D327A</sup> (kind gift of Dr. Reyland at University of Colorado) (DeVries et al., 2002) as template and the same primer pairs used for amplification of PKC $\delta$ -WT. To prepare PKC $\delta$ -DN, full-length mouse PKC $\delta$  cDNA with a point mutation at 1489 (A to G) that abolishes the ATP binding site of PKC $\delta$  was amplified with pPKC $\delta$ <sup>K376R</sup>-EGFP (kind gift of Dr. Reyland at University of Colorado) as template and the same primer pairs used for amplification of PKC $\delta$ -WT. All PCR reactions were performed with *Pfu* DNA polymerase to maintain the fidelity of the sequence. All PCR products were directly cloned in-frame into a V5-tagged expression vector (at the C terminal) pLenti/TOPO from Invitrogen, to get pLenti/PKC $\delta$ -CF, pLenti/PKC $\delta$ -RF, pLenti/PKC $\delta$ - $\Delta$ NLS, pLenti/PKC $\delta$ -WT, pLenti/PKC $\delta$ -DN, and pLenti/PKC $\delta$ -CRM. All positive clones were confirmed by sequencing.



### **Generation of PKC $\delta$ -CRM, PKC $\delta$ - $\Delta$ NLS, PKC $\delta$ -DN, and PKC $\delta$ -WT stably expressing dopaminergic neuronal (N27) cell line**

ViraPower Lentiviral gene expression system from Invitrogen (Carlsbad, CA) was employed for the establishment of a stable cell line. To produce lentiviral particles containing different constructs, pLenti/PKC $\delta$ -CRM, pLenti/PKC $\delta$ - $\Delta$ NLS, pLenti/PKC $\delta$ -DN, or pLenti/PKC $\delta$ -WT, as well as supporting plasmids (provided with the kit) were co-transfected into human 293FT cells with the use of lipofectamine 2000, respectively, as described in the instruction of the kit. The lentiviral particles in the medium were then collected by centrifuging at 3000 rpm for 15 min at 48-72 hr post-transfection. To generate stably expressing cell lines, lentiviral particles containing different PKC $\delta$  constructs were added into cultured N27 cells ( $2 \times 10^5$ ) followed by polybrene (6  $\mu$ g/ml), cells were incubated for 24 hr, and fresh medium was added and old medium was removed. Positive N27 cells were selected by keeping blasticidin (10  $\mu$ g/ml) in medium for up to 2 weeks. N27 cells stably expressing lacZ (pLenti/lacZ was supplied with the kit) were also established to serve as a vector control. PKC $\delta$ -CRM, PKC $\delta$ - $\Delta$ NLS, or PKC $\delta$ -WT stably expressing N27 cells were identified by immunostaining of the C-terminal V5 epitope.

### **Transient transfection of N27 cells**

Transient transfection of N27 cells was performed with the use of lipofectomine 2000 from Invitrogen, Inc (Carlsbad, CA). Briefly, cells ( $0.7-0.8 \times 10^6$ ) were pre-plated in poly L-lysine coated glass cover slips in a 6-well plate. After 16-24 hr, 4  $\mu$ g plasmid (PKC $\delta$ -CF or PKC $\delta$ -RF) and 10  $\mu$ l lipofectomine 2000 were first diluted in 250  $\mu$ l Opti-MEM medium,

separately. After a 5 min incubation at RT, diluted plasmid was mixed with diluted lipofectomine 2000 and incubated for another 20 min for the formation of DNA-lipid complex. The DNA-lipid complex was then added to the cells in a 6-well plate and incubated for 16-24 hr at 37<sup>0</sup>C.

### **Preparation of nuclear and cytosolic fractions**

Nuclear and cytosolic fractions were prepared by employing NE-PER<sup>TM</sup> nuclear and cytosolic extraction reagent from Pierce Biotechnology, Inc (Rockford, IL). Briefly, the N27 cells (10x10<sup>6</sup>) were harvested with trypsin/EDTA and spun at 200xg for 5 min. Cell pellets were then washed twice with ice-cold PBS and resuspended in 200 µl of CERI buffer (pH7.5, 10 mM HEPES, 10 mM KCl, 1.5 mM MgCl<sub>2</sub> and 1:100 dilution of protease inhibitor). To lyse the cells, 0.1% Nonide P-40 (NP-40) was added into the sample and incubated for 3 min on ice. The lysates were then centrifuged for 30 min at 14,000xg at 4<sup>0</sup>C and supernatants were collected as cytosolic fraction. The nuclei pellets were further resuspended in 50 µl NER buffer (420 nM NaCl, 20 mM HEPES, 1.5 mM MgCl<sub>2</sub>, 0.2 mM EDTA, and 25% glycerol, pH7.9) for 40 min on ice. The nuclear suspension was centrifuged for 10 min at 14,000xg at 4<sup>0</sup>C and supernatants were collected as nuclear fraction. The relative purity of cytosolic and nuclear fractions was examined by the corresponding marker proteins lactase dehydroxylase (LDH) and lamin B.

### **Preparation of whole cell homogenates**

After treatment, the N27 cells (10x10<sup>6</sup>) were harvested with trypsin/EDTA and spun at 200xg for 5 min. Cell pellets were then washed twice with ice-cold PBS and resuspended

in 200  $\mu$ l of homogenization buffer (pH8.0, 20 mM Tris, 10 mM EGTA, 2 mM EDTA, 2 mM DTT, 0.5% Triton X-100 and 1:100 dilution of protease inhibitor). After incubation on ice for 5 min, the cell lysates were centrifuged for 30 min at 14,000xg at 4°C and supernatants were collected as whole cell lysates.

### **Western blotting**

Equal amount of protein was loaded in each lane and separated on SDS-polyacrylamide gel as described previously. Proteins were then transferred to nitrocellulose membrane by electro-blotting overnight (4°C, 25V). Non-specific binding sites were blocked by treating the nitrocellulose membranes with 5% non-fat dry milk TBST solution (10 mM Tris, 150 mM NaCl, and 0.1% Tween 20) for 1 hr. The nitrocellulose membranes were then incubated with primary antibodies (1:1000) for 1 hr at RT. The primary antibody treatment was followed by treatment with secondary HRP-conjugated anti-rabbit or anti-mouse IgG (1:2000) for 1 hr at RT. Secondary antibody-bound proteins were detected using an ECL chemiluminescence kit (Amersham). To confirm equal protein loading, blots were re probed with  $\beta$ -actin antibody (1:5000). Gel photographs and densitometric analysis were performed with a Kodak image station (Model 1000R, Rochester, New York).

### **Quantitative real time RT-PCR**

After treatment, cells were lysed in 1 ml TRIZOL reagent and total RNA was isolated by chloroform extraction and precipitated by ethanol. Total RNA was first treated with DNase I to degrade contaminated DNA and then reversely transcribed into first strand cDNA using the SuperScript III first-strand synthesis system (Invitrogen, Inc, Carlsbad, CA) as

described in the kit instructions. To detect the abundance of PKC $\delta$  mRNA in the sample, quantitative real time PCR was performed with TaqMan rat PKC $\delta$  and control 18s ribosome RNA (rRNA) assay kits. Briefly, about 50 ng cDNA was mixed with primers, TaqMan probe, as well as 2x PCR master mix to set up the reaction. For each sample, triplicates were run on the same plate. The PCR reaction was performed and data were analyzed in a Mx4000 multiplex Quantitative PCR system (stratagene, La Jolla, CA).

### **Immunocytochemistry**

Cells grown on poly L-lysine coated glass cover slips were first fixed in 4% paraformaldehyde, then permeabilized and blocked with blocking reagent (0.4% BSA, 5% goat serum, and 0.2% Triton-X 100 in PBS) for 20 min. Cells were then incubated with primary antibody (1:1000 in blocking reagent) overnight at 4°C and then washed for 4x8 min with PBS. Endogenous PKC $\delta$ , cleaved caspase-3, Ser 14 phosphorylated histone H2B, or overexpressed PKC $\delta$ -WT, PCK $\delta$ -CRM, or PKC $\delta$ - $\Delta$ NLS was visualized by incubation with Alexa 488-conjugated goat anti-rabbit secondary antibody or Cy3-conjugated goat anti-mouse secondary antibody (1:2000 in PBS) at RT for 90 min. After another 4x8 min PBS wash, Hoechst 33342 (final concentration of 10  $\mu$ g/ml in PBS) was added to stain the cell nuclei at RT for 3 min. Finally, cells were mounted on a slide with antifade mounting medium. The cells were observed under regular fluorescence or confocal microscopy. For regular fluorescence microscopy, a Nikon inverted fluorescence microscope (Model TE-2000U) was used and pictures were captured with a SPOT digital camera (Diagnostic Instruments, Sterling Heights, MI). For confocal microscopy, a TCS/NT confocal

microscopy system (Leica, Bannockburn, IL) was employed. All images were processed in MetaMorph 5.07 from Universal imaging (Downingtown, PA).

### **Immunoprecipitation kinase assay**

PKC $\delta$  enzymatic activity was assayed using an immunoprecipitation kinase assay as previously described (Anantharam et al., 2002; Reyland et al., 1999). After treatment with dieldrin, nuclear lysates of N27 cells ( $20 \times 10^6$ ) were first prepared as described above. About 0.1-0.2 mg protein was immunoprecipitated overnight at 4°C using 2  $\mu$ g of anti-PKC $\delta$  antibody. The immunoprecipitates were then incubated with protein-A-sepharose for 1 hr at 4°C. The protein-A bound antigen-antibody complexes were then washed 3 times with 1x PBS, 3 times with kinase buffer (40 mM Tris, pH7.4, 20 mM MgCl<sub>2</sub>, 20  $\mu$ M ATP, and 2.5 mM CaCl<sub>2</sub>), and resuspended in 20  $\mu$ l of kinase buffer. Reactions were started by adding 20  $\mu$ l of reaction buffer containing 0.4 mg purified histone H2B and 5  $\mu$ Ci of [ $\gamma$ -<sup>32</sup>P] ATP (3,000 Ci/mM) to the immunoprecipitated samples and incubated for 10 min at 30°C. 2xSDS gel loading buffer was then added to terminate the reaction, the samples were boiled for 5 min, and the products were separated on a 12% SDS-PAGE gel. The phosphorylated histone bands were detected using a Personal Molecular Imager (FX model, Bio-Rad) and quantified using Quantity One 4.2.0 software (Bio-Rad, Hercules, CA).

### **Acid extraction of histone mixtures**

Briefly, the N27 cells ( $10 \times 10^6$ ) were harvested with trypsin/EDTA and spun at 200xg for 5 min. Cell pellets were then washed twice with ice-cold PBS and resuspended in 200  $\mu$ l

of homogenization buffer (pH7.5, 10 mM HEPES, 10 mM KCl, 1.5 mM MgCl<sub>2</sub> and 1:100 dilution of protease inhibitor). To lyse the cells, 0.5% Triton-X-100 was added into the sample and incubated for 5 min on ice. The lysates were then centrifuged for 5 min at 14,000xg to collect the nuclei pellets. To extract the histones, nuclei pellets were resuspended with 100 µl 0.2 M HCl and shaken at 4<sup>0</sup>C for 3 hr. Nuclear lysates were then centrifuged at 14,000xg at 4<sup>0</sup>C for 10 min and histone mixtures were collected from the supernatant.

### **Quantification assay for DNA fragmentation**

DNA fragmentation was measured using a recently developed Cell Death Detection ELISA plus Assay Kit (Molecular Biochemicals, Indianapolis, IN). Briefly, cells were spun down at 200xg for 5 min and washed twice with 1X PBS. Cells were then incubated with lysis buffer (supplied with the kit) at RT. After 30 min, samples were centrifuged and 20 µl aliquots of the supernatant were then dispensed into streptavidin-coated 96 well microtiter plates followed by addition of 80 µl of HRP-conjugated antibody cocktail, and incubated for 2 hr at RT with mild shaking. After incubation, unbound components were removed by washing with the incubation buffer supplied with the kit. The nucleosomes retained by the antibody cocktail in the immunocomplex were quantified spectrophotometrically with ABTS as an HRP substrate. Measurements were made at 405nm and 490nm using a SpectroMax 190 spectrophotometer (Molecular Devices, Sunnyvale, CA). The difference of absorbance between OD 405 and OD 490 nm was used to measure the actual DNA fragmentation level.

**Data analysis**

Data analysis was performed using Prism 3.0 software (GraphPad Software, San Diego, CA). Data from PKC $\delta$  kinase, DNA fragmentation, and QRT-PCR were first analyzed using one-way ANOVA. Bonferroni's post-test was then performed to compare all groups and differences with  $p < 0.05$  were considered significant.

**RESULTS****Caspase-3 is primarily activated and remains in the cytoplasm of dopaminergic neuronal (N27) cells following dieldrin exposure**

Activation of key apoptotic protease caspase-3 following dieldrin exposure was first determined by monitoring the production of cleaved (activated) caspase-3 on immunoblots with the use of specific anti-cleaved caspase-3 antibody. Also, to determine the subcellular localization of activated caspase-3, the cytosolic and nuclear fractions of N27 cells following dieldrin exposure were prepared and separated by 15% SDS-PAGE. As shown in Figure 1A, cleaved caspase-3 can be detected starting at 0.5 hr in the cytosolic fraction and the maximum intensity of cleaved caspase-3 on immunoblot of the cytosolic fraction is reached at the 1 hr time point. However, cleaved caspase-3 is barely detected at the 0.5 hr time point on immunoblot of the nuclear fraction, and there is only a weak increase in the intensity of cleaved caspase-3 at the 1 hr time point. To show the relative purity of the cytosolic and nuclear fractions, cytosolic and nuclear fractions were separated again by SDS-PAGE and immunoblotted by the cytosolic fraction marker Lactase dehydroxylase (LDH) or nuclear fraction marker lamin B. As shown in Figure 1A, only very little LDH was detected in the

nuclear fraction and no clear lamin B was detected in the cytosolic fraction. To visualize the localization of activated caspase-3 *in situ*, immunostaining of cleaved caspase-3 and counterstaining of nuclei was performed in N27 cells at 1 hr following dieldrin exposure. As shown in Figure 1B, the immunoreactivity of cleaved caspase-3 was significantly elevated following dieldrin exposure for 1 hr. The increased immunoreactivity was also predominantly localized in cytoplasm as seen in Figure 1Bf. Taken together, this result suggests that caspase-3 was primarily activated and retained in the cytoplasm; only a very small fraction of activated caspase-3 translocated to the nucleus at the later time point.

#### **Dieldrin exposure induces PKC $\delta$ cleavage without changing its expression level in dopaminergic neuronal (N27) cells**

PKC $\delta$  was recently identified as one of the downstream targets of caspase-3 that can be proteolytically activated in apoptotic cells (Brodie and Blumberg, 2003; Kikkawa et al., 2002). Here, we examine the cleavage of PKC $\delta$  induced by dieldrin exposure in dopaminergic neuronal cells. Anti-PKC $\delta$  antibody from Santa Cruz Biotechnology (Santa Cruz, CA), which recognizes the C-terminal epitope of PKC $\delta$ , was employed. As shown in Figure 2A, cleaved PKC $\delta$  fragments (41/38KDa) were detected from whole cell lysates of N27 cells starting at 1 hr after dieldrin exposure and decreased at the 3 hr time point, which matches the time for caspase-3 activation shown in Figure 1A. To demonstrate that the activated caspase-3 indeed starts to cleave its substrates, cleavage of the classical substrate of activated caspase-3, poly (ADP-ribose) polymerase (PARP) (Tewari et al., 1995), was also examined. The whole cell lysates of N27 cells after dieldrin treatment were separated by



7.5% SDS-PAGE and immunoblotted with anti-PARP antibody. As shown in Figure 2B, the cleaved PARP (85KDa) was detected as early as 0.5 hr and the intensity of cleaved PARP on immunoblot increased over time up to 3 hr after dieldrin treatment. Both membranes were reprobbed with anti- $\beta$ -actin antibody and the results showed that equal amounts of proteins were loaded on the gel.

To examine whether dieldrin exposure induces transcriptional change in PKC $\delta$  mRNA in N27 cells, the relative abundance of PKC $\delta$  mRNA copies in control and dieldrin-treated N27 cells was determined by quantitative real-time RT-PCR assay. After dieldrin treatment of 1 and 3 hr, total RNA from control and dieldrin-treated N27 cells was isolated and reversely transcribed into cDNA. Equal amounts of cDNAs were then used to perform real-time PCR with the use of a TaqMan rat PKC $\delta$  probe. The 18s ribosome RNA (rRNA) probe was employed to serve as endogenous control to equalize the RNA used in the real-time PCR assay. The real-time amplification plots from control and dieldrin-treated samples were shown in Figure 2C and the fluorescence intensity generated as the result of the amplification of PKC $\delta$  cDNA was nearly identical, suggesting that the same amount of PKC $\delta$  between control and dieldrin-treated N27 cells was amplified during PCR. The relative quantity of PKC $\delta$  mRNA in control and dieldrin-treated N27 cells converted by the formula  $2^{-(\Delta Ct \text{ PKC}\delta - \Delta Ct \text{ 18s rRNA})}$  (Ct: threshold of cycle) (Bustin, 2000, 2002) is presented in Figure 2D; no significant difference was found. This result indicates that short exposures to dieldrin induce no transcriptional change in PKC $\delta$  in N27 cells.

### **Nuclear accumulation of cleaved fragments of PKC $\delta$ in N27 cells following dieldrin exposure**

Subcellular localization of PKC $\delta$  after its proteolytic activation in neurotoxin-induced apoptotic dopaminergic neuronal cells has not been determined. We first examined the localization of PKC $\delta$  by immunostaining in N27 cells following dieldrin exposure. The immunostaining of PKC $\delta$  was performed at 1 hr following dieldrin exposure. The immunoreactivity of PKC $\delta$  was predominantly found in the cytoplasm rather than in the nucleus in control N27 cells (Figure 3Ac). However, in dieldrin-treated N27 cells, a dramatic shift of immunoreactivity of PKC $\delta$  from the cytoplasm to the nucleus was observed (Figure 3Af). To determine the dieldrin-induced subcellular localization change of both full-length and cleaved PCK $\delta$ , nuclear and cytosolic fractions from N27 cells following dieldrin exposure up to 3 hr were prepared, separated by 10% SDS-PAGE and immunoblotted with anti-PKC $\delta$  antibody. As shown in Figure 3B, full-length PKC $\delta$  was largely found in the cytosolic fraction and dieldrin exposure did not induce the elevation of PKC $\delta$  protein level, which is consistent with the quantitative RT-PCR result shown in Figure 2D. In addition, no significant localization change between the cytoplasm and the nucleus for full-length PKC $\delta$  in N27 cells following dieldrin exposure was observed. On the other hand, the cleaved fragments of PKC $\delta$  can be detected in the cytosolic fraction of N27 cells as early as 0.5 hr after dieldrin exposure, while cleaved fragments of PKC $\delta$  in the nuclear fraction of N27 cells only appeared after the 1 hr time point following dieldrin exposure.

Since caspase-3 was primarily activated and retained in the cytoplasm as shown in Figure 1, and the cleaved fragments of PKC $\delta$  in the cytosolic fraction appeared at an earlier

time point as compared to the nuclear fraction of N27 cells following dieldrin exposure, this result suggests that the full-length PKC $\delta$  is first cleaved in the cytoplasm and then the cleaved fragments of PCK $\delta$  are translocated to the nucleus. To investigate whether the nuclear accumulation of cleaved fragments of PKC $\delta$  was caspase-3 dependent, N27 cells were co-treated with dieldrin and the caspase-3 specific inhibitor Z-DEVD-FMK. As shown in Figure 3C, cleaved fragments of PKC $\delta$  appeared in both cytosolic and nuclear fractions following dieldrin exposure. Following co-treatment with Z-DEVD-FMK and dieldrin, cleaved fragments of PKC $\delta$  were dramatically decreased in the cytosolic fraction. Similarly, the cleaved fragments in the nuclear fraction were also reduced. Notably, however, the reduction in cleaved fragments of PKC $\delta$  in the nuclear fraction was not as significant as that observed in the cytosolic fraction. Possibly a small fraction of cleaved fragments of PKC $\delta$  was still generated in the cytoplasm due to the incomplete inhibition of Z-DEVD-FMK; therefore, these cleaved fragments of PCK $\delta$  continued to translocate and accumulate in the nucleus. This result matched our previous observation that the cleaved fragments of PKC $\delta$  appeared at an earlier time point in the cytosolic fraction compared to the nuclear fraction, reinforcing the model that the full-length PKC $\delta$  is first cleaved in the cytoplasm and the cleaved fragments of PKC $\delta$  subsequently translocate to the nucleus in N27 cell following dieldrin exposure.

We also tried to directly determine the localization change of the catalytic fragment of PKC $\delta$  in N27 cells following dieldrin exposure. Because antibody specifically detecting the catalytic fragment of PCK $\delta$  is currently unavailable, we then transiently transfected PKC $\delta$ -CF into N27 cells to examine the localization of the catalytic fragment of PKC $\delta$

(PKC $\delta$ -CF). Immunostaining of the V5 tag and counterstaining of the nucleus were performed at 24 hr post-transfection. As shown in Figure 3D, PKC $\delta$ -CF, revealed by V5 immunoreactivity, primarily localizes in the nucleus, further indicating that cleaved fragments of PKC $\delta$  translocate to the nucleus.

**Cleavage resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM) abolishes dieldrin induced proteolytic activation of PKC $\delta$  in N27 cells and protects cells from dieldrin induced apoptosis**

In order to investigate the necessity of caspase-3 mediated proteolytic activation of PKC $\delta$  in dieldrin induced apoptosis of N27 cells, the PKC $\delta$ -CRM stably expressing N27 cell line was generated via the ViraPower<sup>TM</sup> lentiviral expression system (Invitrogen). Figure 4A shows that about 80% of N27 cells in this cell line were PKC $\delta$ -CRM expressing cells, as identified by immunostaining of the V5 tag. PKC $\delta$ -CRM contains a point mutation (D327A) in its caspase-3 recognition and cleavage motif, which abolishes the cleavage of PKC $\delta$  by activated caspase-3 (DeVries et al., 2002; Ghayur et al., 1996). As shown in Figure 4B, in the control (no transfection) cells, PKC $\delta$  cleavage was induced at the 1 hr time point following dieldrin exposure and was abolished by co-treatment with Z-DEVD-FMK and dieldrin; however, in the PKC $\delta$ -CRM expressing N27 cells, cleaved fragments of PKC $\delta$  were barely detected at the 1 hr time point following dieldrin exposure.

The detailed mechanism of the inhibition of PKC $\delta$ -CRM in dieldrin induced cleavage of endogenous PKC $\delta$  is under investigation. Some preliminary results from our lab suggest that overexpressed PKC $\delta$  down-regulates the expression of endogenous PKC $\delta$ . The

overexpressed PKC $\delta$ -CRM might also inhibit the feedback loop between PKC $\delta$  and caspase-3 (Leverrier et al., 2002), resulting in the inhibition of continuous activation of caspase-3. It is also possible that the overexpressed PKC $\delta$ -CRM simply out-competes endogenous PKC $\delta$  for activated caspase-3, thus leaving endogenous PKC $\delta$  intact. With the co-treatment of Z-DEVD-FMK and dieldrin in PKC $\delta$ -CRM cells, dieldrin induced cleavage of PKC $\delta$  was completely blocked. Meanwhile, the PKC $\delta$  kinase activity was also examined in PKC $\delta$ -CRM expressing cells. As shown in Figure 4C, dieldrin treatment for 1 hr in the control (no transfection) cells increased PKC $\delta$  kinase activity to 220% in comparison to untreated control cells. However, in PKC $\delta$ -CRM expressing cells, dieldrin exposure for 1 hr increased PKC $\delta$  kinase activity by only 20% compared to untreated PKC $\delta$ -CRM cells.

We next examined whether abolishment of caspase-3 mediated proteolytic activation of PKC $\delta$  by PKC $\delta$ -CRM protects N27 cells against dieldrin induced apoptotic cell death. In control cells, dieldrin exposure for 1 hr induced about 520% increase in the DNA fragmentation level compared to untreated control cells; however, in the PKC $\delta$ -CRM expressing N27 cells, only 50% increase in the DNA fragmentation level was induced following dieldrin exposure for 1 hr in comparison to untreated PKC $\delta$ -CRM expressing cells (Figure 4D). These results clearly suggest that the caspase-3 mediated proteolytic activation of PKC $\delta$  following dieldrin exposure is required for PKC $\delta$ 's pro-apoptotic function in dieldrin induced apoptotic cell death in dopaminergic neuronal cells.

**Lipid-mediated activation of full-length PKC $\delta$  induces neuronal differentiation but not apoptosis in N27 cells**

Other than proteolytic activation, PKC $\delta$  can also be activated through the binding of lipid (diacylglycerol, phorbol esters) to its C1 domain, resulting in subsequent translocation to the plasma membrane (Newton, 2003). To investigate whether the lipid-mediated activation of full-length PKC $\delta$  also contributes to apoptosis of dopaminergic neuronal cells, N27 cells were treated with either 100 nM bistratene A, the specific PKC $\delta$  activator (Frey et al., 2000; Frey et al., 2001) or 100 nM TPA, the classical pan-PKC activator, for 30 min. The immunostaining of PKC $\delta$  was performed after treatment and observed under confocal microscopy. As shown in Figure 5Ai, PKC $\delta$  showed uniform cytoplasmic distribution, and no clear neurites were observed in the untreated N27 cells. After treatment with bistratene A for 30 min, PKC $\delta$  was translocated to the plasma membrane (Figure 5Ad) and differentiation of N27 cells were observed (Figure 5Af). Multiple elongated neurites were induced, and the cell body became more compact. N27 cells were also treated with TPA. As shown in Figure 5Aa, plasma membrane translocation of PKC $\delta$  and differentiation of N27 cells were induced following TPA exposure. No PKC $\delta$  cleavage was induced in N27 cells following either TPA or bistratene A exposure for 30 min, as shown in Figure 5B. Following bistratene A or TPA exposure, the DNA fragmentation level in N27 cells was also determined. As shown in Figure 5C, no significant difference was found in DNA fragmentation levels in N27 cells treated with bistratene A or TPA compared to the untreated cells. Taken together, these results clearly suggest that although full-length PKC $\delta$  can be activated through lipid molecules, the activated full-length PKC $\delta$  contributes to neuronal differentiation, but not the apoptotic death of dopaminergic neuronal cells.

### **Blockade of the nuclear localization of cleaved fragments of PKC $\delta$ protects N27 cells from apoptosis**

As shown above, dieldrin exposure induces not only caspase-3 mediated proteolytic activation of PKC $\delta$ , but also the nuclear translocation of activated cleaved PKC $\delta$ . It has been recently reported that the C-terminal of PKC $\delta$  contains a functional nuclear localization signal (NLS) (DeVries et al., 2002). Point mutation of this NLS abolishes the nuclear translocation of PKC $\delta$  in rat parotid salivary cells (DeVries et al., 2002). To investigate whether the nuclear translocation of activated cleaved PKC $\delta$  is essential for its function in apoptosis, we first prepared PKC $\delta$ - $\Delta$ NLS with the deletion of the complete nuclear localization signal (NLS) and generated the N27 cell line stably expressing PKC $\delta$ - $\Delta$ NLS and PKC $\delta$ -WT with the use of the ViraPower<sup>TM</sup> lentiviral expression system (Invitrogen).

The schematic representation of the primary structure of PKC $\delta$ -WT, PKC $\delta$ - $\Delta$ NLS, and PKC $\delta$ -CRM is shown in Figure 6A. An N27 cell line stably expressing  $\beta$ -galactosidase (LacZ, supplied with the kit) was also generated as a vector control. Expressed PKC $\delta$ - $\Delta$ NLS or PKC $\delta$ -WT could be identified by immunostaining of the V5 tag at the C terminal. Because the V5 tag is located at the C-terminal, immunostaining of the V5 tag identified both the full-length and cleaved catalytic fragment of PKC $\delta$ . In the PKC $\delta$ -WT expressing cells, PKC $\delta$ -WT, revealed by V5 immunoreactivity, was primarily localized in the cytoplasm in the untreated cells (Figure 6Ba). At 1 hr following dieldrin exposure, V5 immunoreactivity accumulated in the nucleus, as shown in Figure 6Bd, which is consistent with our observation of the endogenous PKC $\delta$  (Figure 3A). In the PKC $\delta$ - $\Delta$ NLS expressing cells, PKC $\delta$ - $\Delta$ NLS, revealed by V5 immunoreactivity, localized only in the cytoplasm regardless of the treatment

with dieldrin (Figure 6Bb&e). The subcellular localization of PKC $\delta$ -CRM was also examined. As shown in Figure 6Bc&f, PKC $\delta$ -CRM, revealed by V5 immunoreactivity, also showed predominant localization in the cytoplasm with or without treatment with dieldrin, which suggests again that only cleaved fragments of PKC $\delta$ , not the full-length PKC $\delta$ , translocates to the nucleus.

We next examined the DNA fragmentation level in PKC $\delta$ -WT and PKC $\delta$ - $\Delta$ NLS expressing cells following dieldrin exposure. As shown in Figure 6C, DNA fragmentation levels following dieldrin exposure only increased by 60% in PKC $\delta$ - $\Delta$ NLS expressing cells when compared to untreated PKC $\delta$ - $\Delta$ NLS cells; however, an approximate 210% DNA fragmentation level was induced following dieldrin exposure in both PKC $\delta$ -WT expressing and vector control cells. Together with the DNA fragmentation result from Figure 4D, our study clearly indicates that not only the proteolytic activation of full-length PKC $\delta$ , but also the subsequent nuclear translocation of activated cleaved PCK $\delta$ , are both necessary for PKC $\delta$ 's pro-apoptotic function in dieldrin-induced apoptosis of dopaminergic neuronal (N27) cells.

#### **Activated cleaved PKC $\delta$ mediates Ser14 phosphorylation of histone H2B following its nuclear translocation in dieldrin induced apoptotic N27 cells**

Phosphorylation of histones has been suggested to play a role in the formation of chromatin condensation in apoptotic cells (Ajiro, 2000). In particular, histone H2B phosphorylation at Ser14 has been ubiquitously found in apoptotic cells (Cheung et al., 2003). To investigate whether activated cleaved fragments of PKC $\delta$  mediate H2B phosphorylation



following nuclear translocation, we first examined the Ser14 phosphorylation in dieldrin-induced apoptotic N27 cells. The immunostaining of phosphorylated H2B was performed with the use of anti-phospho-Histone H2B (Ser14) antibody in N27 cells at the 1 hr time point following dieldrin exposure. As shown in Figure 7Aa, Ser14 phosphorylated H2B was clearly detected in dieldrin-induced apoptotic cells. To ensure that it occurred inside the nucleus, nuclei were also counterstained with Hoechst 33342. As shown in Figure 7Ab, a condensed nucleus was also observed in the same apoptotic cell and the merged image (Figure 7Ac) confirms the co-staining. Histone mixtures were also extracted from the nuclei of N27 cells following dieldrin treatment alone or after co-treatment with Z-DEVD-FMK and dieldrin, separated by 15% SDS-PAGE, and immunoblotted with anti-phospho-Histone H2B (Ser14) antibody. As shown in Figure 7B, Z-DEVD-FMK co-treatment reduced dieldrin-induced Ser14 phosphorylation of H2B, indicating that Ser14 phosphorylation of H2B is caspase-3 dependent.

To directly examine whether PKC $\delta$  mediated the phosphorylation of H2B, PKC $\delta$  was immunoprecipitated from N27 cells following co-treatment of Z-DEVD-FMK and dieldrin or dieldrin treatment alone. Immunoprecipitated PKC $\delta$  was then performed with an *in vitro* kinase assay with purified H2B as substrate in the presence of  $^{32}\text{P}$ . As shown in Figure 7C, PKC $\delta$  immunoprecipitated from cells treated only with dieldrin showed a significant increase in phosphorylation of H2B over time (from 1 hr to 3 hr) compared to untreated cells, however, Z-DEVD-FMK co-treatment reduced dieldrin-induced phosphorylation of H2B by immunoprecipitated PKC $\delta$ .

PKC $\delta$ -CRM and PKC $\delta$ - $\Delta$ NLS have been shown above to inhibit the nuclear translocation of activated cleaved PKC $\delta$ . To investigate whether PKC $\delta$ -CRM and PKC $\delta$ - $\Delta$ NLS also block dieldrin-induced Ser14 phosphorylation of H2B, double immunostaining of V5 and Ser14 phosphorylated H2B was performed in PKC $\delta$ -CRM and PKC $\delta$ - $\Delta$ NLS stably expressing N27 cells following dieldrin exposure. In addition, double staining of V5 and Ser14 phosphorylated H2B was also performed in dieldrin treated PKC $\delta$ -WT and PKC $\delta$ -DN stably expressing N27 cells to determine whether PKC $\delta$  indeed mediates Ser14 phosphorylation of H2B. As shown in Figure 7Da-d, Ser14 phosphorylated H2B was clearly detected in PKC $\delta$ -WT expressing N27 cells, and fragmentation of the nucleus was also observed after dieldrin treatment. However, Ser14 phosphorylated H2B staining could not be detected in PKC $\delta$ -DN (Figure 7Df), PKC $\delta$ -CRM (Figure 7Dj) and PKC $\delta$ - $\Delta$ NLS (Figure 7Dn) expressing cells. Nuclei of these cells are also intact after dieldrin treatment. The effective inhibition of PKC $\delta$ -DN, PKC $\delta$ -CRM, and PKC $\delta$ -NLS indicates that the cleaved, kinase-active fragments of PKC $\delta$ , after nuclear translocation, mediate Ser14 phosphorylation of H2B and promote dieldrin induced apoptotic death of dopaminergic neuronal cells.

### **Catalytic fragment of PKC $\delta$ directly induces Ser14 phosphorylation of histone H2B and apoptosis in dopaminergic neuronal cells**

Next, we directly introduced the catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF) in the N27 cells to investigate whether PKC $\delta$ -CF itself can induce Ser14 phosphorylation of H2B and apoptosis in N27 cells. PKC $\delta$ -CF was introduced into the N27 cells through lipofectamine-mediated transfection. PKC $\delta$ -RF was also introduced into the N27 cells to serve as a control.

About 48 hr after transfection, double immunostaining of Ser14 phosphorylated H2B and the V5 tag as well as counterstaining of nuclei were performed to visualize the localization of PKC $\delta$ -CF and phosphorylation of H2B. As shown in Figure 8a, PKC $\delta$ -CF, revealed by V5 immunoreactivity, only localizes in the nucleus, and strong staining of Ser14 phosphorylated H2B was also observed in the same cell (Figure 8b). Nucleus counterstaining showed that the nucleus was also broken apart and chromatin became condensed (Figure 8c), confirming that this cell indeed underwent apoptosis. In contrast, the nucleus of a PKC $\delta$ -RF positive N27 cell is still intact (Figure 8g) and no clear staining of Ser14 phosphorylated H2B could be observed (Figure 8f). The direct induction of Ser14 phosphorylation of H2B and apoptosis by the nuclear localized PKC $\delta$ -CF is consistent with our results above that proteolytically activated cleaved PKC $\delta$  mediates neurotoxin-induced Ser14 phosphorylation of H2B and apoptosis of dopaminergic neuronal cells. Interestingly, we first tried to generate PKC $\delta$ -CF stably expressing N27 cells with the use of ViraPower<sup>TM</sup> lentiviral expression system; however, generation of a PKC $\delta$ -CF stably expressing N27 cell line was unsuccessful after many attempts. N27 cells were either refractory to PKC $\delta$ -CF or quickly died several days after application of the selection antibiotic, blasticidin. This also suggests that PKC $\delta$ -CF itself is toxic and could induce cell death by itself.

## DISCUSSION

In the present study, we investigated the downstream events after proteolytic cleavage of PKC $\delta$  in dieldrin induced apoptosis of dopaminergic neuronal cells. We demonstrated that

the full-length PKC $\delta$  was first cleaved in the cytoplasm and the activated cleaved fragments of PKC $\delta$  subsequently translocated into the nucleus. By employing the NLS deletion mutant (PKC $\delta$ - $\Delta$ NLS) and cleavage resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM), we showed that the proteolytic activation of full-length PKC $\delta$  and nuclear translocation of activated cleaved PKC $\delta$  are both necessary for PKC $\delta$ 's pro-apoptotic function in dieldrin-induced apoptosis of dopaminergic neuronal cells. Furthermore, we also demonstrated that the activated cleaved fragments of PKC $\delta$ , after nuclear translocation, mediate Ser14 phosphorylation of histone H2B. The caspase-3 inhibitors Z-DEVD-FMK, PKC $\delta$ -CRM, PKC $\delta$ - $\Delta$ NLS, and PKC $\delta$ -DN all inhibit Ser14 phosphorylation of H2B, while PKC $\delta$ -CF itself can directly induce Ser14 phosphorylation of H2B and apoptosis. Our study suggests that proteolytically activated PKC $\delta$  translocates to the nucleus and mediates Ser14 phosphorylation of histone H2B in neurotoxin-induced apoptotic death of dopaminergic neuronal cells.

Proteolytic activation of PKC $\delta$  is associated with its nuclear translocation in apoptotic cells. Depending on the cell type and apoptotic stimuli, the nuclear translocation of PKC $\delta$  either precedes (Blass et al., 2002; DeVries et al., 2002) or follows (Cross et al., 2000; Scheel-Toellner et al., 1999) its proteolytic activation in apoptotic cells. The early translocation of the full-length PKC $\delta$  to the nucleus before its proteolytic activation has been suggested to regulate the mitochondrial mediated apoptotic pathway and subsequent activation of caspase-3 (DeVries et al., 2002). In etoposide induced apoptotic glioma cells, proteolytic activation of PKC $\delta$  occurred in the nucleus after full-length PKC $\delta$  was translocated to the nucleus. The inhibition of nuclear translocation of the full-length PKC $\delta$  blocked caspase-3 activation and cleavage (Blass et al., 2002). Early nuclear translocation of

the full-length PKC $\delta$  is also implicated in early nuclear events to regulate the mitochondrial mediated apoptotic pathway in apoptotic C5 rat parotid salivary acinar cells (DeVries et al., 2002). In contrast, the late translocation of the activated cleaved PKC $\delta$  to the nucleus (after its proteolytic activation) is more often implicated as a direct effector to accelerate the apoptotic process by facilitating caspase-3 mediated cleavage of nuclear substrates, like lamin B (Cross et al., 2000) or inactivating survival mechanisms in apoptotic cells (Bharti et al., 1998).

In dieldrin-induced apoptotic dopaminergic neuronal cells, we demonstrated here that full-length PKC $\delta$  is first cleaved in the cytoplasm and only the activated cleaved fragments of PKC $\delta$  subsequently translocate to the nucleus. By employing the cleavage resistant mutant (PKC $\delta$ -CRM) and NLS deletion mutant (PKC $\delta$ - $\Delta$ NLS), we have further shown that the nuclear translocation of activated cleaved PKC $\delta$  was necessary for its function in dieldrin-induced apoptosis of dopaminergic neuronal cells. In addition, although few studies reported that the allosteric activation of full-length PKC $\delta$  by TPA treatment promoted the cytochrome C release and apoptosis (Majumder et al., 2000), our results show that allosteric activation of full-length PKC $\delta$  by treatment with TPA or a PKC $\delta$  specific activator, bistratene A, induces differentiation of dopaminergic neuronal cells, but not apoptotic death. By employing the cleavage resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM), we further demonstrate that proteolytic activation of PKC $\delta$  is required for its pro-apoptotic function in dieldrin induced apoptosis of dopaminergic neuronal cells. Since many other studies have reported that activation of the full-length PKC $\delta$  by lipids mediates signal transduction in a range of normal physiological processes, our study suggests that proteolytic activation is the favorable mode for PKC $\delta$ 's

activation and pro-apoptotic function in apoptotic dopaminergic neuronal cells. Our study further provides insight for the design of better inhibitors that specifically inhibit the proteolytic activation of PKC $\delta$ , and target only the activated cleaved fragments of PKC $\delta$  for protection against neurotoxin induced apoptosis in dopaminergic neuronal cells.

The downstream nuclear events following nuclear translocation of PKC $\delta$  in apoptosis have just begun to be explored as more and more nuclear targets of PKC $\delta$  have recently been identified. In DNA damage-induced apoptosis, the PKC $\delta$  catalytic fragments phosphorylate the catalytic subunit of DNA dependent protein kinase (DNA-PK) (Bharti et al., 1998), inhibiting the function of DNA-PK to form complexes with DNA and to phosphorylate its downstream target, p53 (Ferri and Kroemer, 2001). PKC $\delta$  was also found to interact with hRad9, a member of the human DNA damage sensor family to regulate interaction of hRad9 with Bcl-2 and the hRad9-mediated apoptotic response to DNA damage (Yoshida et al., 2003). PKC $\delta$  also phosphorylates transcriptional factors, including p73 (Ren et al., 2002) and STAT1 (DeVries et al., 2004), and regulates gene expression in apoptosis. PKC $\delta$  not only regulates the apoptotic signal, but also directly accelerates the collapse of nuclear structure in apoptotic cells. It was shown that PKC $\delta$  can phosphorylate lamin B, which is one of the major structural proteins involved in the assembly of the nuclear envelope (Cross et al., 2000). The phosphorylation of lamin B increases its susceptibility to caspase mediated cleavage, eventually leading to the disassembly of nuclear lamina.

Phosphorylation of histone H2B at Ser14 has been ubiquitously found in apoptotic cells in diverse species ranging from frogs to humans (Cheung et al., 2003). The H2B phosphorylation and amino-terminal tail of H2B (de la Barre et al., 2001), but not other

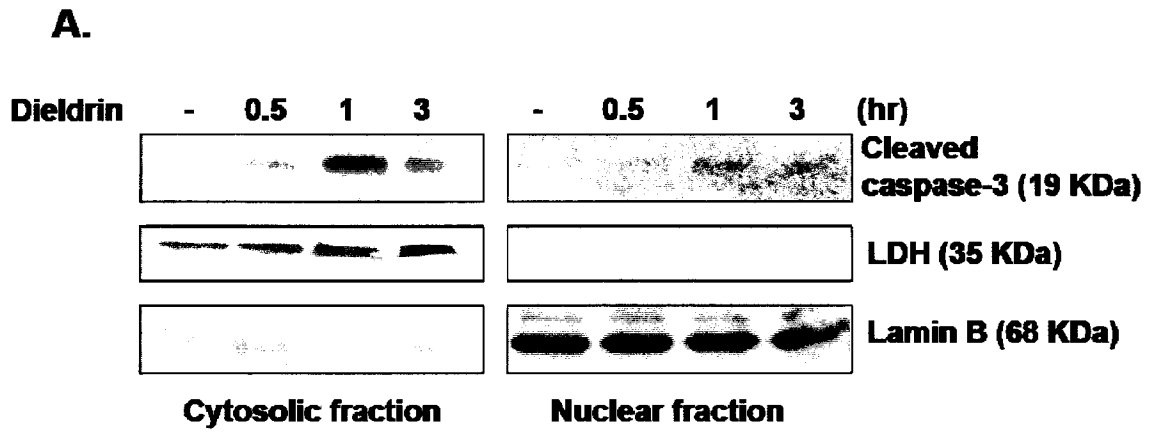
histones, are essential for chromatin condensation, one of the hallmarks of apoptotic cells. Mammalian sterile twenty 1 (Mst1) kinase has been identified as responsible for Ser14 phosphorylation of H2B (Cheung et al., 2003). Interestingly, Mst1 kinase also undergoes caspase-3 mediated proteolytic activation, and activated cleaved fragments of Mst1 kinase also translocate to the nucleus (Graves et al., 1998; Ura et al., 2001). In dopaminergic neuronal cells, we demonstrated that dieldrin exposure induces Ser14 phosphorylation of H2B, and activated PKC $\delta$  recovered from N27 cells exposed to dieldrin can phosphorylate H2B *in vitro* in a caspase-3 dependent manner. We further showed that the PKC $\delta$  catalytic fragment (PKC $\delta$ -CF) itself induces phosphorylation of H2B. These results suggest that other than Mst1, activated cleaved fragments of PKC $\delta$  also mediate phosphorylation of H2B directly by itself or indirectly by phosphorylating downstream kinases in apoptotic dopaminergic neuronal cells. During preparation of our manuscript, a recent study also reported that PKC $\delta$  mediates phosphorylation of H2B (Mecklenbrauker et al., 2004).

In conclusion, we demonstrate that the activated cleaved fragments of PKC $\delta$  translocate to the nucleus after proteolytic activation. We also show that proteolytic activation of the full-length PKC $\delta$  and nuclear translocation of the activated cleaved PKC $\delta$  are both necessary for its function in dieldrin-induced apoptosis of dopaminergic neuronal cells. In addition, the nuclear active PKC $\delta$  mediates phosphorylation of H2B and accelerates the apoptotic process in dopaminergic neuronal cells. Understanding the detailed mechanisms of PKC $\delta$  activity in neurotoxin-induced apoptosis of dopaminergic neuronal cells provides insight for drug design to protect dopaminergic neurons against neurotoxin induced degeneration.

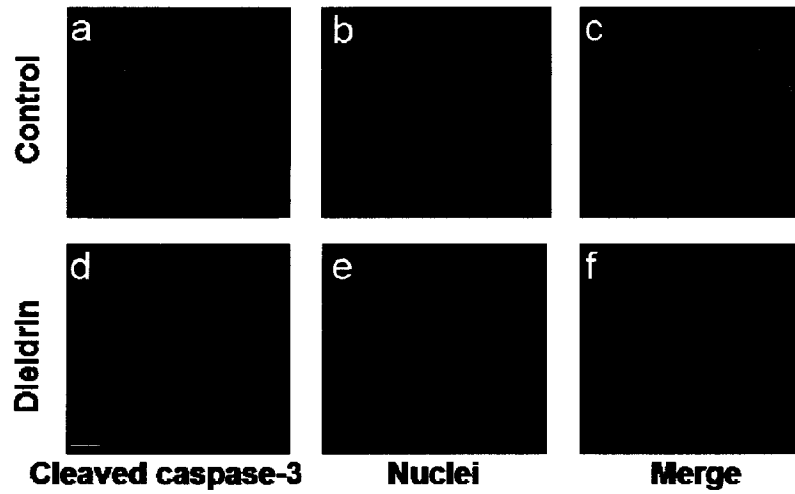
**Figure 1: Subcellular localization of activated caspase-3 in dopaminergic neuronal cells following dieldrin exposure.**

(A) Immunoblot of cleaved caspase-3 in cytosolic and nuclear fractions of N27 cells following dieldrin exposure. After treatment with dieldrin (60  $\mu$ M) for up to 3 hr in serum-free medium, cytosolic and nuclear fractions of N27 cells were prepared and separated on 15% SDS-PAGE. Cleaved (activated) caspase-3 was then detected on the immunoblots with the use of specific anti-cleaved caspase-3 antibody. Immunoblot of LDH and lamin B was also performed on separate gels for relative purity of cytosolic and nuclear fractions. (B) Immunostaining of cleaved caspase-3 in dopaminergic neuronal cells following dieldrin (60  $\mu$ M) exposure for 1 hr in serum-free medium. After treatment, cells were fixed and stained with anti-cleaved-caspase-3 antibody. The immunoreactivity of cleaved caspase-3 was visualized by Alexa488 conjugated secondary antibody (green fluorescence). The cells were observed under an LCS/NT confocal microscopy system (Bar = 10  $\mu$ m). Experiments were repeated three times and representative images are presented.



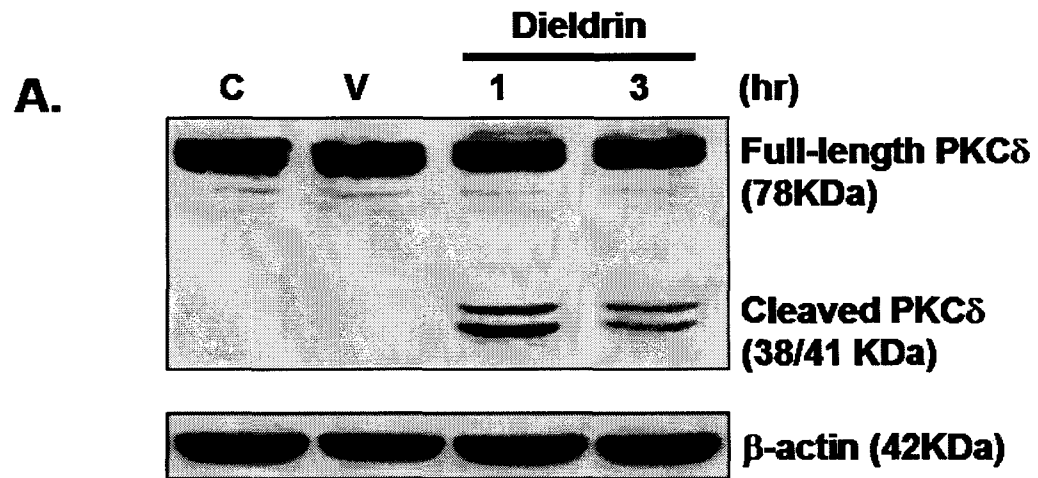


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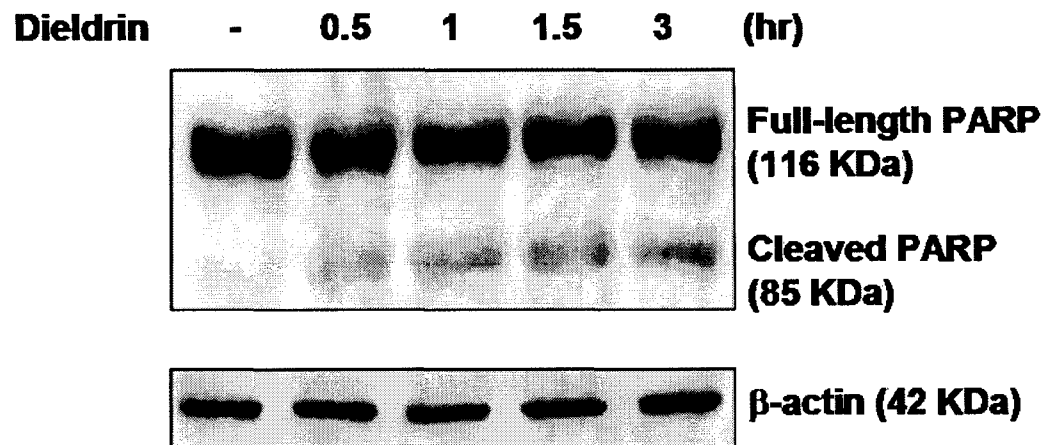


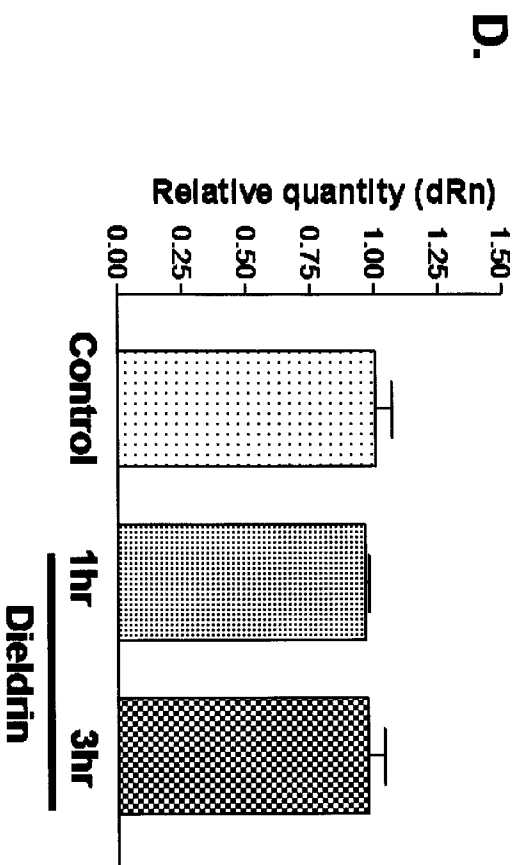
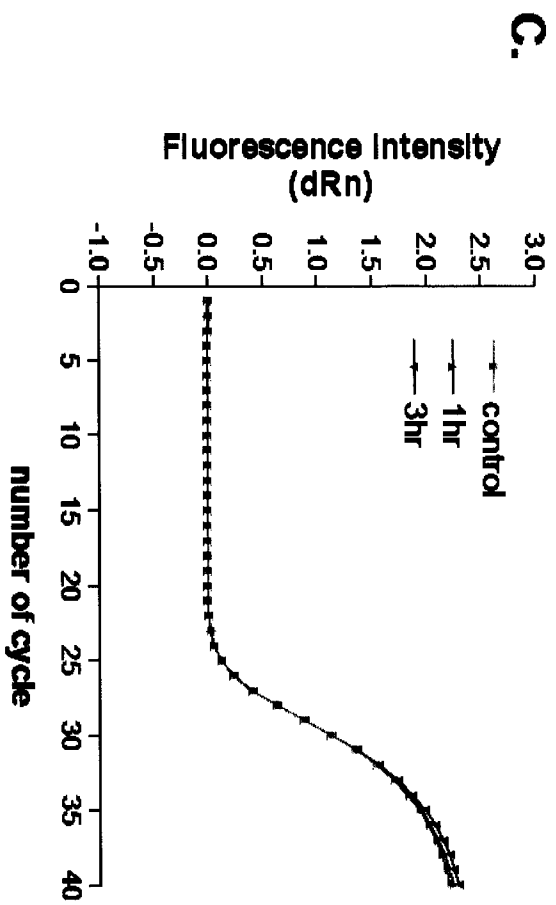
**Figure 2: Dieldrin exposure induces PKC $\delta$  cleavage without changing its expression in N27 cells**

(A) Cleaved fragments of PKC $\delta$  (38-41kDs) were induced in N27 cells following dieldrin exposure. (B) Dieldrin exposure also induced the generation of cleaved fragments of PARP (85KD) in N27 cells. N27 cells were treated with 60  $\mu$ M dieldrin for up to 3 hr in serum-free medium. Cells were then lysed and the lysate was used for Western blot analysis to detect both the PKC $\delta$  and PARP cleavage. To confirm equal protein loading in Western blots, the membranes were reprobed with  $\beta$ -actin antibody. (C) Amplification plot of quantitative RT-PCR of PKC $\delta$  mRNA in N27 cells following dieldrin exposure. (D) Relative quantity of PKC $\delta$  mRNA copies in N27 cells following dieldrin exposure. N27 cells were treated with 60  $\mu$ M dieldrin for up to 3 hr in serum-free medium. Cells were then lysed and total RNA was isolated with TRIZOL reagent and converted to cDNA. The PCR reaction was then set up by mixing 50 ng cDNA, rat PKC $\delta$  TaqMan expression assay reagent as well as 2x PCR master mix in a 96-well plate. The PCR reaction was performed in a Mx4000 multiplex Quantitative PCR system (Stratagene, La Jolla, CA). To ensure that equal amounts of RNA were used in the PCR reaction, 18s ribosome RNA (18s rRNA) was used as an endogenous control. The relative quantity of PKC $\delta$  mRNA was calculated based on the formula  $2^{-(\Delta C_t^{PKC\delta - \Delta C_t^{18s\ rRNA}})}$  (Ct: threshold of cycle), and the control was used as a calibrator for comparison with other samples. The Ct value was determined by software installed on the Mx4000 multiplex Quantitative PCR system. The data represent the mean  $\pm$  SEM from three separate experiments in triplicate.



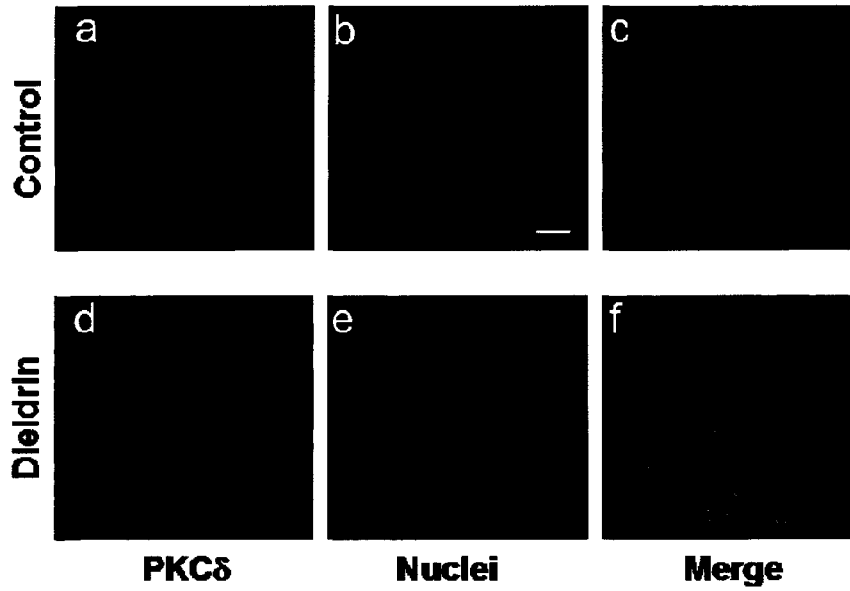
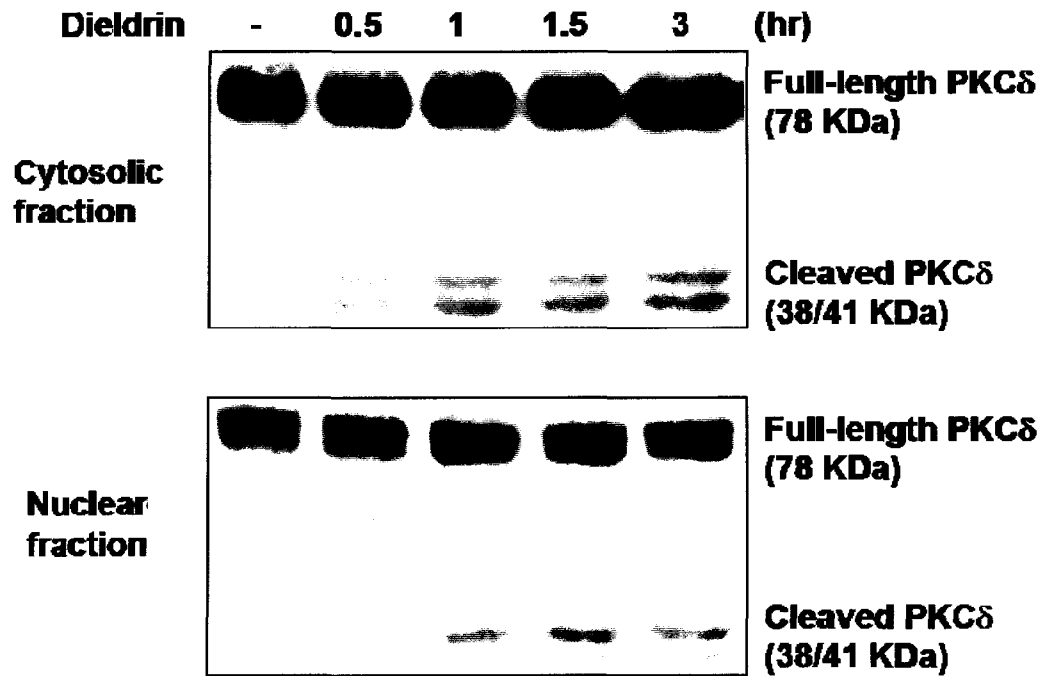
**B.**



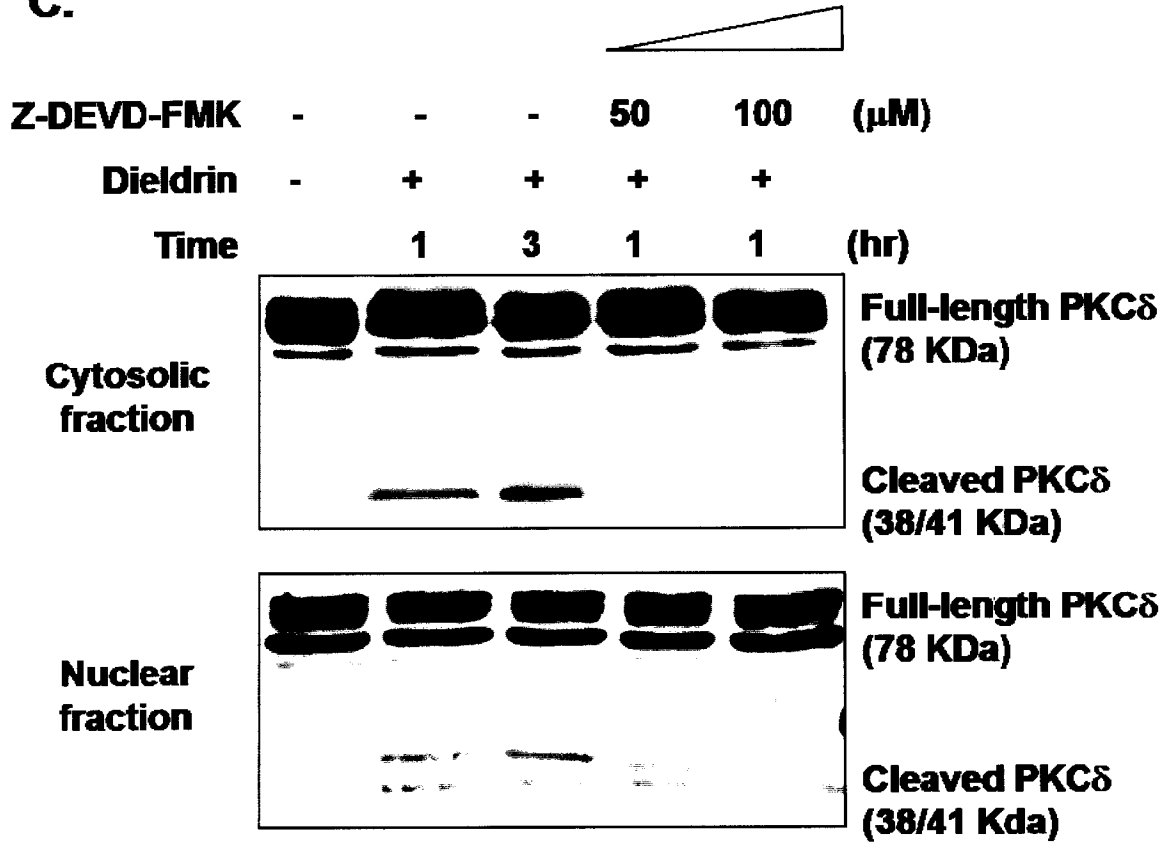


**Figure 3: Dieldrin exposure induces nuclear translocation of cleaved fragments of PKC $\delta$  in N27 cells**

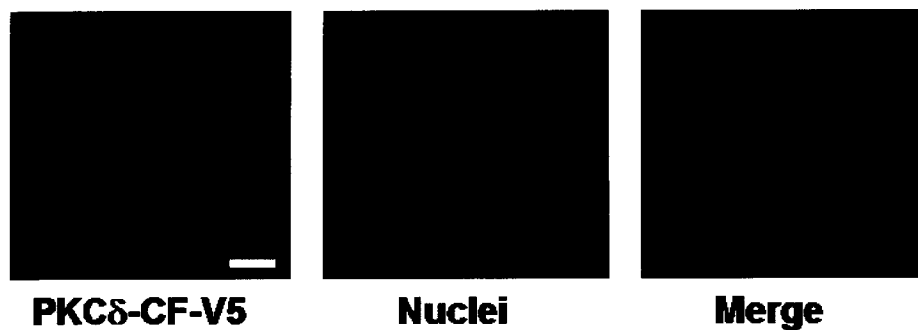
(A) Nuclear accumulation of PKC $\delta$  immunoreactivity in N27 cells following dieldrin exposure. After dieldrin (60  $\mu$ M) treatment for 1 hr, N27 cells were fixed and stained with anti-PKC $\delta$  antibody (1:1000). The PKC $\delta$  was visualized then by Alex488 conjugated secondary antibody (1:2000) and images were taken under TCS/NT confocal microscopy (B). Dieldrin exposure induced nuclear translocation of cleaved fragments of PKC $\delta$  in N27 cells. (C) Co-treatment of N27 cells with Z-DEVD-FMK reduced dieldrin induced PKC $\delta$  cleavage and nuclear translocation of cleaved fragments of PKC $\delta$ . Cells were treated with dieldrin (60  $\mu$ M) alone or co-treated with Z-DEVD-FMK (50  $\mu$ M or 100  $\mu$ M) and dieldrin (60  $\mu$ M) for up to 3 hr. Cytosolic and nuclear fractions were then prepared and separated on 10% SDS-PAGE. Cleaved fragments of PCK $\delta$  were then detected on both immunoblots with the use of anti-PKC $\delta$  antibody. (D) Nuclear localization of overexpressed PKC $\delta$ -CF in the N27 cells. Immunostaining of V5 was performed 24 hr after transfection. Immunoreactivity of V5 was visualized by Cy3 conjugated anti-mouse secondary antibody (1:2000). Nuclei were counterstained by Hoechst 33342. Cells were observed under a LCS/NT confocal microscopy system (Bar = 10  $\mu$ m).

**A.****B.**

C.



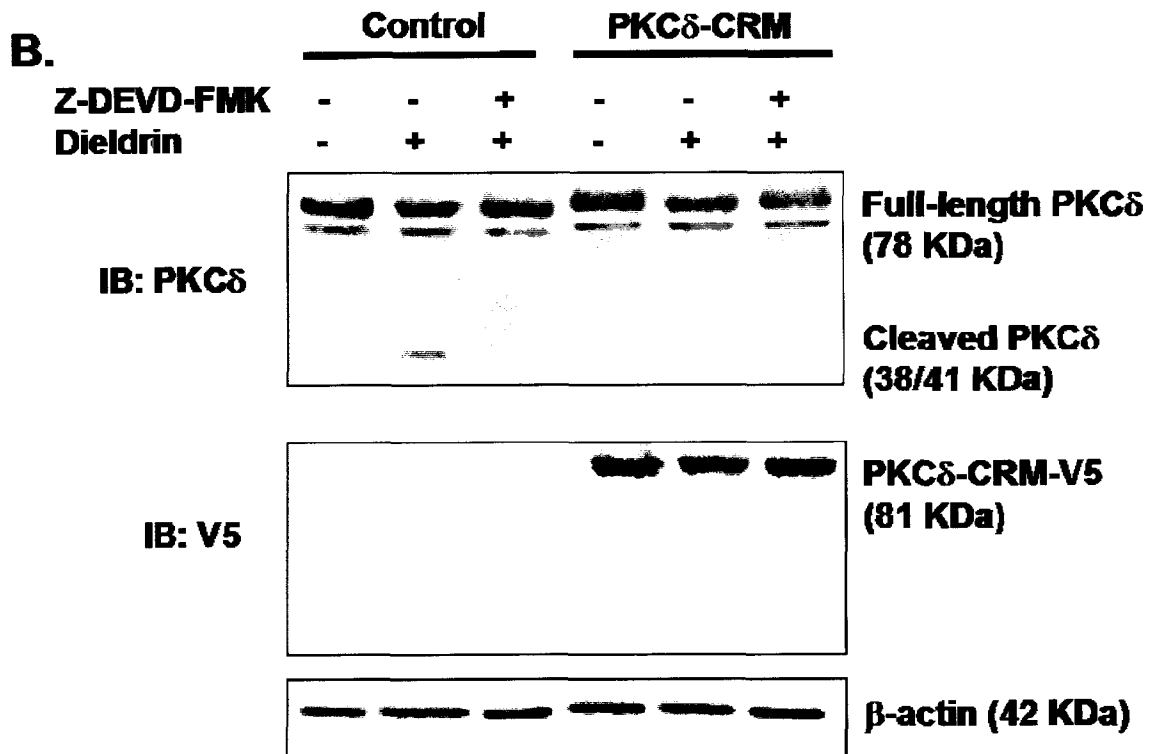
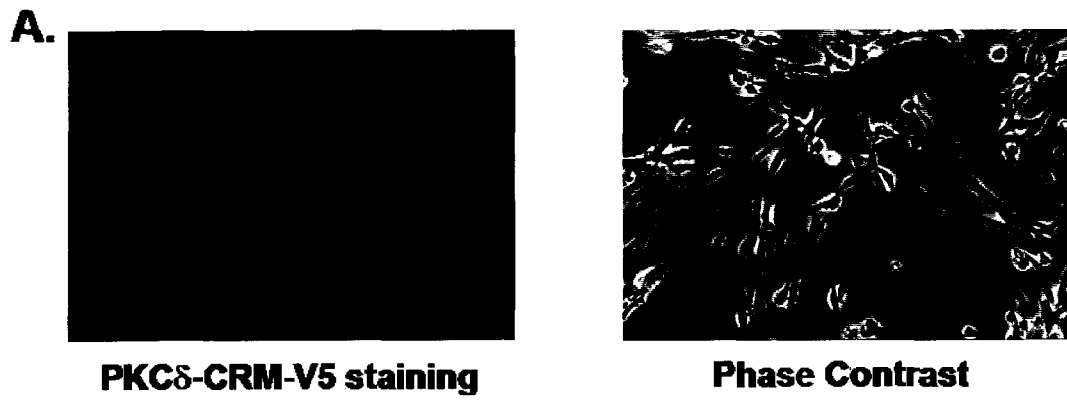
D.

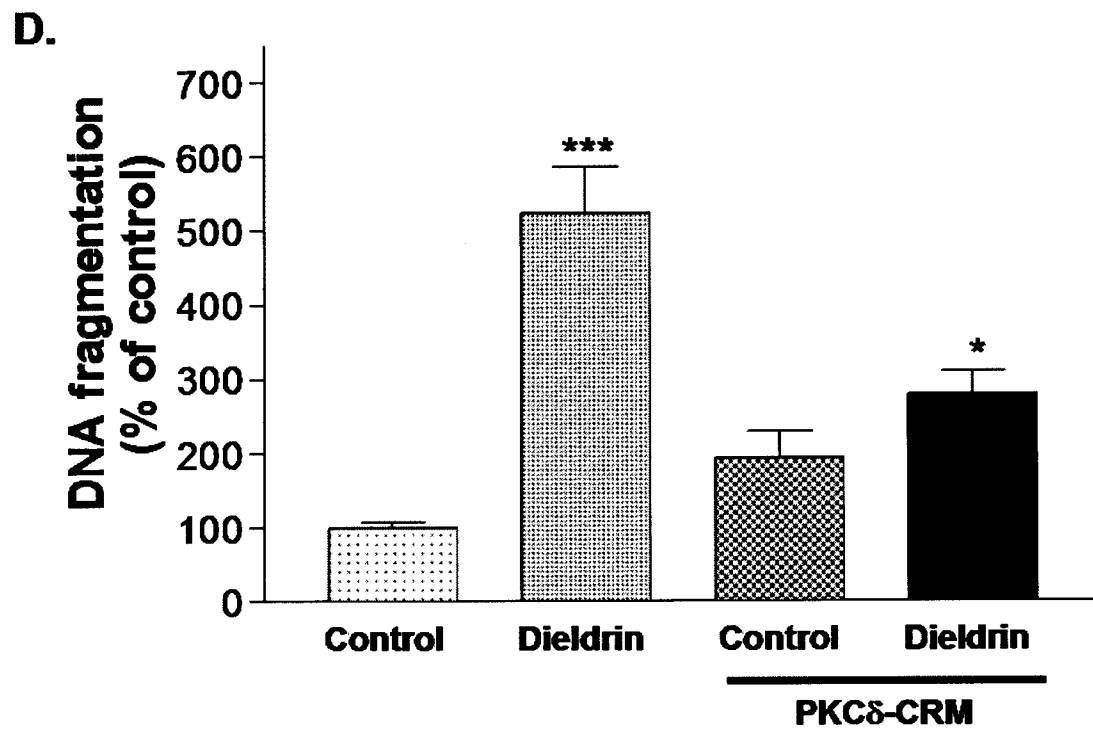
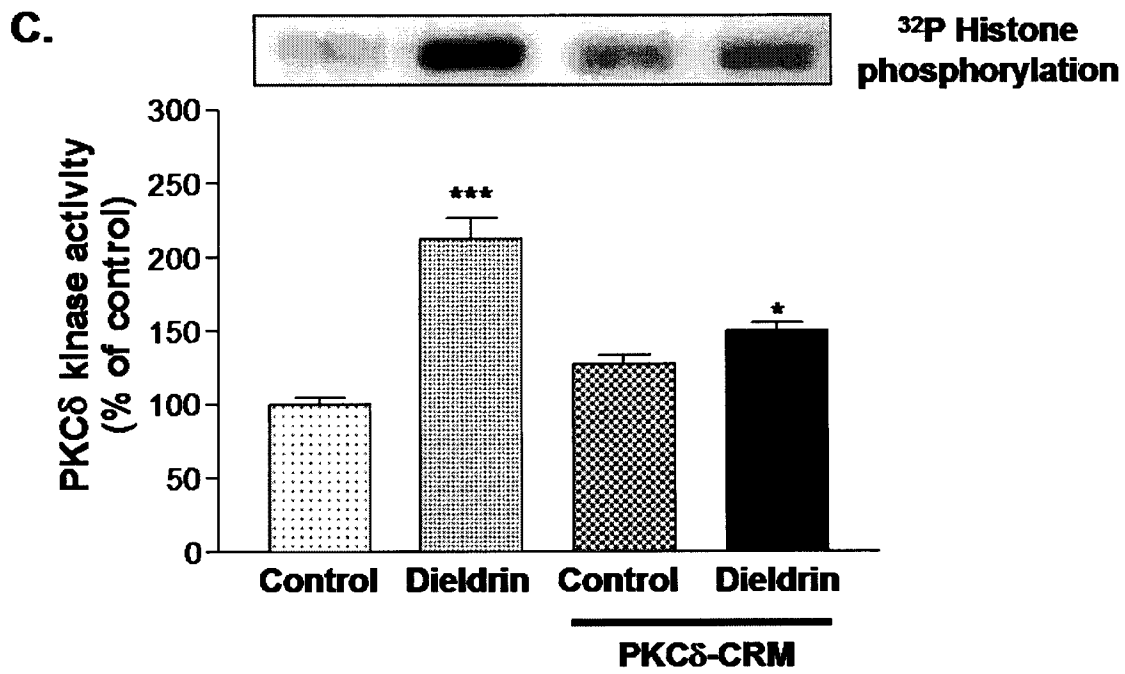


**Figure 4: Cleavage resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM) abolishes dieldrin induced proteolytic activation of PKC $\delta$  and protects cells from dieldrin induced apoptosis in N27 cells.**

(A) Stable expression of PKC $\delta$ -CRM in dopaminergic neuronal (N27) cells. A ViraPower Lentiviral gene expression system (Invitrogen, Inc. Carlsbad, CA) was employed for generation of a PKC $\delta$ -CRM expressing cell line. PKC $\delta$ -CRM stably expressing cells were maintained in normal medium supplemented with 10  $\mu$ g/ml blasticidin. To identify PKC $\delta$ -CRM expressing cells, cells were fixed and stained with anti-V5 antibody (1:1000) and Cy3-conjugated secondary anti-mouse antibody (1:2000). Cells were observed under a Nikon inverted fluorescence microscope (Model TE-2000U). (B) Dieldrin induced PKC $\delta$  cleavage was abolished in PKC $\delta$ -CRM expressing cells. Control cells and PKC $\delta$ -CRM expressing cells were treated with dieldrin (60  $\mu$ M) alone or co-treated with Z-DEVD-FMK (50  $\mu$ M) and dieldrin (60  $\mu$ M) for 1 hr. The cells were lysed and whole cell lysate was used for Western blot analysis to detect the PKC $\delta$  cleavage. Membrane was reprobbed with anti-V5 antibody (1:5000) to ensure abundant PKC $\delta$ -CRM was expressed only in the PKC $\delta$ -CRM expressing cell line. (C) Dieldrin exposure induced PKC $\delta$  kinase activity was attenuated in PKC $\delta$ -CRM stably expressing N27 cells. The cells were lysed and PKC $\delta$  was first immunoprecipitated and an *in vitro* kinase assay was performed. Significance of difference in kinase activity was compared to untreated control cells. (D) PKC $\delta$ -CRM protects against dieldrin induced apoptosis in N27 cells. Significance of difference in DNA fragmentation was compared to untreated control cells. The data represent the mean  $\pm$  SEM from two separate experiments in triplicate (\*,  $p < 0.05$ ; \*\*\*,  $p < 0.001$ ; N=6).



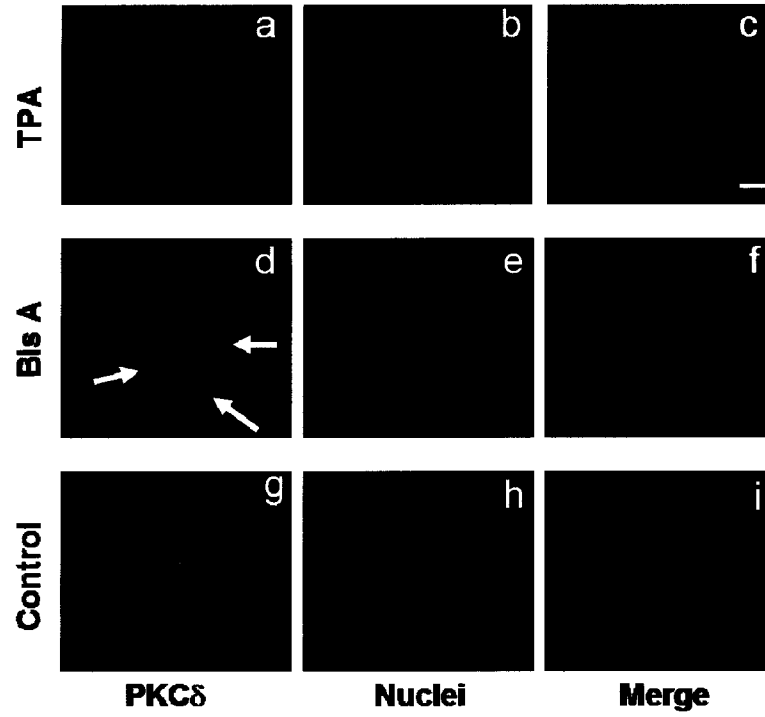




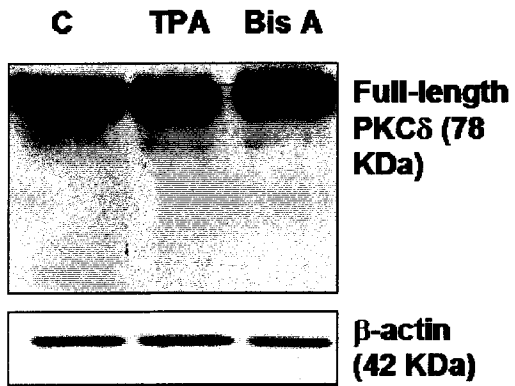
**Figure 5: Lipid-mediated activation of full-length PKC $\delta$  induces the differentiation of N27 cells but not apoptotic death.**

(A) Plasma membrane translocation of PKC $\delta$  and differentiation of N27 cells were induced by bistratene A or TPA treatment. N27 cells were treated with 100 nM bistratene A or TPA for 30 min. PKC $\delta$  immunostaining was then performed to visualize its subcellular distribution and cellular morphological changes. Stained cells were observed under confocal microscopy (Bar = 10  $\mu$ m). (B) TPA and Bistratene A treatment didn't induce PKC $\delta$  cleavage in N27 cells. N27 cells were treated with 100 nM TPA or Bis A for 30 min and whole cell lysates were isolated. (C) Apoptotic death was not induced in N27 cells following bistratene A or TPA treatment. After treatment with 100 nM bistratene A or TPA for 30 min, N27 cells were lysed for DNA fragmentation assay. The data represent the mean  $\pm$  SEM from two separate experiments in triplicate (N=6).

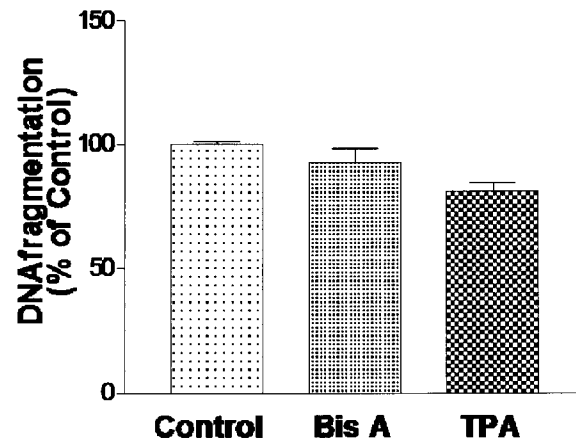
A.



B.

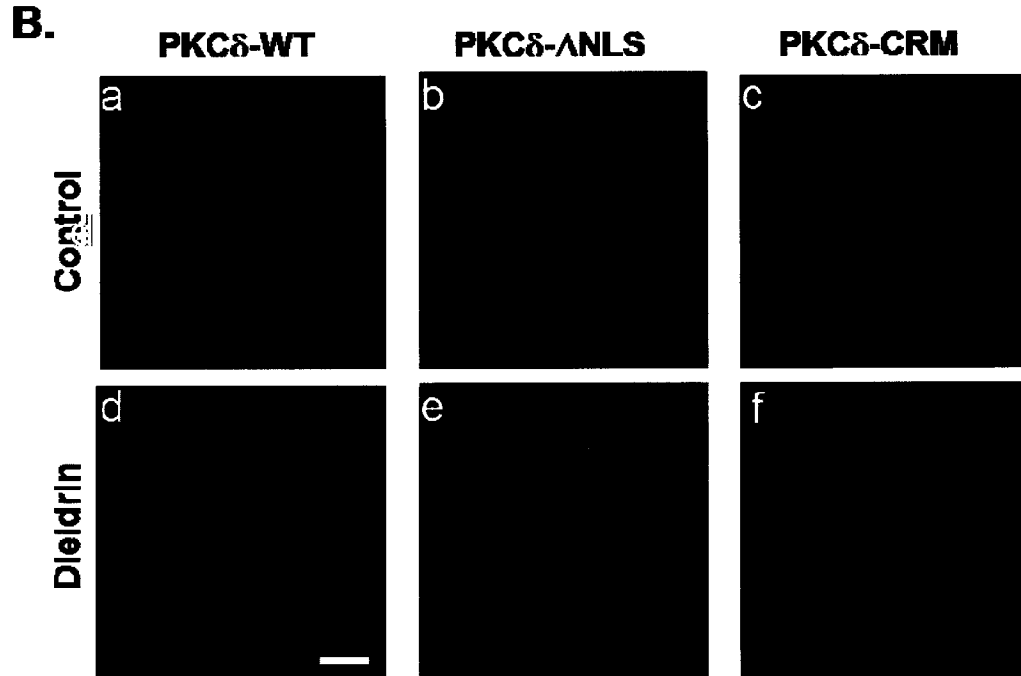
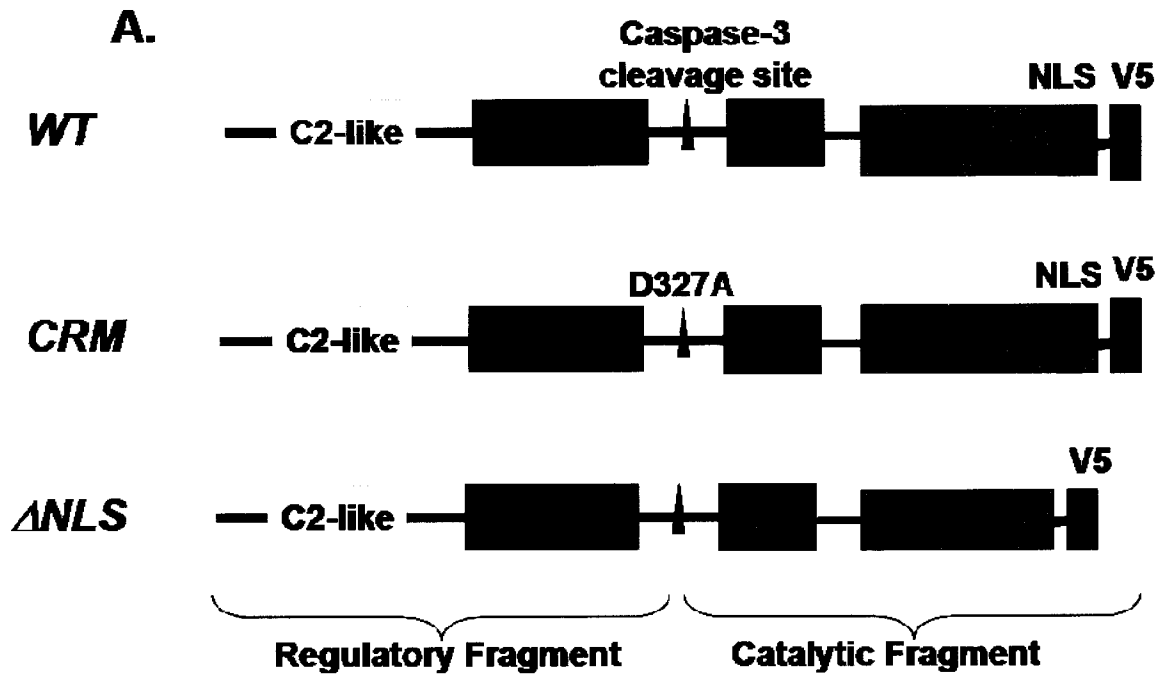


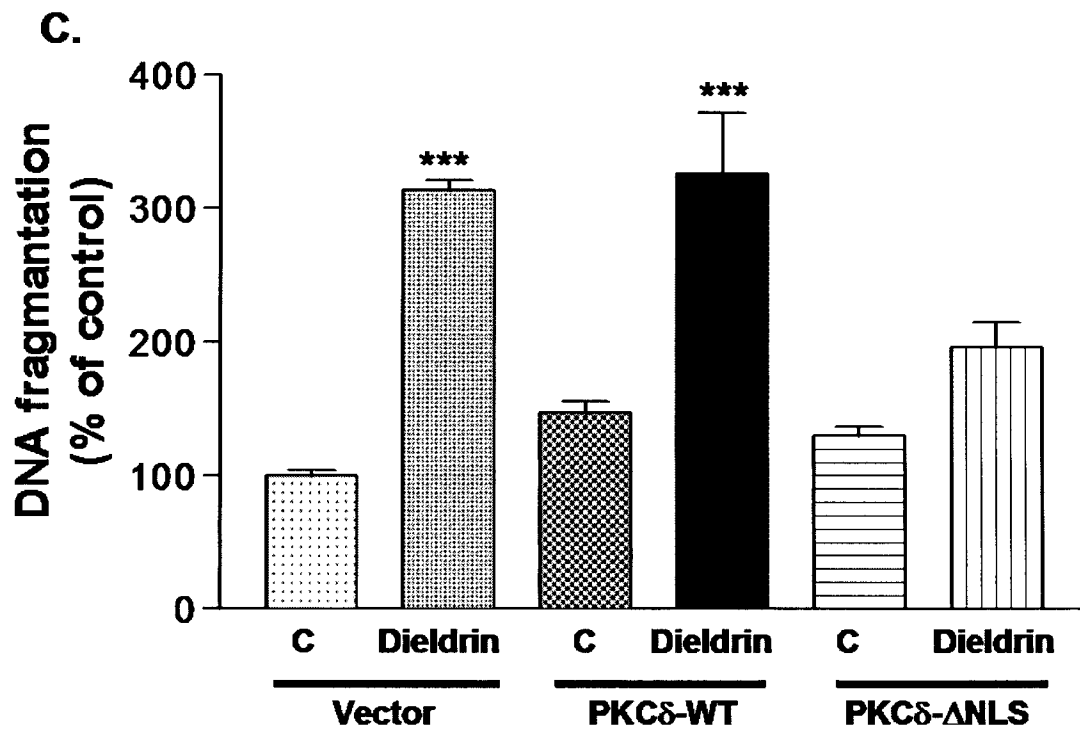
C.



**Figure 6: Blockade of nuclear localization of cleaved fragments of PKC $\delta$  protects N27 cells from dieldrin induced apoptosis.**

(A) Schematic representation of primary structure of PKC $\delta$ -WT, PKC $\delta$ -CRM, and PKC $\delta$ - $\Delta$ NLS. The V5 tag locates at the C-terminal of the fused protein. (B) Subcellular localization of PKC $\delta$ -WT, PKC $\delta$ - $\Delta$ NLS, and PKC $\delta$ -CRM in N27 cells following dieldrin exposure. PKC $\delta$ -WT and PKC $\delta$ - $\Delta$ NLS stably expressing N27 cell lines were also established via ViraPower Lentiviral gene expression system (Invitrogen, Inc. Carlsbad, CA). After dieldrin (60  $\mu$ M) exposure for 1 hr, subcellular distribution of PKC $\delta$ -WT, PKC $\delta$ - $\Delta$ NLS, and PKC $\delta$ -CRM was determined by immunostaining of the C-terminal V5 tag (Bar = 10  $\mu$ m). (C) Exclusion of PKC $\delta$  from the nucleus significantly abolished dieldrin induced apoptosis in N27 cells. Vector control (LacZ), PKC $\delta$ -WT, and PKC $\delta$ - $\Delta$ NLS stably expressing N27 cells were exposed to dieldrin for 1 hr and cells were then lysed for the DNA fragmentation assay. Significance of difference in DNA fragmentation was compared to untreated vector control cells. The data represent the mean  $\pm$  SEM from two separate experiments in triplicate (\*\*\*,  $p < 0.001$ ; N=6).

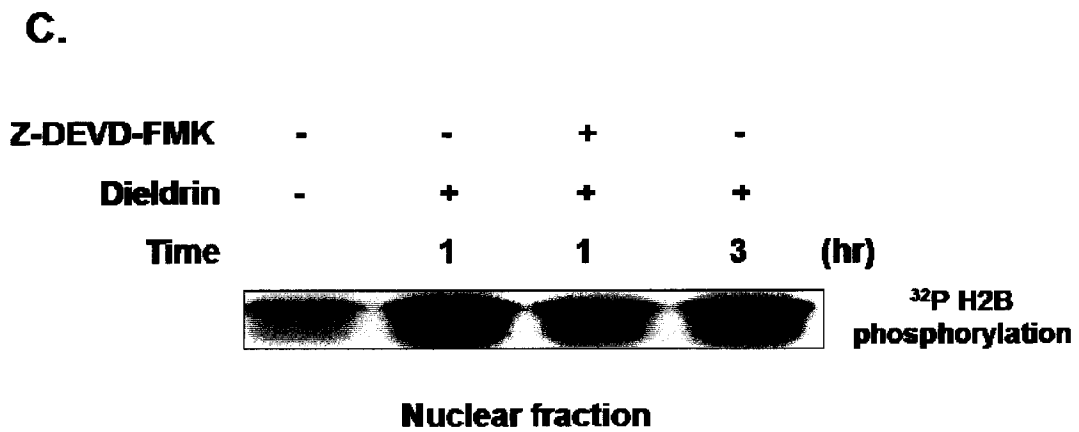
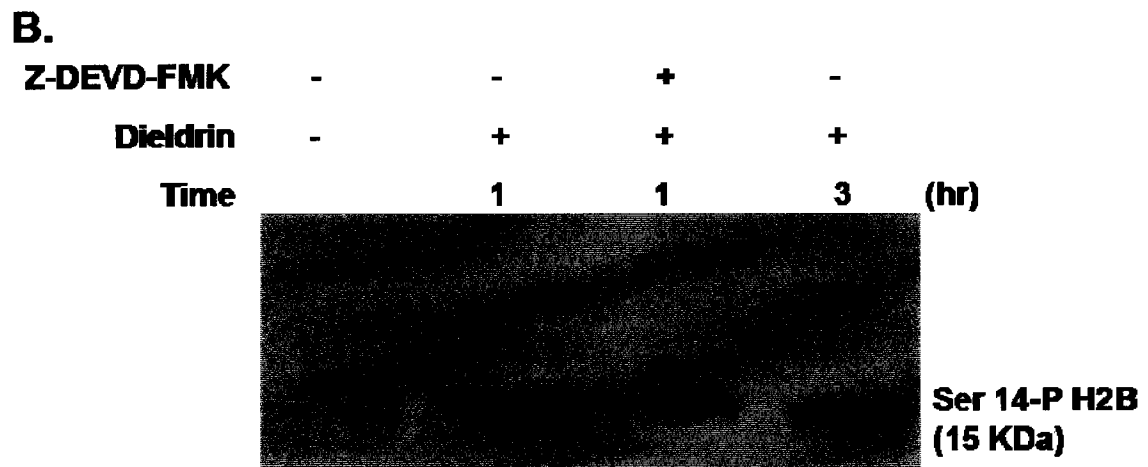
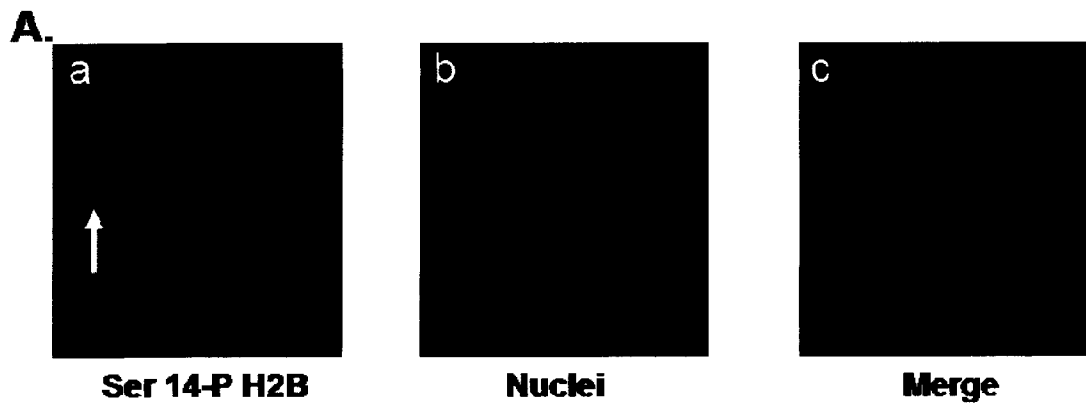


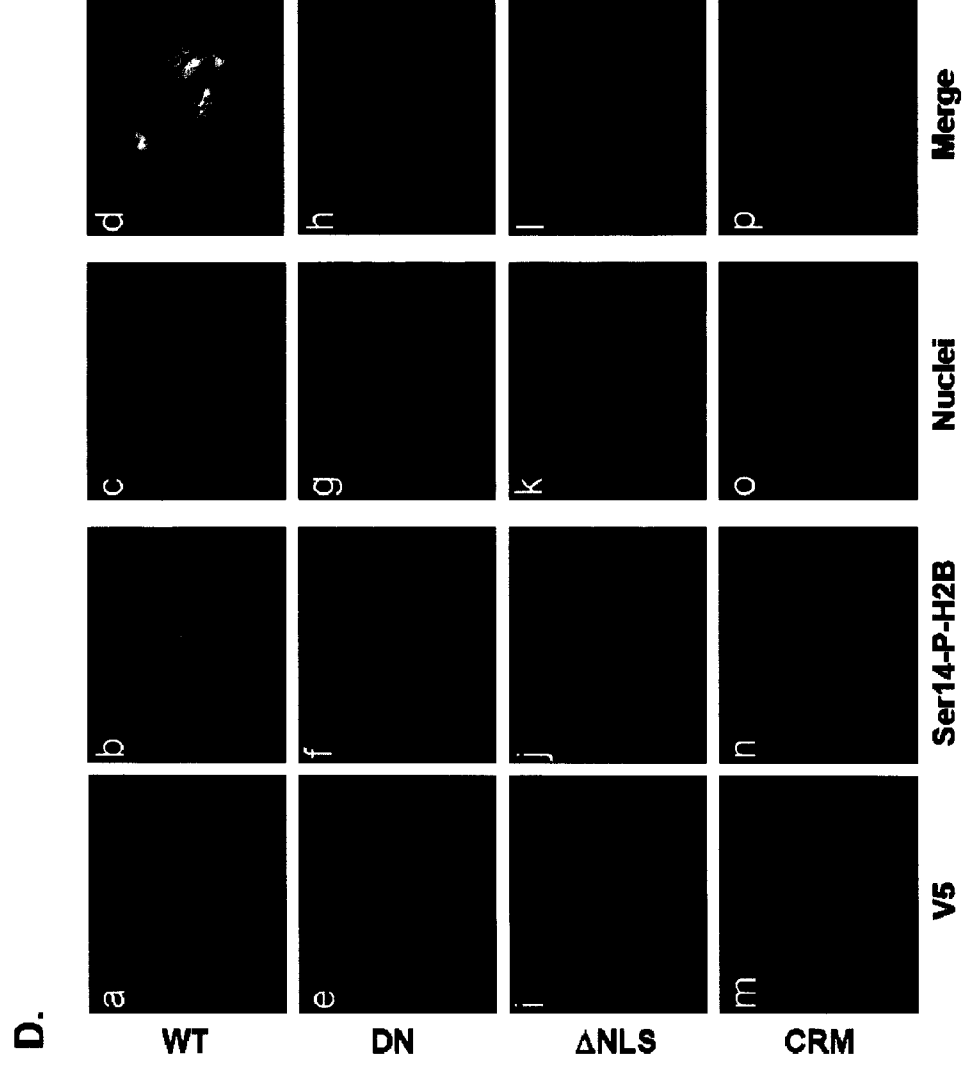


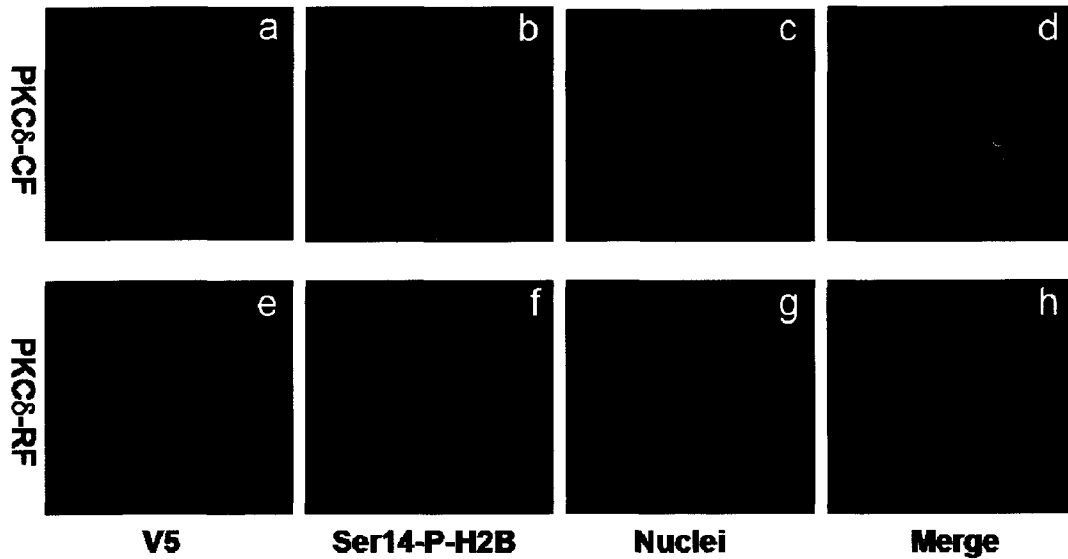
**Figure 7: Cleaved fragments of PKC $\delta$  mediate Ser14 phosphorylation of histone H2B in dieldrin induced apoptotic N27 cells.**

(A) *In situ* detection of Ser14 phosphorylated H2B in dieldrin induced apoptotic cells. After dieldrin exposure (60  $\mu$ M) for 1 hr, N27 cells were fixed and stained with Anti-phospho-histone H2B (Ser14) antibody (1:1000) and Alex488 conjugated anti-rabbit secondary antibody (1:2000). Apoptotic nuclei were also shown by counterstaining of nuclei with Hoechst 33342. Cells were observed under a Nikon inverted fluorescence microscope (Model TE-2000U). (B) Dieldrin induced Ser14 phosphorylation of H2B was caspase-3 dependent. (C) *In vitro* phosphorylation of H2B by PKC $\delta$  was caspase-3 dependent. Cells were treated with dieldrin (60  $\mu$ M) alone for up to 3 hr or co-treated with Z-DEVD-FMK (50  $\mu$ M) and dieldrin (60  $\mu$ M) for 1 hr. To detect Ser14 phosphorylation of H2B, histone mixtures were then isolated from the nuclear fraction of cells and separated by 15% SDS-PAGE for immunoblot analysis. For the kinase assay, PKC $\delta$  was immunoprecipitated from nuclear lysate of cells and an *in vitro* kinase assay was performed with purified H2B as substrate. (D) PKC $\delta$ -CRM, PKC $\delta$ -DN, and PKC $\delta$ - $\Delta$ NLS blocked dieldrin-induced Ser14 phosphorylation of Histone H2B. Double immunostaining of V5 and Ser14 phosphorylated H2B was performed after dieldrin treatment for 1 hr. Nuclei were also counterstained by Hoechst 33342. Cells were observed under a Nikon inverted fluorescence microscope (Model TE-2000U). Experiments were repeated three times and representative images are presented.









**Figure 8: Catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF) directly induces Ser14 phosphorylation of H2B.**

PKC $\delta$ -CF and PKC $\delta$ -RF were introduced into N27 cells by electroporation. Double immunostaining of V5 and Ser14 phosphorylated H2B was then performed 48 hr after transfection. Immunoreactivity of V5 and Ser14 phosphorylated H2B was visualized by Cy3 conjugated anti-mouse secondary antibody (1:2000) or Alex488 conjugated anti-rabbit secondary antibody (1:2000), respectively. Nuclei were counterstained with Hoechst 33342. Cells were observed under a Nikon inverted fluorescence microscope (Model TE-2000U).

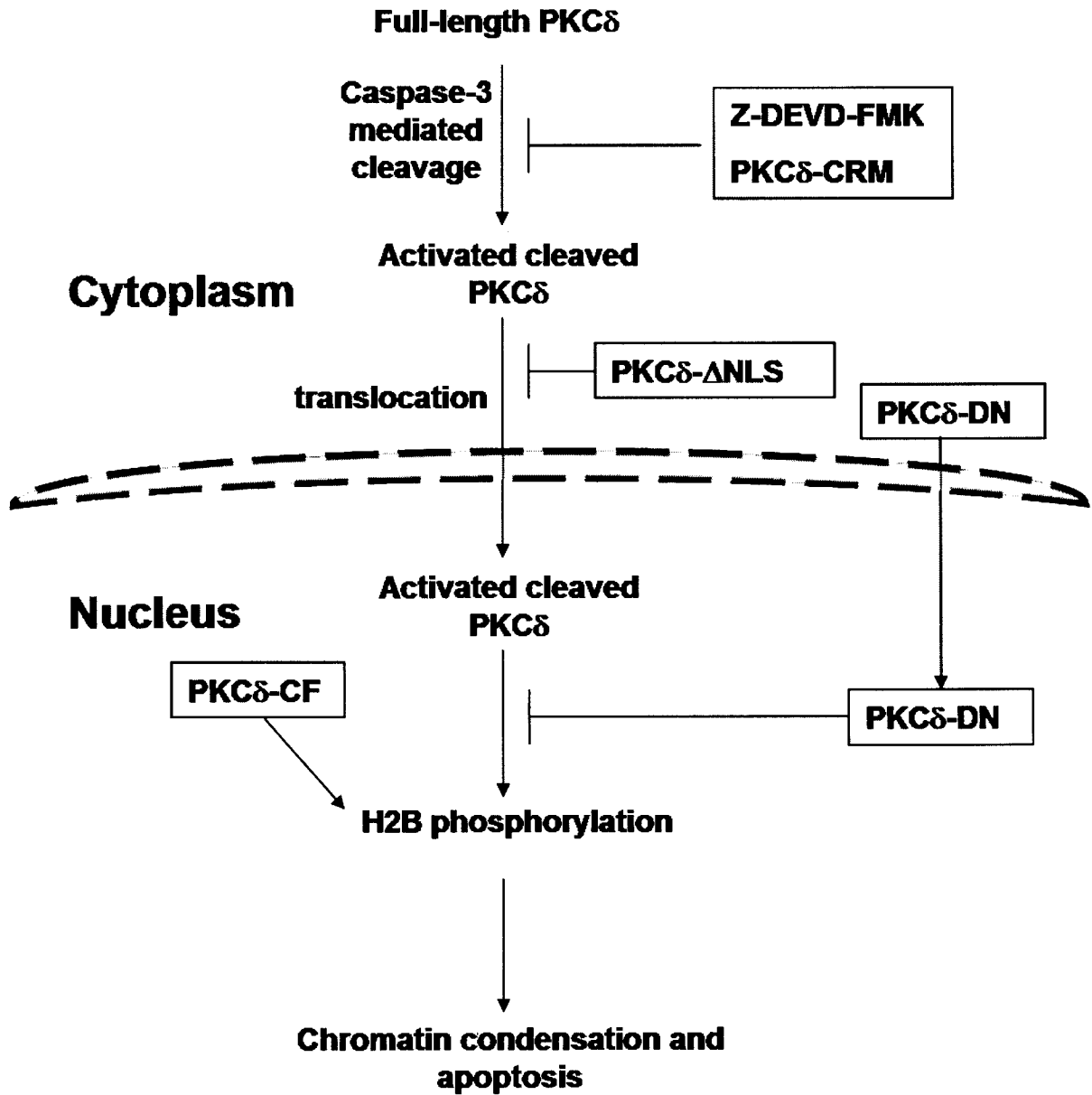


Figure 9: Proposed integrated mechanisms of PKC $\delta$  in dieldrin-induced apoptotic death of dopaminergic neuronal (N27) cells.

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**CHAPTER IV: NUCLEAR LOCALIZATION OF PKC $\delta$  IS REGULATED BY  
PROXIMITY OF N-TERMINAL C2-LIKE DOMAIN TO THE C-TERMINAL  
NUCLEAR LOCALIZATION SIGNAL (NLS)**

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**ABSTRACT**

PKC $\delta$  belongs to the novel PKC subfamily that contains a Ca<sup>2+</sup>-insensitive C2-like domain followed by a lipid-binding C1 domain in its N-terminal regulatory moiety. Although a functional nuclear localization signal (NLS) has been identified in the C-terminal of PKC $\delta$ , it primarily localizes in the cytosol. The mechanisms by which PKC $\delta$  is retained in the cytosol and by which the nuclear/cytosolic trafficking of PKC $\delta$  is regulated are not known. In the present study, we demonstrated that the N- and the C-terminals of PKC $\delta$  are in close proximity in the tertiary structure by fluorescence resonance energy transfer (FRET). FRET analysis of N-terminal CFP-FRET and C-terminal YFP FRET of PKC $\delta$  gives rise to a significant FRET signal. Furthermore, by employing the C1 or C2-like domain deletion mutants of PKC $\delta$  (PKC $\delta$ - $\Delta$ C1 or PKC $\delta$ - $\Delta$ C2), we show that deletion of the C2-like domain, but not the C1 domain, induces a strong nuclear localization of PKC $\delta$ . The exogenously expressed catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF) also primarily localizes to the nucleus.

Sequence analysis of the C2-like domain revealed a possible leucine-rich nuclear export signal (NES); however, the C2-like domain is not sensitive to the nuclear export inhibitor leptomycin B, suggesting that this leucine-rich motif is not a functional NES. Moreover, the C2-like domain alone was fused to the N-terminal of a NES mutated form of Rev protein, the RNA binding protein of Equine Infectious Anemia Virus (EIAV), to generate the Rev chimera. Interestingly, the Rev chimera with the C2-like domain is still primarily localized in the nucleus. Together, our studies suggest that the N-terminal C2-like domain regulates the subcellular localization of PKC $\delta$  by masking the C-terminal NLS through the position obstacle in the tertiary structure, but not by employing NES or interacting with anchoring proteins.

## INTRODUCTION

Protein kinase C (PKC) is one of the major cellular signal transducers that mediates and regulates signals involved in a range of cellular processes, including cell growth, differentiation, apoptosis, neurotransmitter release, and carcinogenesis (Newton, 2003; Spitaler and Cantrell, 2004). All PKC family members share a highly conserved C-terminal catalytic moiety containing the kinase core; however, their regulatory moiety varies dramatically in composition and organization. The function of PKC, as observed in most of protein A, B, and C kinases, is primarily regulated by its regulatory moiety (Newton, 2003). Two key regulation roles of the regulatory moiety in PKC have been identified so far: the regulation of kinase membrane targeting through the C1 and C2 domains and the regulation of kinase activity through the pseudosubstrate.



As a member of the novel PKC (nPKC) subfamily ( $\delta$ ,  $\epsilon$ ,  $\eta$ ,  $\theta$ ), PKC $\delta$  contains a Ca<sup>2+</sup>-insensitive C2-like domain followed by a pseudosubstrate that normally binds to the catalytic site of the kinase core to inactivate the kinase (Orr et al., 1992) and a lipid-binding C1 domain in the N-terminal regulatory moiety. The C1 domain is a small globular structure (~8 KDa) that contains binding sites for small lipid molecules, including diacylglycerol (DAG), phorbol esters, and non-hydrolysable analogues of the endogenous ligand (Newton, 1995; Zhang et al., 1995). Recent studies have further characterized that the C1 domain can be divided into two sub-domains: C1A and C1B. These two sub-domains in different PKC isoforms preferentially bind to different lipid molecules (Bogi et al., 1999; Toker, 1998). In PKC $\delta$ , C1B is primarily responsible for the binding of DAG (Szallasi et al., 1996). The binding of lipid molecules to the C1 domain recruits PKC $\delta$  to the membrane and promotes a remarkably high affinity interaction between PKC $\delta$  and the membrane. This membrane interaction provides the energy to promote the conformational change which results in the release of pseudosubstrate from the catalytic site and activation of the kinase (Toker, 1998). In the conventional PKC (cPKC) subfamily ( $\alpha$ ,  $\beta$ I,  $\beta$ II, and  $\gamma$ ), the lipid-mediated translocation and activation of kinase is through the synergic action of both the C1 and C2 domains. The C2 domain in cPKC provides a binding site for anionic phospholipids and Ca<sup>2+</sup> (Nalefski and Falke, 1996; Newton and Johnson, 1998; Ponting and Parker, 1996), and together with the binding of lipid to the C1 domain promotes the high affinity interaction of cPKC with the membrane and subsequent activation of kinase.

Unlike the conserved C1 domain whose function in the regulation of the kinase core has been well characterized, the function of the C2-like domain in PKC $\delta$ , as well as in all

other nPKC isoforms, is not fully understood. In particular, the C2-like domain is incapable of binding to  $\text{Ca}^{2+}$ , and therefore loses the response to the  $\text{Ca}^{2+}$  signal though it shares significant homology with the C2 domain in cPKC (Newton, 1995). The crystallized structure of the C2-like domain from PKC $\delta$  (Pappa et al., 1998) and PKC $\epsilon$  (Ochoa et al., 2001) suggests that it can still interact with the membrane by binding to phospholipids (phosphatidic acid and phosphatidylserine) in a  $\text{Ca}^{2+}$  independent manner. Pepio, A.M et al. showed that phosphorylation of Ser36 in the C2-like domain of Apl II, an nPKC isoform from *Aplysia*, increases the binding to phosphatidylserine and induces more efficient translocation of kinase to the membranes (Pepio and Sossin, 2001). The C2-like domain of PKC $\delta$  also mediates direct interaction with filamentous actin (F-actin) in neutrophils to regulate the migration of neutrophils in host-defense mechanisms against invading pathogens (Lopez-Lluch et al., 2001), as well as with non-smooth muscle F-actin in airway epithelial cells (Liedtke et al., 2003; Smallwood et al., 2005).

The function of PKC $\delta$  in the cell is closely associated with its subcellular localization. The precise localization is always the premise for kinase to receive upstream signals and transduce them downstream (Teruel and Meyer, 2000). Lipid-mediated translocation of PKC $\delta$  to the membrane allows PKC $\delta$  to effectively respond to the second messengers produced from different receptors (Nishizuka, 1992). PKC $\delta$  also translocates to the mitochondria, Golgi, endoplasmic reticulum (ER), and the nucleus in response to other stimuli (Brodie and Blumberg, 2003). However, the mechanisms that regulate the subcellular localization of PKC $\delta$  are poorly understood. Although it has been speculated that the isoform-specific localization of PKC is controlled by specific anchoring proteins (Mochly-

Rosen and Gordon, 1998; Newton, 1997; Newton and Johnson, 1998), like receptors for activated C kinase (RACK), very little information is known about the interaction of PKC isoforms with different anchoring proteins. Recently, a functional nuclear localization signal (NLS) has been identified in the C-terminal of PKC $\delta$  that induces PKC $\delta$  translocation to the nucleus in response to apoptotic stimuli (DeVries et al., 2002). This NLS alone can also localize GFP to the nucleus. Other studies also observed that the exogenously expressed catalytic fragment of PKC $\delta$  itself is primarily localized in the nucleus (Blass et al., 2002; DeVries et al., 2002). Interestingly, though PKC $\delta$  contains the functional NLS at the C-terminal of the kinase core that drives kinase into the nucleus in response to stimuli, PKC $\delta$  primarily localizes in the cytosol rather than the nucleus in a variety of normal cells. On the other hand, the nuclear export signal (NES) has been identified only in the atypical PKC (aPKC) isoforms ( $\lambda$  and  $\zeta$ ) (Perander et al., 2001), but not in all other cPKC and nPKC isoforms. The mechanisms that retain PKC $\delta$  in the cytosol and regulate the nuclear/cytosolic trafficking of PKC $\delta$  in normal cells are not clear.

From the primary structure of PKC $\delta$ , the pseudosubstrate at the middle of the regulatory moiety and kinase core at the catalytic moiety are distant from each other (Newton and Johnson, 1998). However, the pseudosubstrate constantly binds to the kinase core in normal cells to keep the kinase inactive. In order to do that, the primary structure of PKC $\delta$  has to be properly folded to form a specific conformation that brings the pseudosubstrate and the kinase core closer for their interaction in the tertiary structure. Although the structure of full-length PKC $\delta$  has not been crystallized, the fold of primary structure certainly brings the regulatory and catalytic moieties together. Since the C2-like domain is at the beginning of the

regulatory moiety and the NLS is located at the C-terminal of the kinase core, the fold of the primary structure may bring the C2-like domain closer to the NLS, which may implicate a role of the C2-like domain in the regulation of subcellular localization of PKC $\delta$ . In the present study, we investigate the mechanisms that regulate the cytosolic localization of PKC $\delta$ . We demonstrate that the C2-like domain retains PKC $\delta$  in the cytosol by directly masking the NLS through the close proximity of the N-terminal to the C-terminal in the tertiary structure, rather than by binding to potential anchoring proteins or employing functional NES.

## MATERIALS AND METHODS

### **Cell culture and treatment**

The immortalized rat mesencephalic dopaminergic neuronal (N27) cell line was a kind gift from Dr. Kedar N. Prasad, University of Colorado Health Sciences Center (Denver, CO) (Prasad et al., 1998). N27 cells were grown in RPMI 1640 medium containing 10% fetal bovine serum, 2 mM L-glutamine, 50 units penicillin, and 50  $\mu$ g/ml streptomycin. Cells were grown in a humidified atmosphere of 5% CO<sub>2</sub> at 37<sup>0</sup>C as previously described. For dieldrin treatment, dieldrin was prepared in DMSO and cells were exposed to serum-free RPMI medium containing dieldrin (final concentration 100  $\mu$ M) for up to 1 hr. For leptomycin B (LMB) treatment, LMB was dissolved in ethanol and cells were exposed to normal growth medium containing LMB (final concentration 0.5-5 ng/ml) for up to 30 min.

**Cell transfection**

Transient transfection of N27 cells was performed by lipid or electroporation mediated approaches. For lipid-mediated transfection, lipofectamine 2000 from Invitrogen (Carlsbad, CA) was used. Briefly, cells ( $0.7-0.8 \times 10^6$ ) were plated in 35 mm glass bottom dishes (MatTek Corporation, Ashland, MA). After 16-24 hr, 4  $\mu\text{g}$  plasmid as well as 10  $\mu\text{l}$  lipofectamine 2000 were first diluted in 250  $\mu\text{l}$  Opti-MEM medium, separately. After 5 min, diluted plasmid was mixed with diluted lipofectamine 2000 and incubated for another 20 min for DNA-lipid complex formation. The DNA-lipid complex was then added into a glass bottom dish. After 16-24 hr, cells were directly observed under TCS/NT confocal microscopy. For electroporation, a nucleofector kit for adherent cell transfection from Amaxa biosystems (Cologne, Germany) was employed. Briefly, cultured N27 cells were trypsinized and spun down. About  $1-2 \times 10^6$  cells were resuspended with 100  $\mu\text{l}$  nucleofector solution mixed with 2  $\mu\text{g}$  plasmid and transferred into a cuvette. The cuvette was then put in a nucleofector device (Amaxa biosystems, Cologne, Germany) for electroporation. After electroporation, cells were transferred to a 6-well plate and incubated at  $37^\circ\text{C}$ .

**Preparation of constructs**

Full-length mouse PKC $\delta$  (mPKC $\delta$ ) cDNA was amplified from pGFP-PKC $\delta$  (a kind gift from Dr. Reyland at University of Colorado Health Sciences Center, Denver, CO) (DeVries et al., 2002) by using the following primer pairs that contain Hind III and BamH I sites at each end. Forward primer: 5' atatatataagcttatggcacccttctctgcgc 3'; reverse primer: 5' atatatatggatccaatgtccaggaattgctcaaa 3'. The PCR product was digested with Hind III/BamH I and then cloned into Hind III/BamH I sites of pEYFP-N1 or pECFP-C1 (Clontech, Palo Alto,

CA) to generate the pEYFP $\delta$  or pECFP $\delta$ . pEYFP $\delta$  was then subjected to Xho I/Xba I digestion to digest out the fragment containing mPKC $\delta$  together with EYFP. This fragment was subcloned into Xho I/Xba I site of pECFP-C1 to generate the pFRET $\delta$  construct.

For the preparation of expression vectors containing PKC $\delta$ -WT (wild type), PKC $\delta$ - $\Delta$ C2 (C2-like domain deletion mutant), PKC $\delta$ - $\Delta$ NLS (nuclear localization signal deletion mutant), and PKC $\delta$ -CF (catalytic fragment), 14-2035bp, 428-2035bp, 14-1843bp, and 995-2035bp of mPKC $\delta$  cDNA was amplified individually with the following primer pairs. For PKC $\delta$ -WT: 5' caccatggcacccttctctgccc 3' (F), 5' aatgtccaggaattgctcaaac 3' (R); for PKC $\delta$ - $\Delta$ C2: 5' caccatgtttccaaccatgaaccgtcgt 3' (F), 5' aatgtccaggaattgctcaaac 3' (R); for PKC $\delta$ - $\Delta$ NLS: 5' caccatggcacccttctctgccc 3' (F), 5' ctccaggaggaccagtt 3' (R); for PKC $\delta$ -CF: 5' caccatgaacaacgggacctatggcaa 3' (F), 5' aatgtccaggaattgctcaaac 3' (R). To prepare PKC $\delta$ - $\Delta$ C1 (C1 domain deletion mutant), the C2-like domain and catalytic fragment (CF) was first amplified with the following primer pairs. For the C2-like domain: 5' caccatggcacccttctctgccc 3' (F) and 5' atatatatgaattcctttgctctctctacta 3' (R); for CF: 5' atcccagacgaattcaacaacgggacc 3' (F) and 5' aatgtccaggaattgctcaaac 3' (R). These two PCR fragments were then ligated after EcoR I digestion and purification. The ligation reaction was used as template for amplification with the following primer pairs: 5' caccatggcacccttctctgccc 3' (F) and 5' aatgtccaggaattgctcaaac 3' (R). All PCR reactions were performed with *pfu* DNA polymerase to ensure the fidelity of amplification. All PCR products were directly subcloned into the V5-tagged (at the C-terminal) expression vector pLenti/TOPO from Invitrogen, Inc. (Carlsbad, CA) to generate pLenti/PKC $\delta$ -WT, pLenti/PKC $\delta$ - $\Delta$ C2, pLenti/PKC $\delta$ - $\Delta$ C1, pLenti/PKC $\delta$ - $\Delta$ NLS, and pLenti/PKC $\delta$ -CF.

Plasmids pEGFP-Rev and pEGFP-RDM4 (nuclear export signal deletion mutant of Rev) were kind gifts from Dr. Susan Carpenter (Iowa State University, Ames, IA). To prepare pEGFP-C2RDM4, the C2-like domain of PKC $\delta$  was first amplified with the following primer pairs that contain a Hind III and EcoR I site at each end. Forward primer: 5' atatatataagccttatggcacccttctctgcgc 3'; reverse primer: 5' atatatatgaattcctttgcctctctcacta 3'. The PCR product was digested with Hind III/EcoR I and cloned into Hind III/EcoR I sites of pEGFP-RDM4 to generate the pEGFP-C2RDM4. All constructs were confirmed by sequencing.

#### **Establishment of PKC $\delta$ - $\Delta$ C2, PKC $\delta$ - $\Delta$ C1, PKC $\delta$ - $\Delta$ NLS, and PKC $\delta$ -WT stably expressing N27 cell lines**

A ViraPower Lentiviral gene expression system from Invitrogen (Carlsbad, CA) was used to generate PKC $\delta$ - $\Delta$ C2, PKC $\delta$ - $\Delta$ C1, PKC $\delta$ - $\Delta$ NLS, and PKC $\delta$ -WT stably expressing N27 cell lines. To produce lentivirus, pLenti6/PKC $\delta$ - $\Delta$ C2, pLenti/PKC $\delta$ - $\Delta$ C1, pLenti/PKC $\delta$ - $\Delta$ NLS or pLenti/PKC $\delta$ -WT as well as supporting plasmids (provided with the kit) were co-transfected into human 293FT cells with the use of lipofectamine 2000 as described in the instruction of the kit. The lentivirus particles in the medium were collected by centrifuging at 3000 rpm for 15 min 48-72 hr post-transfection. To generate a stably expressing cell line, lentivirus containing individual pLenti/PKC $\delta$ - $\Delta$ C2, pLenti/PKC $\delta$ - $\Delta$ C1, pLenti/PKC $\delta$ - $\Delta$ NLS or pLenti/PKC $\delta$ -WT as well as polybrene (6  $\mu$ g/ml) was added into cultured N27 cells ( $2 \times 10^5$ ) for 24 hr and replaced with fresh medium. Positive N27 cells were selected by keeping blasticidin (10  $\mu$ g/ml) in the medium for up to 2 weeks. PKC $\delta$ - $\Delta$ C2, PKC $\delta$ - $\Delta$ C1, PKC $\delta$ -

$\Delta$ NLS, or PKC $\delta$ -WT expressing N27 cells were identified by immunostaining of the C-terminal V5 tag.

### **Preparation of whole cell homogenates**

After dieldrin treatment or electroporation, the N27 cells were harvested with trypsin/EDTA and spun at 200xg for 5 min. Cell pellets were then washed twice with ice-cold PBS and resuspended in 200  $\mu$ l of homogenization buffer (pH 8.0, 20 mM Tris, 10 mM EGTA, 2 mM EDTA, 2 mM DTT, 0.5% Triton X-100 and 1:100 dilution of protease inhibitor). After incubation on ice for 5 min, the cell lysates were centrifuged for 30 min at 14,000xg at 4<sup>o</sup>C and supernatants were collected as whole cell lysates.

### **Immunoblotting**

An equal amount of protein was loaded in each lane and separated on SDS-polyacrylamide gel as described previously (Yang et al., 2004). Proteins were then transferred to nitrocellulose membrane by electro-blotting overnight (4<sup>o</sup>C, 25 V). Non-specific binding sites were blocked by treating the nitrocellulose membranes with 5% non-fat dry milk TBST solution (10 mM Tris, 150 mM NaCl, and 0.1% Tween 20) for 1 hr. The nitrocellulose membranes were then incubated with primary antibodies (1:1000) for 1 hr at RT. The primary antibody treatment was followed by treatment with secondary HRP-conjugated anti-rabbit or anti-mouse antibody (1:2000) for 1 hr at RT. Secondary antibody-bound proteins were detected using an ECL chemiluminescence kit (Amersham). To confirm equal protein loading, blots were reprobbed with  $\beta$ -actin antibody (1:5000). Gel photographs were analyzed with a Kodak image station (Model 1000R, Rochester, New York).



**Immunostaining**

Immunostaining of the V5 tag was performed in PKC $\delta$ -WT, PKC $\delta$ - $\Delta$ C1, PKC $\delta$ - $\Delta$ C2 and PKC $\delta$ - $\Delta$ NLS expressing cells, as well as in PKC $\delta$ -CF transiently transfected N27 cells. Cells cultured on poly L-lysine coated glass cover slips were gently washed with PBS twice, fixed in 4% paraformaldehyde, washed for 3x7 min with PBS, permeabilized, and blocked with blocking reagent (0.4% BSA, 5% goat serum, and 0.2% Triton-X 100 in PBS) for 20 min. Cells were then incubated with anti-V5 mouse antibody (1:1000 in blocking reagent) overnight at 4°C and then washed for 3x7 min with PBS. The V5 tag was visualized by incubation with Cy3-conjugated goat anti-mouse secondary antibody (1:2000 in PBS) at RT for 90 min. After PBS wash, Hoechst 33342 was added to stain the cell nuclei at RT for 3 min. Finally, cells were washed twice in PBS and mounted on a slide with antifade mounting medium. The cells were observed under TCS/NT confocal systems (Leica, Bannockburn, IL). All images were processed in MetaMorph 5.07 (Downingtown, PA).

**Live cell imaging**

Cells were first transfected with plasmid. After 24 hr, transfected cells cultured in glass bottom dishes (MatTek Corporation, Ashland, MA) were observed by inverted confocal microscopy. To observe the *in vivo* FRET, cells were excited by Argon laser line at 458 nm and image was acquired by using an LP515 emission filter. For ECFP, cells were excited by Argon laser line at 458 nm and image was acquired by using a 475 $\pm$ 66 emission filter. For EYFP, cells were excited by Argon laser line at 488 nm and image was acquired by using an LP515 emission filter. For transmitted light images, cells were excited by Krypton laser line at 568 nm through a 488/568 double dichroic excitation filter and image was acquired by

using a 490±40 emission filter. For time-lapse acquisition of image, FRET, CFP, and YFP images were acquired every 5 min for up to 60 min. For visualization of pEGFP-Rev, pEGFP-RDM4, and pEGFP-C2RDM4, N27 cells cultured in glass bottom dishes were first transfected with plasmid. After 24 hr, Hoechst 33342 was added to the dish and incubated at RT for 15 min. The dishes were washed several times with 1x PBS and replaced with normal growth medium. The cells were then observed under confocal microscopy. The EGFP fluorescence was excited by Argon laser line at 488 nm and image was acquired by using a BP525/50 emission filter. All images were acquired by a TCS/NT confocal system controlled by TCS NT software (Leica, Bannockburn, IL) and processed in MetaMorph 5.07 from Universal Imaging (Downingtown, PA).

## RESULTS AND DISCUSSION

### **Design and characterization of PKC $\delta$ -FRET**

To test whether the N-terminal is in close proximity to the C-terminal in the tertiary PKC $\delta$  structure, the hybrid protein PKC $\delta$ -FRET was designed and genetically engineered. The PKC $\delta$ -FRET is composed of ECFP fused to the N-terminal, followed by the full-length mouse PKC $\delta$  cDNA, and EYFP fused to the C-terminal (Figure 1A). The ECFP-PKC $\delta$  and PKC $\delta$ -EYFP were also constructed as a negative control for PKC $\delta$ -FRET. Because of the nature of FRET, in the PKC $\delta$ -FRET, resonance energy transfer from ECFP to EYFP can be observed when the N-terminal is in close proximity to the C-terminal in the tertiary structure (Figure 1A). When PKC $\delta$  undergoes caspase-3 mediated cleavage, the close proximity of

the N-terminal to the C-terminal is disrupted, as the regulatory fragment is separated from the catalytic fragment (Emoto et al., 1995; Kanthasamy et al., 2003). Because the ECFP and EYFP are not covalently linked, resonance energy transfer from ECFP to EYFP can no longer be observed. Similar FRET systems have been successfully demonstrated in the proteolysis of Bid protein (Onuki et al., 2002) and in monitoring of caspase-3 activity in apoptosis (Lee and Segal, 2004; Wang et al., 2005). The resonance energy transfer from ECFP to EYFP in hybrid protein PKC $\delta$ -FRET was directly visualized by employing the confocal microscopy system. Live N27 cells transfected with pFRET $\delta$  were excited with an Argon laser line at 458 nm, and emission was monitored by using either a 475 $\pm$ 66 (ECFP) or LP515 (EYFP) emission filter. The *in vivo* ECFP fluorescence or fluorescence transferred from ECFP to EYFP (FRET) was observed (Figure 1Bb&c), as well as the EYFP fluorescence when excited with 488 nm (Figure 1Ba). In contrast, when cells transfected with pEYFP $\delta$  were excited with 458 nm and emission was monitored by using either a 475 $\pm$ 66 or LP515 emission filter, no fluorescence was observed (Figure 1Be&f), while fluorescence of EYFP was observed with excitation at 488 nm and emission at LP515nm (Figure 1Bd). Similarly, no EYFP and FRET fluorescence was observed in cells expressing pECFP $\delta$  with excitation at 488nm and emission at LP515 (Figure 1Bg&i), while the ECFP fluorescence was observed with excitation at 458 nm and emission at 475 $\pm$ 66 (Figure 1Bh).

Although the structure of full PKC $\delta$  has not been successfully crystallized, many attempts to elucidate the structure of PKC have suggested that regulatory and catalytic moieties of PKC are close to each other, and the full protein is tightly compacted and globularly shaped (Newton and Johnson, 1998). The tight binding of pseudosubstrate to the

kinase core in the tertiary structure of PKC also suggests that the regulatory and catalytic moieties must be properly folded. By using FRET, we determined that the N- and C-terminal of PKC $\delta$  are in close proximity in the tertiary structure. Since the C2-like domain is located at the beginning of the N-terminal and NLS is located at the very end of the C-terminal kinase core, the close proximity of the N- and C-terminals suggests that the C2-like domain is very close to the NLS in the tertiary structure. In order to mediate the nuclear translocation of protein, the NLS must be recognized and must bind with the nuclear import receptor (Kaffman and O'Shea, 1999). The close proximity of the C2-like domain to the NLS may provide a position obstacle for the recognition and binding of the NLS with the nuclear import receptor, further inhibiting the nuclear localization of PKC $\delta$ .

#### **Proteolytic cleavage of PKC $\delta$ abolishes FRET *in vivo***

PKC $\delta$  has been identified as one of the downstream targets of activated caspase-3 in apoptotic cells (Brodie and Blumberg, 2003; Emoto et al., 1995). We first examined PKC $\delta$  cleavage in dopaminergic neuronal cells exposed to the neurotoxin dieldrin (100  $\mu$ M) for up to 60 min. Anti-PKC $\delta$  antibody that recognizes the C-terminal epitope was employed. As shown in Figure 2A, cleaved PKC $\delta$  was detected starting from 30 min and increased up to 60 min following dieldrin exposure. The caspase-3 cleavage site of PKC $\delta$  has been mapped on the hinge region that connects the regulatory and the catalytic moieties (Emoto et al., 1995); therefore, the cleavage of PKC $\delta$  completely separates regulatory and catalytic fragments. To test whether the separation of regulatory and catalytic fragments by cleavage disrupts the close proximity of the N- to C-terminal in the tertiary structure of PKC $\delta$ , N27 cells

transfected with pFRET $\delta$  were treated with dieldrin (100  $\mu$ M) for up to 60 min. During the treatment, live cells were excited with an Argon laser line at 458 nm and emission was monitored by using either a 475 $\pm$ 66 or LP515 emission filter, and the *in vivo* CFP fluorescence or fluorescence transferred from ECFP to EYFP (FRET) was recorded every 5 min. The ratio of ECFP/EYFP was calculated to represent the FRET efficiency (Violin et al., 2003). When the close proximity of the N- to C-terminal is disrupted, resonance energy transfer from ECFP to EYFP is abolished. Therefore, the ECFP/EYFP ratio increases as more ECFP fluorescence is emitted and less EYFP fluorescence is transferred from ECFP. As shown in Figure 2Ba, the ECFP/EYFP ratio showed no significant change over time, though the value at each time point fluctuated up and down in control N27 cells. In contrast, the ECFP/EYFP ratio gradually increased over time in dieldrin-treated N27 cells, indicating that the close proximity of the N- to C-terminal was partially disrupted during the period of dieldrin treatment. Rapid increases in the ECFP/EYFP ratio were also observed from 15 min to 20 min and from 45 min to 60 min, suggesting that disruption of the close proximity of the N- to C-terminal was intensive during that period of time. The time period of the two rapid increases in FRET efficiency matches closely with the time point that cleaved PKC $\delta$  appeared (Figure 2A), which indicates that the separation of the regulatory and the catalytic fragments by cleavage disrupts the close proximity of the N- to C-terminal.

To demonstrate that the hybrid protein PKC $\delta$ -FRET indeed undergoes proteolytic cleavage, the N27 cells transfected with pFRET $\delta$  were treated with dieldrin (100  $\mu$ M) for up to 60 min. Cells were lysed and subjected to immunoblot analysis by using anti-GFP antibody. As shown in Figure 2C, hybrid protein PKC $\delta$ -FRET was cleaved and the cleaved CF-YFP/RF-CFP was detected at 60 min following dieldrin exposure. Since antibody

specifically detecting the catalytic fragment of PKC $\delta$  is currently unavailable, the localization change of the catalytic fragment of PKC $\delta$  in N27 cells following dieldrin exposure cannot be directly explored. Thus, we transiently transfected the catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF) into N27 cells in order to examine the localization of the catalytic fragment of PKC $\delta$ . Immunostaining of the C-terminal V5 tag and counterstaining of the nucleus were performed 24 hr post transfection. As shown in Figure 2D, PKC $\delta$ -CF revealed by V5 immunoreactivity primarily localizes in the nucleus.

These results suggest that there is no covalent link between regulatory and catalytic moieties. The separation of the regulatory and catalytic moieties by proteolytic cleavage disrupts the close proximity of the N- to C-terminal and abolishes the FRET. We also demonstrate that the catalytic fragment of PKC $\delta$ , by itself, primarily localizes in the nucleus, which is consistent with previous studies (Blass et al., 2002; DeVries et al., 2002). The primary nuclear localization of PKC $\delta$ -CF indicates that the recognition of the NLS by the nuclear import receptor is not inhibited and the catalytic fragment itself does not contain a functional NES to transport PKC $\delta$ -CF out of the nucleus.

### **Deletion of the C2-like domain leads to nuclear localization of PKC $\delta$**

A functional nuclear localization signal (NLS) has been identified at the C-terminal (611-623) of the kinase core in PKC $\delta$  (DeVries et al., 2002). Nuclear translocation of PKC $\delta$  was inhibited with mutated NLS. Also, the NLS alone localizes GFP in the nucleus. Interestingly, though PKC $\delta$  contains the C-terminal NLS, it is mainly distributed in the cytosol in cells. We demonstrated that the N-terminal is in close proximity to the C-terminal

in the tertiary structure of PKC $\delta$ , and PKC $\delta$ -CF primarily localizes to the nucleus. The regulatory moiety is probably involved in the regulation of the nuclear localization of PKC $\delta$ .

We next investigated the involvement of the regulatory moiety in the regulation of nuclear localization of PKC $\delta$ . Expression vectors that express wild-type PKC $\delta$  (PKC $\delta$ -WT), the C1 or C2-like domain deletion mutant (PKC $\delta$ - $\Delta$ C1 or PKC $\delta$ - $\Delta$ C2), or the NLS deletion mutant (PKC $\delta$ - $\Delta$ NLS) were first constructed. The schematic representation of these constructs is shown in Figure 3A. The PKC $\delta$ -WT, PKC $\delta$ - $\Delta$ C1, PKC $\delta$ - $\Delta$ C2, and PKC $\delta$ - $\Delta$ NLS stably expressing N27 cells were then generated by using the ViraPower Lentiviral gene expression system from Invitrogen, Inc. (Carlsbad, CA). V5 immunostaining and nucleus counterstaining were performed to investigate the subcellular distribution of wild type and mutated PKC $\delta$  protein. As shown in Figure 3B, PKC $\delta$ -WT revealed by V5 immunoreactivity was primarily localized in the cytosol, though a little was in the nucleus (Figure 3Bc). In the PKC $\delta$ - $\Delta$ NLS expressing cells, the PKC $\delta$ - $\Delta$ NLS was completely excluded from the nucleus as expected (Figure 3Bf). Strikingly, PKC $\delta$ - $\Delta$ C2 was primarily localized in the nucleus, with only very light V5 immunoreactivity observed in the cytosol (Figure 3Bi), while PKC $\delta$ - $\Delta$ C1 was still primarily localized in the cytosol (Figure 3Bi). The dramatic shift in V5 immunoreactivity from the cytosol to the nucleus in PKC $\delta$ -WT and PKC $\delta$ - $\Delta$ C2 strongly suggests that the C2-like domain is involved in the regulation of the nuclear localization of PKC $\delta$ .

Since the C2-like domain is located at the beginning of the N-terminal regulatory moiety, and we demonstrated above that the N-terminal is in close proximity to the C-terminal, the C2-like domain might regulate the nuclear localization of PKC $\delta$  by

preoccupying the position near the NLS to block the potential contact of the nuclear import receptor to the NLS. This likely results in the inhibition of the nuclear import of PKC $\delta$  and the normal primary cytosolic localization of PKC $\delta$ . Although the C1 domain could also be in close proximity to the NLS in the tertiary structure and block the contact of NLS with the nuclear import receptor, the deletion of the C1 domain did not result in the shift of PKC $\delta$  localization from the cytosol to the nucleus. When the C2-like domain is deleted or the whole regulatory fragment is removed by cleavage, the position obstacle effect of the C2-like domain to the NLS disappears, leading to the exposure of the NLS to the nuclear import receptor and resulting in the import of PKC $\delta$  into the nucleus. It is also possible, though, that the C2-like domain contains a functional nuclear export signal (NES) to export PKC $\delta$  out of the nucleus, causing the primary cytosolic localization of PKC $\delta$ . The C2-like domain might also interact with anchoring proteins of PKC and inhibit the nuclear import of PKC $\delta$ , which also induces the primary cytosolic localization of PKC $\delta$ .

### **C2-like domain does not contain CRM1-dependent nuclear export signal (NES)**

Similar to the nuclear import, nuclear export of protein is also regulated by the recognition of the nuclear export signal (NES) by its receptor (Kaffman and O'Shea, 1999). Although new NES and corresponding receptors are being identified, the leucine-rich NES and its receptor CRM1 is the major and currently most characterized nuclear export pathway in yeast and mammalian cells (Fornerod et al., 1997; Fukuda et al., 1997; Stade et al., 1997). To investigate whether the C2-like domain contains leucine-rich NES, the leucine-rich motif in the C2-like domain (1-138) was first predicted by using the NETNES 1.1 Server (la Cour



et al., 2004). NETNES is specifically designed for the prediction of leucine-rich NES in eukaryotic proteins. As shown in Figure 4A, no particular motif has an NES score close to or higher than the NES threshold, suggesting that the putative leucine-rich NES was not found in the C2-like domain. However, we did notice that the sequence from 108-116 contained two leucines and gained an NES score. This motif was then aligned with several validated leucine-rich NES in human immunodeficiency virus type 1 (HIV-1) Rev protein (Fischer et al., 1995), mitogen-activated protein kinase (Fukuda et al., 1996), phospholipase C- $\delta$ 1 (PLC $\delta$ 1) (Yamaga et al., 1999), cAMP-dependent protein kinase inhibitor (PKI) (Wen et al., 1995) as well as two atypical PKC isoforms  $\zeta$  and  $\lambda$  (Perander et al., 2001). The alignment is shown in Figure 4B. The C2-like domain contains only two conserved leucines at the first and third position, but not the second and fourth leucines shared by all other NES. In addition, it contains a hydrophilic cysteine instead of hydrophobic leucine or isoleucine at the fourth conserved leucine position. The fourth leucine at the C-terminal has been shown to be critical for the function of NES (Perander et al., 2001). The point mutation of this leucine abolished the functional nuclear export signal in atypical PKC and caused the accumulation of atypical PKC in the nucleus. The lack of sequence homology of the 108-116 region of the C2-like domain with other validated leucine-rich NES, especially the lack of the fourth leucine, makes it incapable of functioning as a leucine-rich NES.

It has been well characterized that the leucine-rich NES is specifically recognized by its receptor CRM1 in the nuclear export process. This CRM1 mediated nuclear export pathway can be effectively inhibited by the fungicide leptomycin B (LMB) through the covalent binding of LMB to a cysteine of CRM1 (Fornerod et al., 1997; Kudo et al., 1999). The potent and specific inhibition of LMB in the CRM1 mediated pathway provides an

excellent tool for the validation of the leucine-rich NES. To further determine if the C2-like domain contains the leucine-rich NES, PKC $\delta$ -WT stably expressing N27 cells were treated with LMB (0.5 ng/ml) for up to 30 min. As shown in Figure 4C, LMB did not induce change in the subcellular distribution of PKC $\delta$ -WT, as revealed by V5 immunoreactivity. Cells were also treated with ethanol (0.1%) as a vehicle control because LMB was prepared in ethanol. Ethanol itself also did not change the subcellular localization of PKC $\delta$ -WT. We also tested a serial combination of LMB concentrations (up to 5 ng/ml) and exposure times (up to 60 min), but no change in subcellular localization of PKC $\delta$ -WT was observed under these conditions. The insensitivity of the C2-like domain to LMB further demonstrates that it does not contain a leucine-rich nuclear export signal.

#### **C2-like domain cannot retain the NES deleted Rev in the cytosol**

We determined above that the C2-like domain does not contain the classical leucine-rich NES. Next, we tried to determine whether the C2-like domain retains PKC $\delta$  in cytosol by employing other types of NES or by interacting with anchoring proteins. To test this, we engineered a C2-like domain as a heterogeneous protein that contains functional NLS but not NES. The functional NLS allows protein importing to the nucleus after synthesis in the cytosol. A NES deleted form of Equine Infectious Anemia Virus (EIAV) Rev protein was employed as the heterogeneous protein because it contains functional NLS and is small in size (23KDa) (Belshan et al., 1998). Rev is a RNA-binding protein of EIAV that contains functional NLS and NES to shuttle itself between the cytosol and nucleus (Fischer et al.,

1995). The deletion of its NES results in the retention of Rev in the nucleus (Belshan et al., 1998).

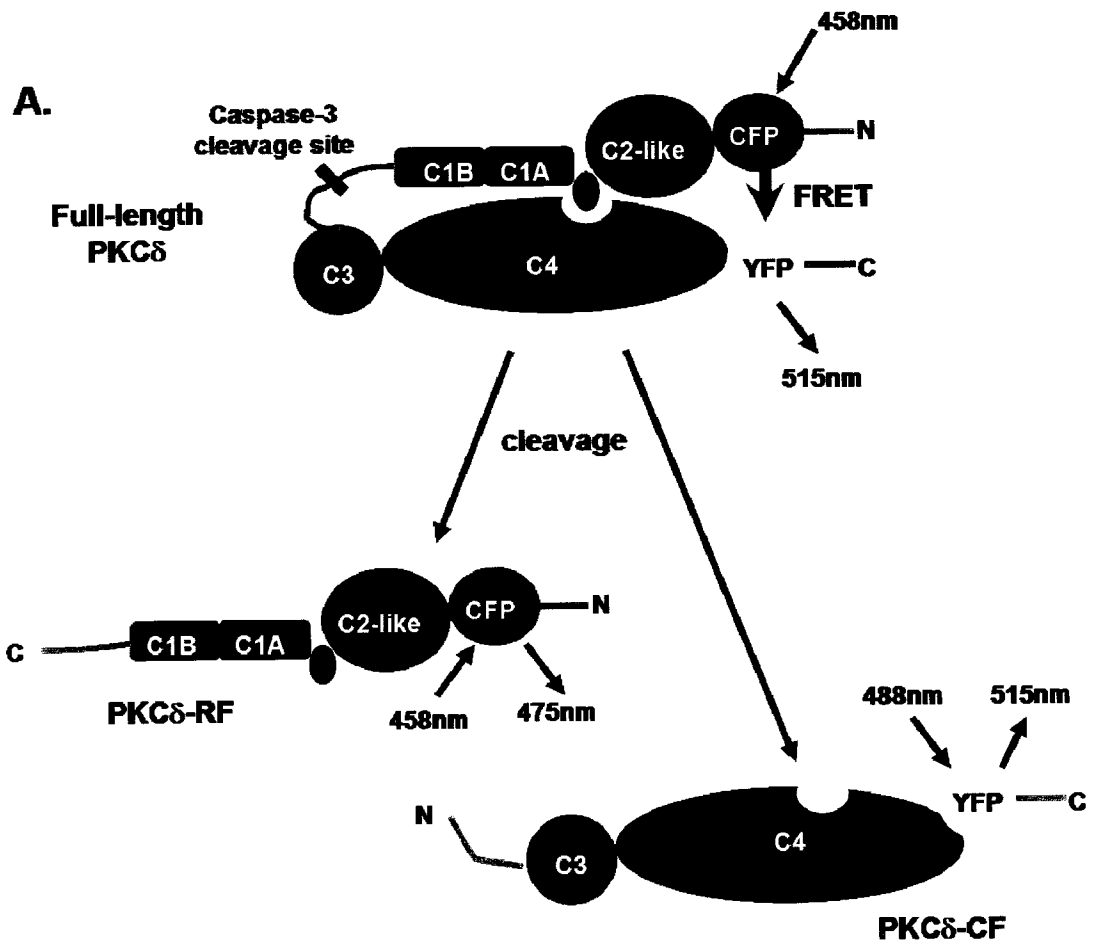
We first obtained pEGFP-Rev-WT and pEGFP-RDM4 (kind gifts of Dr. Susan Carpenter) that express the N-terminal fused wild type Rev or NES deleted form of Rev, respectively. The C2-like domain of PKC $\delta$  was then engineered into the pEGFP-RDM4 to generate the pEGFP-C2RDM4. The schematic presentation of the primary structure of these constructs is presented at Figure 5A. Subcellular localization of these proteins was then visualized by EGFP fluorescence and nucleus staining. In pEGFP-Rev-WT transfected N27 cells, EGFP-Rev-WT showed mixed subcellular localization, as shown in previous studies (Belshan et al., 1998; Belshan et al., 2000). In some cells, EGFP-Rev-WT was mainly localized in the cytosol, but in other cells it was primarily localized in the nucleus. A representative image of the cytosolic localization of EGFP-Rev-WT in N27 cells is shown in Figure 5Ba. However, in pEGFP-RDM4 transfected N27 cells, as shown in Figure 5Bd, EGFP-RDM4 uniformly showed strong nuclear localization in all transfected cells because of the deletion of the functional NES. In pEGFP-C2RDM4 transfected N27 cells, strong nuclear localization of EGFP-C2RDM4 was also uniformly observed in all transfected cells, though a little EGFP fluorescence was also observed in the cytosol (Figure 5Bg). The nucleus was visualized by Hoechst 33342 staining. These results clearly demonstrate that the C2-like domain alone is not capable of compensating for the function of the Rev NES. The failure of the C2-like domain alone to retain Rev chimera in the cytosol indicates that the C2-like domain alone does not contain NES to export the Rev chimera out of the nucleus, nor does it interact with anchoring proteins to retain the Rev chimera in the cytosol in N27 cells.

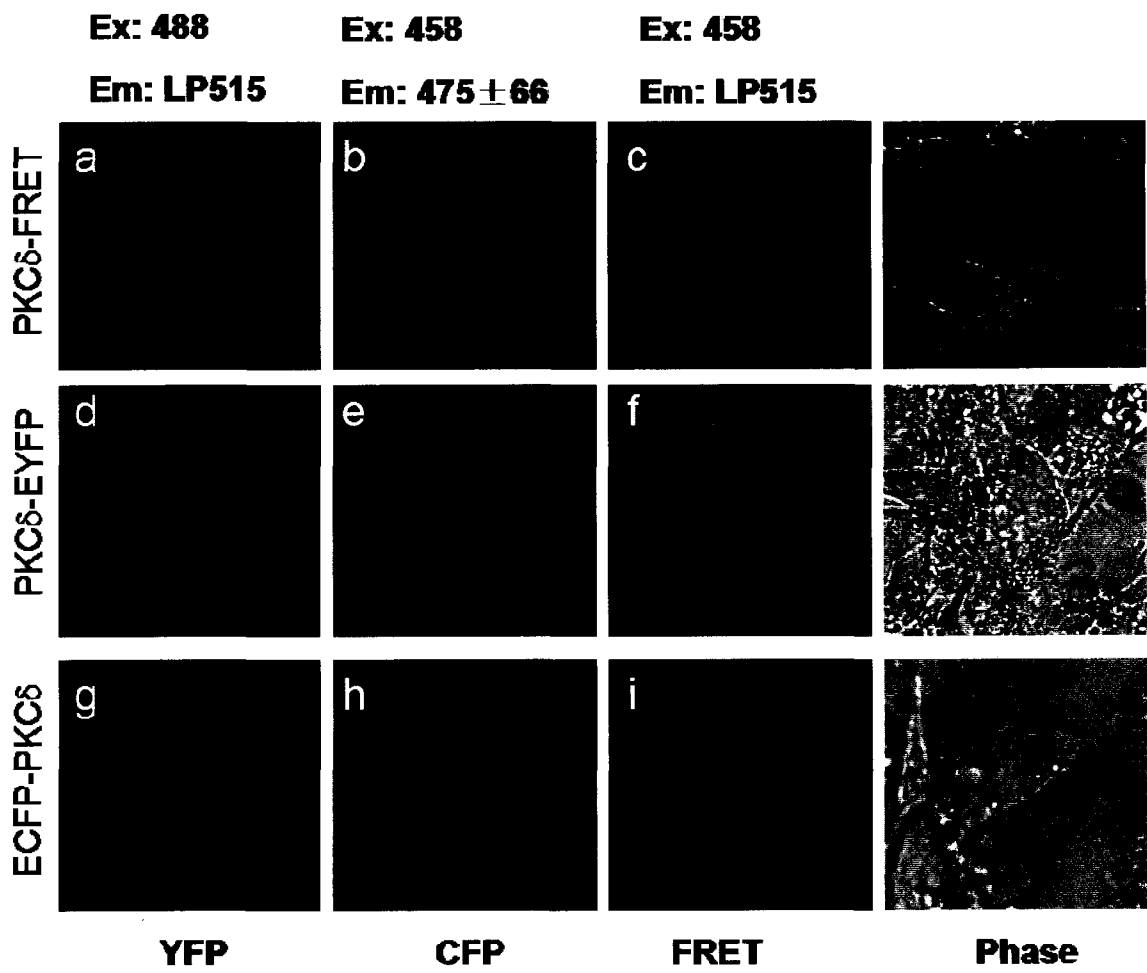
## CONCLUSIONS

In summary, we demonstrate that the C2-like domain at the N-terminal of the regulatory moiety regulates the nuclear localization of PKC $\delta$  (Figure 6). We first show that the N- and C-terminals of PKC $\delta$  are in close proximity in the tertiary structure, which is disrupted by caspase-3 mediated cleavage. The cleavage of PKC $\delta$  or the deletion of the C2-like domain, which both remove the C2-like domain from the NLS, leads to the primary nuclear localization of the kinase. Our results also show that the C2-like domain is not capable of retaining a heterogeneous protein in the cytosol. The C2-like domain regulates the nuclear localization of PKC $\delta$  through the position obstacle effect of the C2-like domain, by masking the NLS and blocking the recognition of the nuclear import receptor to the NLS. Our model suggests that the NLS can be kept incompetent in normal situations. A specific signal, like cleavage, can make NLS competent to be recognized by the nuclear import receptor for further nuclear translocation and downstream signaling. The maintenance of competency of the NLS provides a new and distinct mechanism for kinases to self-regulate their subcellular localization and function.

**Figure 1: Illustration of FRET system in PKC $\delta$ .**

(A) Schematic diagram of the FRET system in PKC $\delta$ . ECFP and EYFP were fused into the N-terminal and C-terminal of PKC $\delta$ , respectively, to generate the PKC $\delta$ -FRET hybrid protein. This FRET system is described in detail in the text. (B) Fluorescent and transmitted light images for CFP, YFP, and FRET in live N27 cells. Plasmid pCFP $\delta$ , pYFP $\delta$ , and pFRET $\delta$  were transfected into N27 cells by using lipofectamine 2000. Cells cultured in glass bottom dishes were directly observed by using the TCS/NT confocal system. The detailed procedures for acquisition of images are described in the materials and methods (Bar = 10  $\mu$ m).

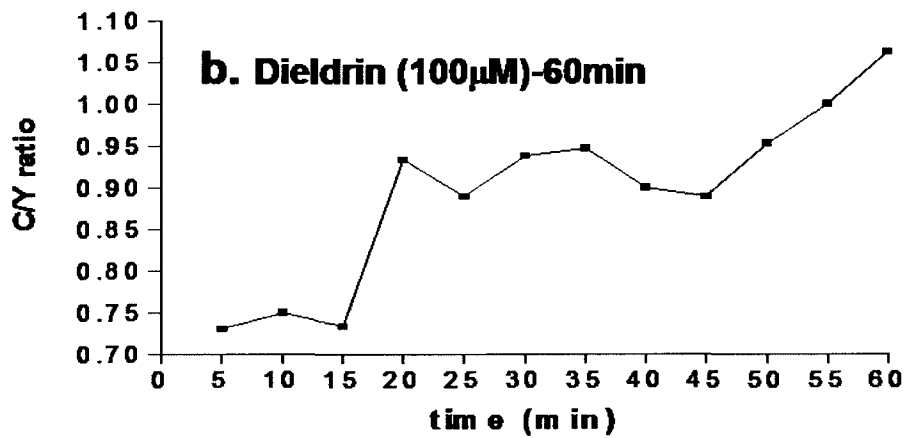
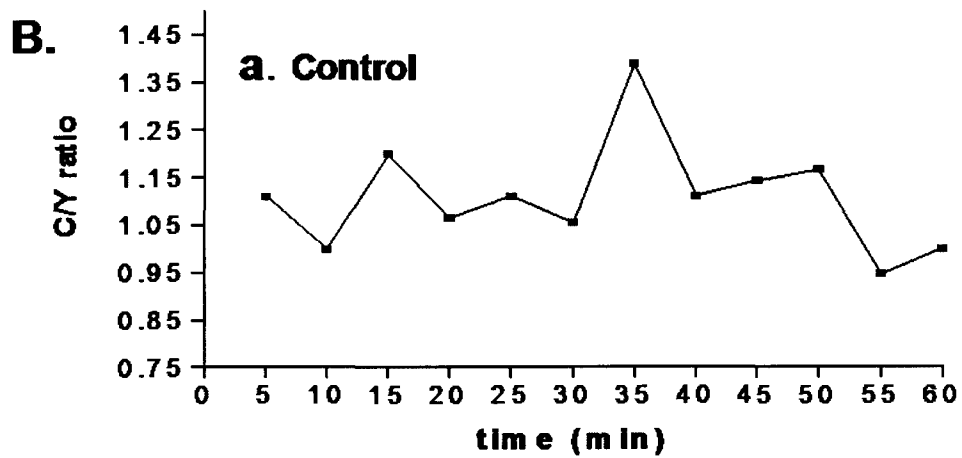
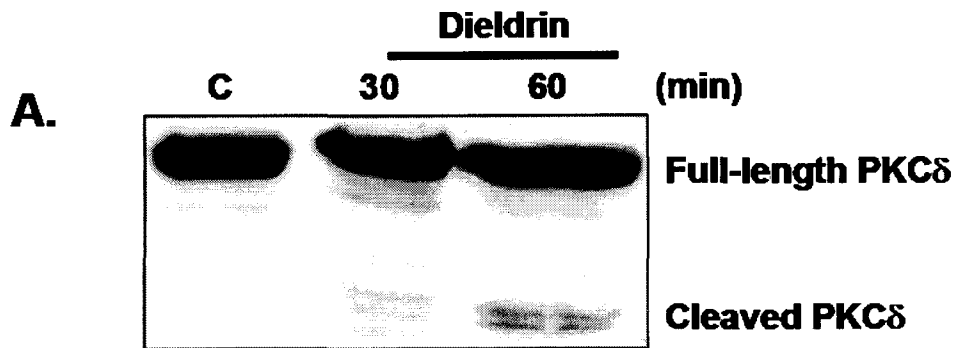


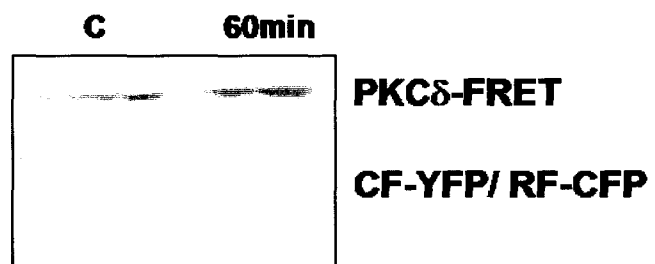
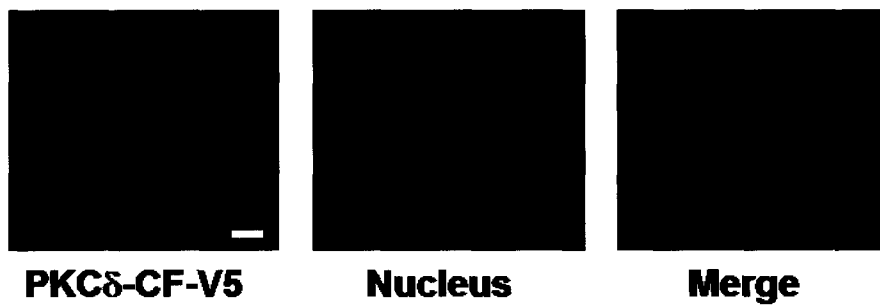


**Figure 2: Separation of regulatory fragment from catalytic fragment of PKC $\delta$  by cleavage abolishes FRET.**

(A) Dieldrin treatment induces PKC $\delta$  cleavage in N27 cells. N27 cells were treated with dieldrin (100  $\mu$ M) in serum-free medium for up to 60 min. Cell homogenates were prepared and separated by 10% SDS-PAGE. PKC $\delta$  cleavage was then detected by using anti-PKC $\delta$ -antibody that recognizes a C-terminal epitope. (B) Time-lapse recording of FRET signal in control and dieldrin-treated N27 cells. N27 cells were first transfected with pFRET $\delta$  for 24 hr and treated with dieldrin (100  $\mu$ M) for up to 60 min. During the treatment, the CFP, YFP, and FRET images were acquired every 5 min by using the corresponding excitation laser wavelength and emission filter set. The intensity of CFP and FRET at each time point was measured in Metamorph 5.07. The intensity ratio of CFP/YFP was calculated and plotted in Prism 3.0. (C) Cleavage of PKC $\delta$ -FRET was indeed induced in pFRET $\delta$  transfected N27 cells following dieldrin exposure. To get the higher transfection efficiency, pFRET $\delta$  was transfected into N27 cells by electroporation. After 24 hr, cells were lysed and whole cell lysates were separated by 7.5% SDS-PAGE. The cleavage of PKC $\delta$ -FRET was detected by using anti-GFP antibody. (D) Nuclear localization of the catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF). PKC $\delta$ -CF was transiently transfected into N27 cells. The localization of PKC $\delta$ -CF was visualized by immunostaining of the V5 tag (Bar = 10  $\mu$ m).

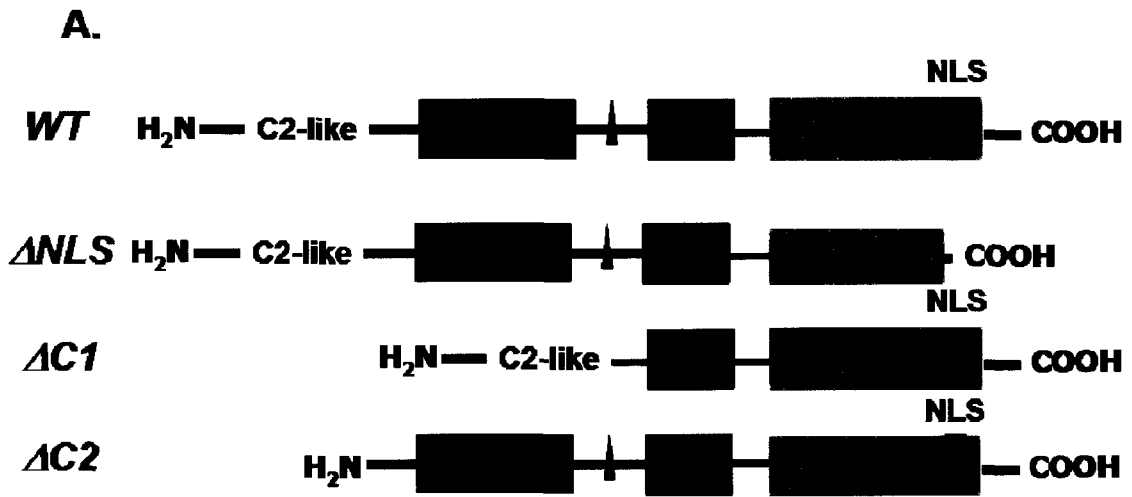




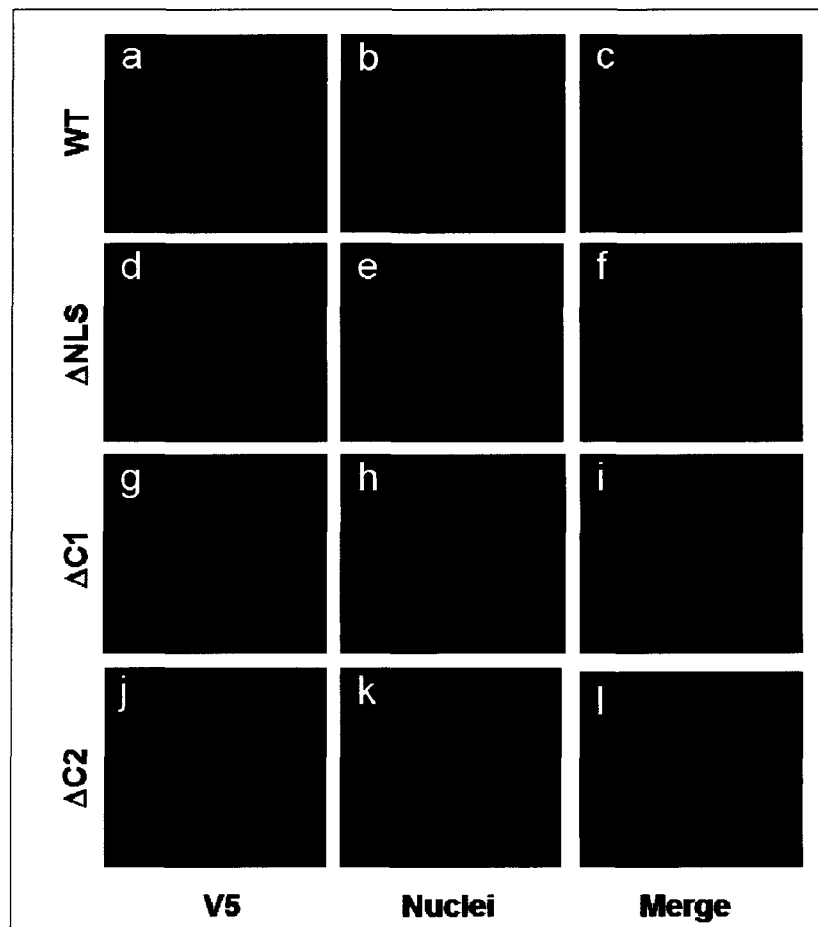
**C.****D.**

**Figure 3: Deletion of C2-like but not C1 domain in PKC $\delta$  induced nuclear localization of PCK $\delta$ .**

(A) Schematic representation of PKC $\delta$ -WT, PKC $\delta$ - $\Delta$ C1, PKC $\delta$ - $\Delta$ C2, and PKC $\delta$ - $\Delta$ NLS. Generation of these constructs is described in detail in the materials and methods. (B) Subcellular localization of PKC $\delta$ -WT, PKC $\delta$ - $\Delta$ C1, PKC $\delta$ - $\Delta$ C2, and PKC $\delta$ - $\Delta$ NLS in N27 cells. PKC $\delta$ -WT, PKC $\delta$ - $\Delta$ C1, PKC $\delta$ - $\Delta$ C2, and PKC $\delta$ - $\Delta$ NLS stably expressing N27 cells were generated via the ViraPower Lentiviral gene expression system (Invitrogen, Inc. Carlsbad, CA). Cells were then fixed, and immunostaining of the V5 tag was performed. To visualize the V5 tag, Cy3-conjugated secondary antibody was used. Subcellular localization of PKC $\delta$ -WT, PKC $\delta$ - $\Delta$ C1, PKC $\delta$ - $\Delta$ C2, and PKC $\delta$ - $\Delta$ NLS was revealed by immunoreactivity of the V5 tag. Nuclei were counterstained by Hoechst 33342. Stained cells were observed under a TCS/NT confocal system and all images were processed in Metamorph 5.07 (Bar = 10  $\mu$ m).



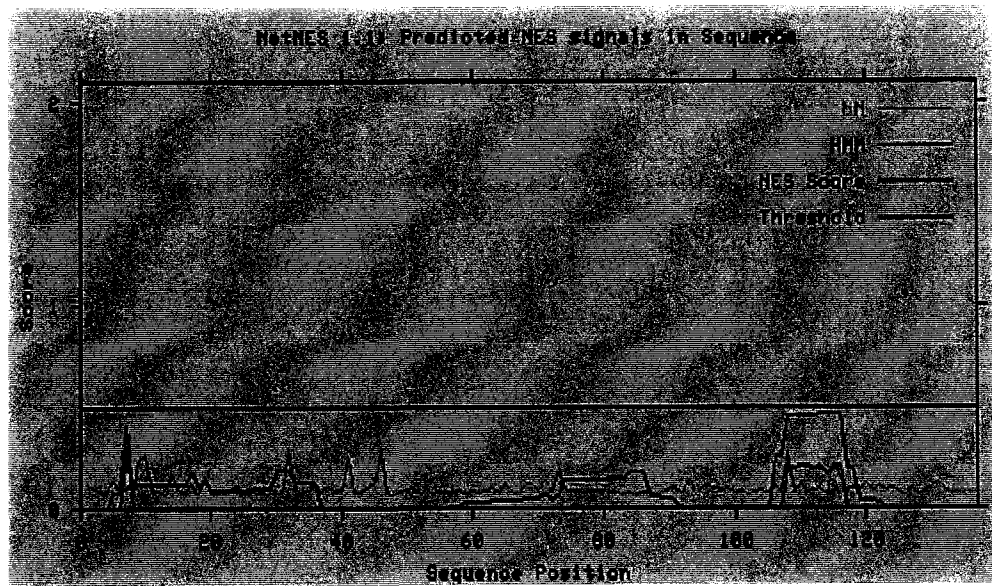
**B.**



**Figure 4: C2-like domain of PKC $\delta$  does not contain leucine-rich nuclear export signal (NES).**

(A) Analysis of the leucine-rich NES motif in the C2-like domain of PKC $\delta$ . The amino acid sequence (1-138) of the C2-like domain was uploaded to the NETNES 1.1 server (<http://www.cbs.dtu.dk/services/NetNES/>) and we performed NES motif prediction. (B) Alignment of the leucine-rich motif in the C2-like domain of PKC $\delta$  with a validated NES motif from Rev, MEK, PLC $\delta$ 1, PKI as well as two atypical PKC isoforms  $\zeta$  and  $\lambda$ . The NES motifs from different proteins were directly aligned with the leucine-rich motif (108-118) of the C2-like domain in ClustalW 1.8 (<http://searchlauncher.bcm.tmc.edu/multi-align/multi-align.html>). (C) Leucine-rich motif in the C2-like domain is not sensitive to the nuclear export inhibitor leptomycin B (LMB). Leptomycin B stock (500 ng/ml) was prepared in ethanol. PKC $\delta$ -WT stably expressing cells were treated with ethanol (0.1%) alone as a vehicle control or with LMB (0.5 ng/ml) for 5 min, and immunostaining of the V5 tag was performed. The immunoreactivity of the V5 tag was visualized by using Cy3-conjugated secondary antibody. Subcellular localization of PKC $\delta$ -WT was revealed by immunoreactivity of the V5 tag. Nuclei were counterstained with Hoechst 33342. Stained cells were observed under a TCS/NT confocal system and all images were processed in Metamorph 5.07 (Bar = 10  $\mu$ m).

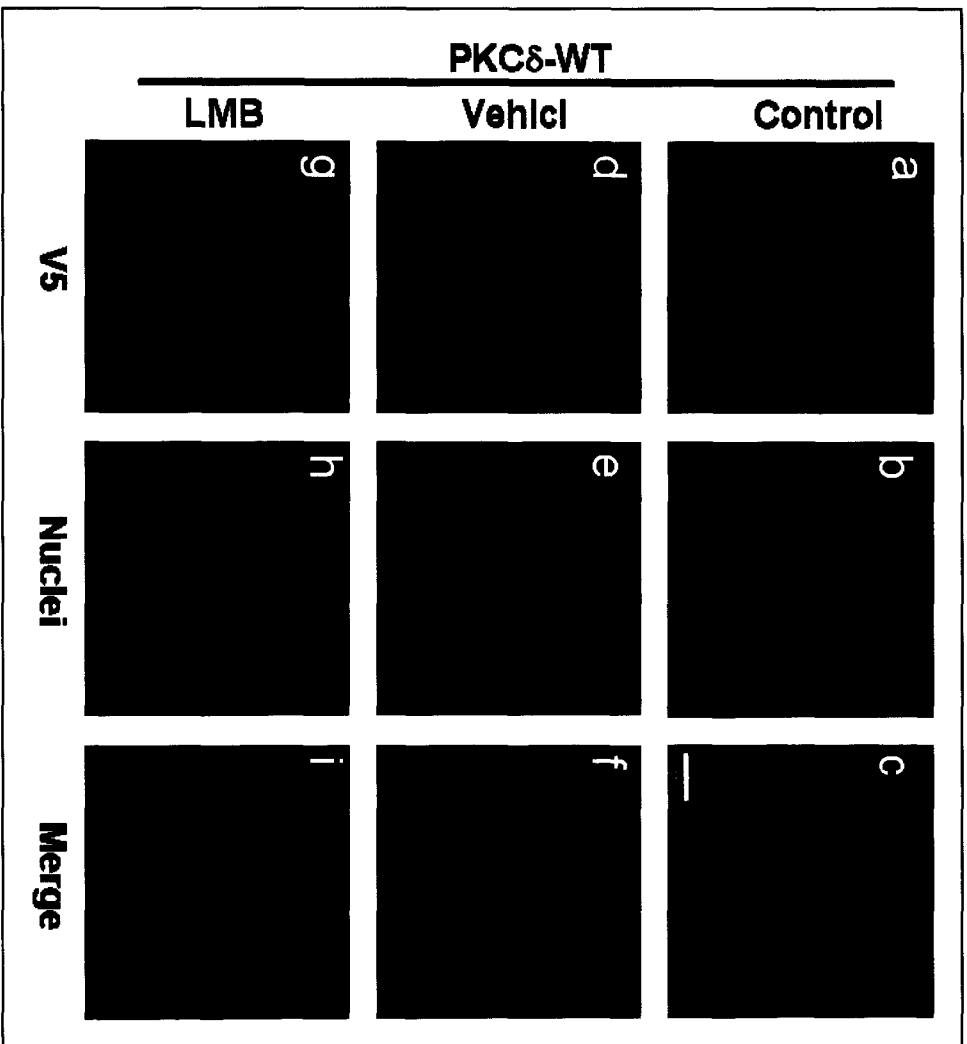
**A.**



**B.**

atypical PKC	Lamda	1	--	S	L	G	L	Q	D	P	D	L	L
	Zeta	1	--	G	L	G	L	Q	D	P	D	L	I
	PKI	1	E	L	A	L	K	L	A	C	L	D	I
	PLC	1	E	L	K	D	F	L	K	E	L	N	I
	Rev	1	-	Q	L	P	P	L	E	R	L	T	D
	MEK	1	A	L	Q	K	K	L	E	E	L	E	L
	C2-domain	1	-	L	Q	P	Q	A	K	V	L	M	C
					1	2	3	4					

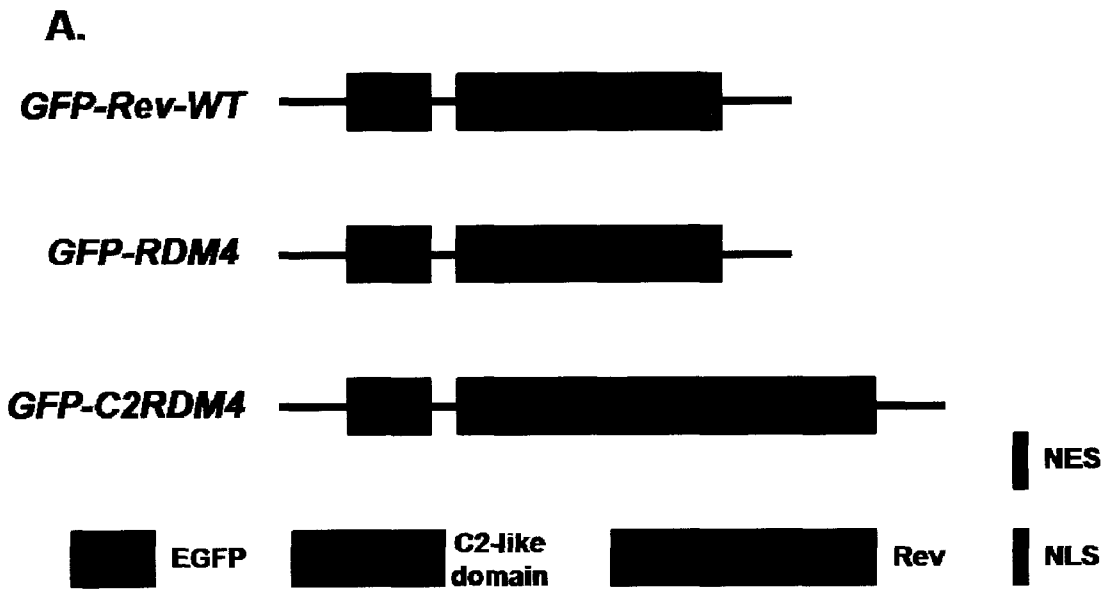
C.



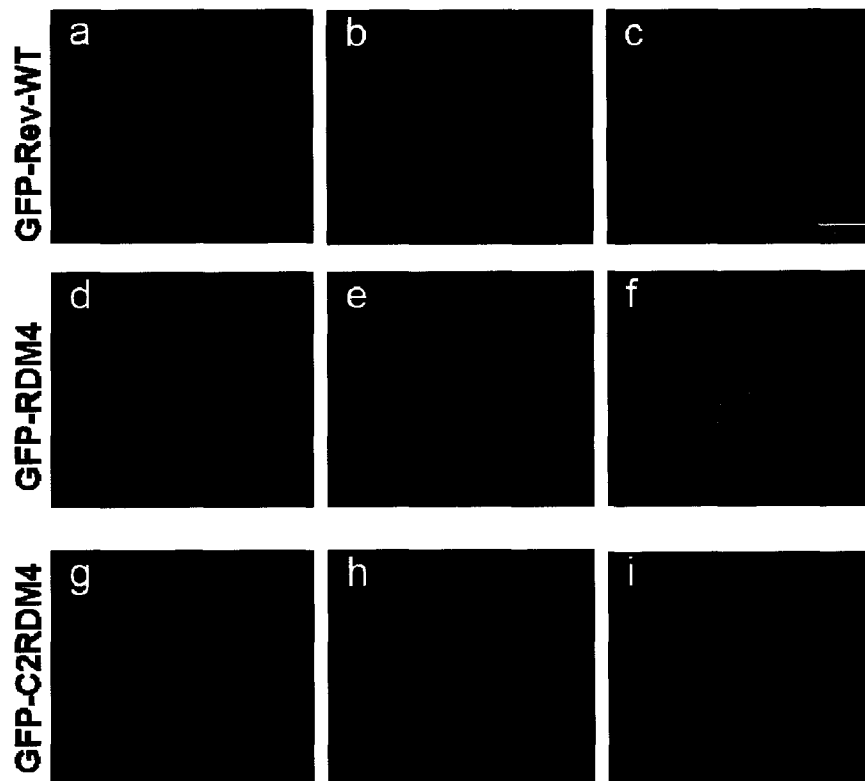
**Figure 5: Incapacity of C2-like domain to retain NES deleted form of Rev in the cytoplasm.**

(A) Schematic representation of the primary structures of EGFP-Rev-WT, EGFP-RDM4, and EGFP-C2RDM4. All functional domains are illustrated as boxes in different colors. (B) Subcellular localization of EGFP-Rev-WT, EGFP-RDM4, and EGFP-C2RDM4 in N27 cells. EGFP-Rev-WT, EGFP-RDM4, and EGFP-C2RDM4 were transfected into N27 cells cultured in glass bottom culture dishes. About 24 hr post-transfection, Hoechst 33342 was added to culture dishes and incubated at RT for 15 min. The culture dishes were then washed with 1xPBS three times and replaced with normal culture medium. To observe the EGFP fluorescence from live cells, cells in culture dishes were then directly observed by confocal microscopy and all images were processed in Metamorph (Bar = 10  $\mu$ m).





**B.**



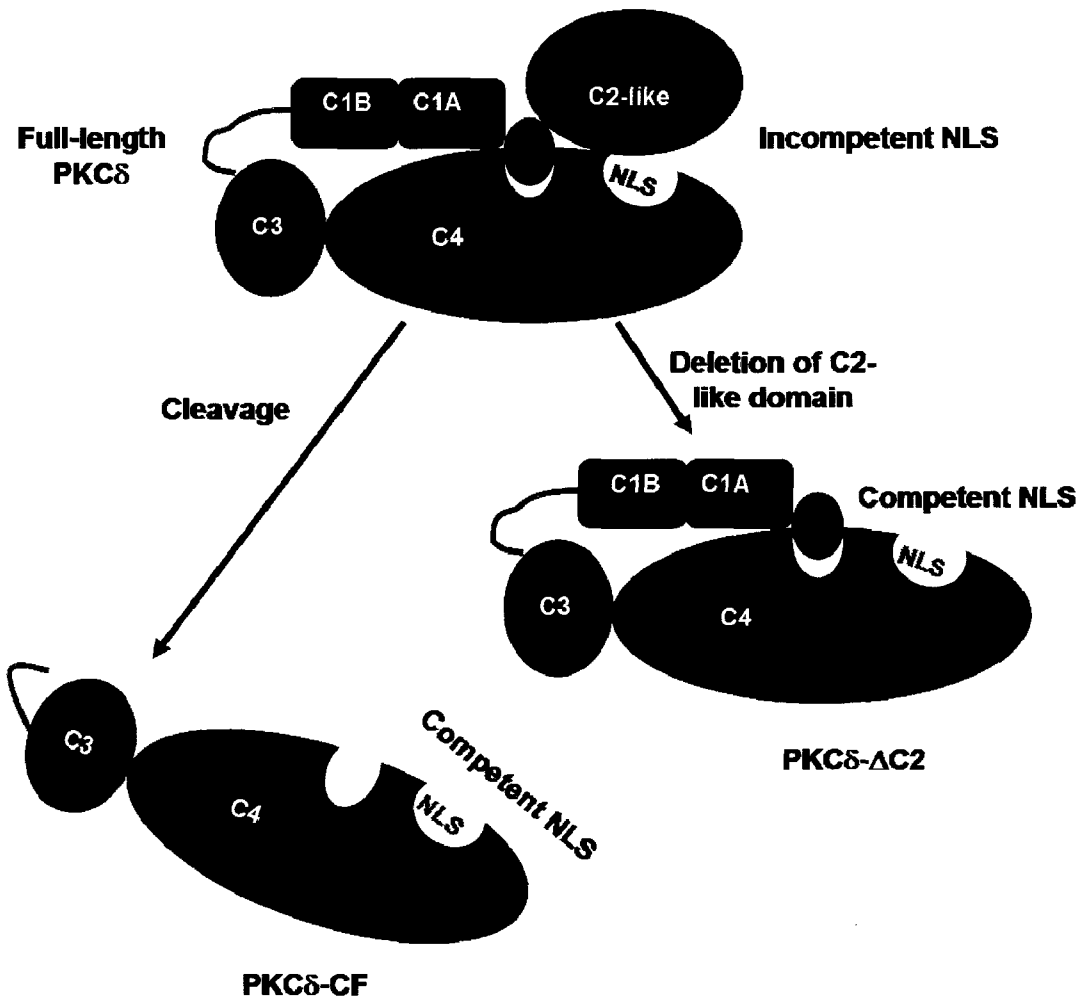


Figure 6: Regulation role of C2-like domain to the nuclear localization of PCK $\delta$

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**CHAPTER V: SELECTIVE EXPRESSION OF OXIDATIVE-STRESS SENSITIVE  
KINASE PROTEIN KINASE C DELTA (PKC $\delta$ ) CONTRIBUTES TO THE  
VULNERABILITY OF NIGRAL DOPAMINERGIC NEURONS TO MPP<sup>+</sup>-INDUCED  
DEGENERATION**

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**ABSTRACT**

Protein kinase C delta (PKC $\delta$ ) has been shown to be an oxidative stress sensitive kinase that promotes neurotoxin-induced apoptotic death of dopaminergic neuronal cells. In the present study, we determined the relative expression levels of PKC isoforms, including PKC $\alpha$ , PKC $\beta$ I, PKC $\delta$ , PKC $\epsilon$ , PKC $\theta$ , and PKC $\zeta$  in the substantia nigra (SN), striatum (St), and cortex (Ctx) regions of rodent brains. By employing immunostaining, immunoblot, and quantitative RT-PCR, selective expression of PKC $\delta$ , but not of other PKC isoforms, was found in the nigral dopaminergic neurons. Co-localization of abundant PKC $\delta$  with tyrosine hydroxylase (TH) in the cytoplasm of nigral dopaminergic neurons was also observed. We further demonstrated that PKC $\delta$  is proteolytically activated in the substantia nigra region of the mouse brain. The blockade of proteolytic cleavage of endogenous PKC $\delta$  by the cleavage

resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM) not only protects dopaminergic neuronal (N27) cells from MPP<sup>+</sup>-induced apoptotic death, but also protects primary dopaminergic neurons from MPP<sup>+</sup>-induced degeneration. Moreover, the catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF), but not the regulatory fragment of PKC $\delta$  (PKC $\delta$ -RF), can directly induce the degeneration of primary dopaminergic neurons. Finally, we demonstrated that the number of nigral dopaminergic neurons and the striatum dopamine level are significantly higher in PKC $\delta$ -/- mice than in PKC $\delta$  +/+ mice after administration of MPTP. Taken together, our studies suggest that abundant PKC $\delta$  is one of the inherent factors that contribute to the vulnerability of nigral dopaminergic neurons to MPP<sup>+</sup>-induced degeneration by its proteolytic activation.

## INTRODUCTION

The severe degeneration of substantia nigra pars compacta (SNc) dopaminergic neurons in Parkinson's disease (PD) causes depletion of the neurotransmitter dopamine in the striatum, and subsequently changes the neuronal circuitry controlling voluntary movement and induces the development of hyperkinesia symptoms, including tremors, bradykinesia, and postural instability. The degeneration of dopaminergic neurons in PD is strikingly selective, i.e., dopaminergic neurons located in the SNc region are selectively degenerated, though degeneration of noradrenergic neurons at the locus coeruleus, serotonergic neurons at the raphe, and cholinergic neurons at the nucleus basalis of meynert, dorsal motor nucleus of vagus, and cerebral cortex are also observed (Dauer and Przedborski, 2003). MPTP, a mitochondrial complex I inhibitor, induces rapid development of an irreversible PD-like

syndrome in humans and primates (Langston et al., 1984; Albanese et al., 1993); the development of MPTP cell culture and animal models of PD paves the path to investigate the mechanism of dopaminergic neuronal degeneration.

Extensive studies have suggested that oxidative stress is one of the major upstream events that contributes to the cell death process of the SNc dopaminergic neurons in PD (Cassarino et al., 1997; Greenamyre et al., 2001; Jenner, 2003). Examination of postmortem PD brains has revealed that the SNc region has a higher level of oxidative stress, as indicated by the level of lipid peroxidation and protein or DNA oxidation (Dexter et al., 1989; Floor and Wetzel, 1998; Jenner, 1998). Dopaminergic neurons are particularly susceptible to oxidative stress, as their neurotransmitter dopamine can be oxidized to generate toxic dopamine-quinone species, superoxide radicals, and hydrogen peroxide (Graham, 1978; Lotharius and Brundin, 2002). Oxidative stress induced by MPTP or its active form MPP<sup>+</sup> (Cassarino et al., 1997; Dauer and Przedborski, 2003; Kaul et al., 2003), as a result of mitochondrial complex I inhibition, has also been shown to trigger a series of apoptotic cascades, including cytochrome c release (Cassarino et al., 1999), caspase activation (Hartmann et al., 2000; Hartmann et al., 2001; Viswanath et al., 2001), and apoptotic cell death in numerous cell culture and animal PD models. However, downstream events of caspase-3 activation induced by oxidative stress in dopaminergic neurons have not been fully characterized.

Protein kinase C is one of the major cellular signal transducers involved in various cellular functions. The PKC family includes 11 isoforms, which are classified mainly into three subgroups based on their dependence upon diacylglycerol (DAG) and Ca<sup>2+</sup> for activation (Newton, 2003). The conventional PKC isoforms ( $\alpha$ ,  $\beta$ I,  $\beta$ II, and  $\gamma$ ) require DAG

and  $\text{Ca}^{2+}$  for activation, the novel PKC isoforms ( $\delta$ ,  $\epsilon$ ,  $\eta$ , and  $\theta$ ) require DAG but not  $\text{Ca}^{2+}$  for activation and the atypical PKCs (PKC  $\zeta$ ,  $\lambda$ , and  $\iota$ ) require neither  $\text{Ca}^{2+}$  nor DAG for activation. Interestingly, a substantial body of evidence has demonstrated that PKC $\delta$  can be proteolytically activated by caspase-3 and promote apoptotic cell death in non-neuronal and neuronal cells (Brodie and Blumberg, 2003; Kitazawa et al., 2003; Yang et al., 2004), although most of the PKC isoforms have anti-apoptotic properties in the cells (Gutcher et al., 2003). Our previous studies have also shown that hydrogen peroxide-induced oxidative stress also induces caspase-3 dependent proteolytic activation of PKC $\delta$  in dopaminergic neuronal cells (manuscript under review), suggesting that PKC $\delta$  might be an important downstream modulator mediating oxidative stress-induced apoptotic death of dopaminergic neurons. Although several expression surveys of PKC isoforms in the central nervous system have found that PKC $\delta$  is highly expressed in the thalamus, septal nuclei, and purkinje cells in the posterior cerebellum (Barmack et al., 2000; Naik et al., 2000), the expression of PKC $\delta$  in the SNc dopaminergic neurons has not been investigated.

Previously, we demonstrated that protein kinase C delta (PKC $\delta$ ) is proteolytically activated by caspase-3 and contributes to the induction of apoptotic death of dopaminergic neuronal cells by various neurotoxins (Kaul et al., 2003; Kitazawa et al., 2003; Yang et al., 2004). Herein, we examined the expression of PKC isoforms in different regions of brain, including the nigral dopaminergic neurons, and investigated the role of proteolytic activation of PKC $\delta$  in MPP $^{+}$ -induced degeneration of nigral dopaminergic neurons in primary mesencephalic neuronal cultures and in the substantia nigra region of mice brains.

## MATERIALS AND METHODS

**Materials**

MPP<sup>+</sup>, protease cocktail, ATP, protein-A-sepharose, and anti- $\beta$ -actin antibody were obtained from Sigma-Aldrich (St. Louis, MO). Antibodies to PKC $\delta$ ,  $\alpha$ , and  $\beta$ I were purchased from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA). Anti-GAD-6 antibody was obtained from the University of Iowa hybridoma facility. TaqMan Rat PKC $\delta$ , Mouse PKC $\delta$ ,  $\epsilon$ , and  $\theta$ , the 18s ribosome RNA expression assay kit, and PCR master mix were purchased from Applied Biosystems (Foster City, CA). Anti-rabbit and anti-mouse secondary antibodies and the ECL chemiluminescence kit were purchased from Amersham Pharmacia Biotech. (Piscataway, NJ). Alexa 488 conjugated anti-rabbit secondary antibody and Hoechst 33342 were purchased from Molecular Probes, Inc. (Eugene, OR). Cy3 conjugated anti-mouse secondary antibody was obtained from Jackson Laboratory (Bar Harbor, Maine) The Cell Death Detection ELISA plus Assay Kit was purchased from Roche Molecular Biochemicals (Indianapolis, IN). [ $\gamma$ -<sup>32</sup>P] ATP was purchased from Perkin Elmer Life Science Products (Boston, MA). The Bradford protein assay kit was purchased from Bio-Rad Laboratories (Hercules, CA). Brilliant SYBR green QPCR reagent, Brilliant QPCR reagent, and *Pfu* DNA polymerase were purchased from Stratagene (La Jolla, CA). SuperScript III first-strand synthesis system, TRIZOL reagent, ViraPower<sup>TM</sup> lentiviral expression system, RPMI, fetal bovine serum, L-glutamine, blasticidin, penicillin, streptomycin, and gentamycin were purchased from Invitrogen, Inc. (Carlsbad, CA). Primers were synthesized in IDT (Coralville, IA).

**Animals**

All male C57 black mice (12-16 weeks old) used in the experiments were maintained in the College of Veterinary Medicine Animal Care Facility of Iowa State University under standard laboratory conditions with water and food available *ad libitum*. PKC $\delta$ <sup>-/-</sup> mice were a kind gift from Prof. Keiichi Nakayama (Kyushu University, Fukuoka, Japan) (Miyamoto et al., 2002). All experimental procedures involving mice have been approved by the Iowa State University Institutional Animal Care and Use Committee.

**Cell culture**

The immortalized rat mesencephalic dopaminergic neuronal cell line (N27) was a gift from Dr. Kedar N. Prasad (University of Colorado Health Sciences Center, Denver, CO) (Prasad et al., 1998). N27 cells were grown in RPMI 1640 medium containing 10% FBS, 2 mM L-glutamine, 50 units penicillin, and 50  $\mu$ g/ml streptomycin. Cells were maintained in a humidified atmosphere of 5% CO<sub>2</sub> at 37<sup>0</sup>C, and 4-5 day old cells were used for the experiments. For MPP<sup>+</sup> treatment, N27 cells and PKC $\delta$ -CRM stably expressing N27 cells were treated with 300  $\mu$ M MPP<sup>+</sup> for 36 hr in serum-containing medium.

**Primary mesencephalic neuronal culture**

Primary mesencephalic neuronal cultures were prepared from the ventral mesencephalon of gestational 15-17 day old rat embryos as described previously (Yang et al., 2004). Briefly, midbrain tissues were maintained in ice-chilled dissection solution (HBS supplemented with 200 units/ml penicillin/streptomycin, 10 mM MgCl<sub>2</sub>, 7 mM pH 7.3 Hepes, and 2 mM L-glutamine) during the dissection. The tissue was collected by centrifugation at

80 g for 5 min and then treated with Trypsin/EDTA for 20-30 min at 37°C. Trypsin was removed by centrifugation and digested tissues were resuspended in culture medium I (DMEM supplemented with 10% FBS). The digested tissues were further separated by pipetting to obtain the homogenous suspension. The cells were counted and plated at equal density ( $0.5 \times 10^6$  cells) on cover slips pre-coated with poly-L-lysine and laminin in 6-well plates. After 24 hr, culture medium I was replaced with culture medium II (Neurobasal-A medium, supplemented with 0.2% insulin, 0.2% transferrin, 5% FBS, 2% B-27 supplement, 2 mM GlutaMAX I, 1 µg/ml gentamycin, and 5 µM cytosine arabinoside). The cells were maintained in a humidified CO<sub>2</sub> incubator (5% CO<sub>2</sub>, 37°C). Half of the culture medium was replaced every 2 days. Approximately 6-7 day old cultures were used for experiments.

### **MPTP administration to mice**

MPTP dissolved in ddH<sub>2</sub>O was administered using an acute dosing regimen of 30 mg/kg intraperitoneally every day for five doses. Control animals were treated with an equal volume of ddH<sub>2</sub>O. All animals were sacrificed the day after the last injection. Experimental groups included MPTP-treated PKCδ<sup>+/+</sup> mice (n=12) and their control (n=12) and MPTP-treated PKCδ<sup>-/-</sup> mice (n=12) and their control (n=12).

### **Immunoblotting**

Different regions of brain, including cortex, striatum, and substantia nigra, were first dissected. To prepare the tissue homogenate, brain tissues were homogenized with a mini homogenizer in lysis buffer (pH 8.0, 20 mM Tris-Cl, 10 mM EGTA, 2 mM EDTA, 2 mM DTT, 0.5% Triton X-100, and 1:100 dilution of protease inhibitor). For cell homogenate

preparation, N27 cells ( $10 \times 10^6$ ) were harvested with trypsin/EDTA and spun at 200xg for 5 min. Cell pellets were then washed twice with ice-chilled PBS and resuspended in 200  $\mu$ l of lysis buffer. After incubation on ice for 5 min, the lysates were centrifuged for 30 min at 14,000xg at 4°C and supernatants were collected as whole lysates. Equal amounts of protein (20-30  $\mu$ g) were loaded in each lane and separated on a 10% SDS-polyacrylamide gel. Proteins were then transferred to nitrocellulose membrane by electro-blotting overnight (4°C, 25 V). Non-specific binding sites were blocked by treating the nitrocellulose membranes with 5% non-fat dry milk TBST solution (10 mM Tris, 150 mM NaCl, and 0.1% Tween 20) for 1 hr. The nitrocellulose membranes were then incubated with primary antibodies (1:1000) for 1 hr at RT. The primary antibody treatment was followed by treatment with secondary HRP-conjugated anti-rabbit or anti-mouse IgG (1:2000) for 1 hr at RT. Secondary antibody-bound proteins were detected using an ECL chemiluminescence kit (Amersham Biosciences). Gel photographs and densitometric analysis were performed with a Kodak image station (Model 1000R, Rochester, New York).

### **RNA preparation and quantitative real time RT-PCR**

Total RNA was prepared from N27 cells or from different regions of rodent (mouse and rat) brains. N27 cells ( $1 \times 10^6$ ) were first collected by centrifugation and washed with PBS. For rodent brain tissue samples, different regions of brain (striatum, cortex, substantia nigra) were dissected and frozen in liquid nitrogen. The absolute RNA RT-PCR miniprep kit (Stratagene, La Jolla, CA) was used for RNA preparation. Briefly, the cell pellet or brain tissue (20 mg) was resuspended in lysis buffer (from the kit). Brain tissue was further homogenized with the mini homogenizer. The homogenate was loaded on the spin column



(from the kit) for the enrichment of RNA in the column. DNase solution (from the kit) was added to the column for the degradation of the remaining DNA. After washing with low-salt buffer, RNA retained on the membrane was eluted out with elution buffer. Total RNA was reversely transcribed into cDNA using the SuperScript III first-strand synthesis system (Invitrogen, Inc., Carlsbad, CA) as described in the kit instructions. For quantitative RT-PCR (QRT-PCR) of rodent PKC $\delta$ , PKC $\epsilon$ , and PKC $\theta$ , a TaqMan expression assay kit was used. About 50 ng cDNA was mixed with TaqMan primer and probe, as well as 2x QPCR master mix to set up the reaction (50  $\mu$ l). For QRT-PCR of mouse PKC $\beta$ I and PKC $\zeta$ , specific primers were designed and SYBR green reagent was employed. Primers used for PKC $\beta$ I were forward: 5' ttctggaagcagttgagctt 3'; reverse: 5' agtgccaaatgtcatttctca 3'; and for PKC $\zeta$ , forward: 5' cagatcacagatgactatgg 3'; reverse: 5' gagattgctctgtctagaag 3'. About 50 ng cDNA was mixed with primer (100 nM), reference dye (30 nM), and Brilliant SYBR green QPCR master mix to set up the reaction (50  $\mu$ l). 18s ribosome RNA (rRNA) was used as an endogenous control for both TaqMan and SYBR green based QRT-PCR. For each sample, triplicates were run on the same plate. All PCR reactions were performed and data were analyzed in a Mx4000 multiplex Quantitative PCR system (Stratagene, La Jolla, CA).

### **Preparation of constructs**

PKC $\delta$ -CRM (cleavage resistant mutant), PKC $\delta$ -CF (catalytic fragment), and PKC $\delta$ -RF (regulatory fragment) expression plasmids were prepared. To prepare PKC $\delta$ -CF and PKC $\delta$ -RF, 995-2035 bp or 14-982 bp of mouse PKC $\delta$  (gi: 6755081) cDNA were first amplified from pGFP-PKC $\delta$  (a kind gift of Dr. Reyland at University of Colorado) (DeVries

et al., 2002) with the following primer pairs, respectively. For PKC $\delta$ -CF: forward primer: 5' caccatgaacaacgggacctatggcaa 3'; reverse primer: 5' aatgtccaggaattgctcaaac 3'; for PKC $\delta$ -RF: forward primer: 5' caccatggcacccttctctgctgcg 3'; reverse primer: 5' actcccagagacttctggctt 3'. To prepare PKC $\delta$ -CRM, full-length mouse PKC $\delta$  cDNA with a point mutation at 993(A-C) that abolishes the caspase-3 cleavage site of PKC $\delta$  was amplified with pGFP-PKC $\delta$ <sup>D-A327</sup> (a kind gift of Dr. Reyland at University of Colorado) as template. The primer pairs used were: forward primer: 5' caccatggcacccttctctgctgcg 3'; reverse primer: 5' aatgtccaggaattgctcaaac 3'. All PCR reactions were performed with *Pfu* DNA polymerase to maintain the fidelity of the sequence. All PCR products were directly cloned in-frame into the V5-tagged expression vector (at the C terminal) pLenti/TOPO from Invitrogen to get pLenti/PKC $\delta$ -CRM, pLenti/PKC $\delta$ -CF, and pLenti/PKC $\delta$ -RF. All positive clones were confirmed by sequencing.

#### **Establishment of PKC $\delta$ -CRM stably expressing N27 cell line**

The ViraPower Lentiviral gene expression system from Invitrogen (Carlsbad, CA) was employed for the establishment of the PKC $\delta$ -CRM stably expressing N27 cell line. To produce lentiviral particles, pLenti/PKC $\delta$ -CRM, as well as supporting plasmids (provided by the kit) were co-transfected into human 293FT cells with the use of lipofectamine 2000, as described in the instruction of the kit. The lentiviral particles in the medium were then collected by centrifuging at 3000 rpm for 15 min at 48-72 hr post-transfection. To generate the PKC $\delta$ -CRM stably expressing cell line, lentiviral particles containing pLenti/PKC $\delta$ -CRM and polybrene (6  $\mu$ g/ml) were added into cultured N27 cells ( $2 \times 10^5$ ). After 24 hr, lentiviral particles were replaced with fresh medium. Positive N27 cells were selected by keeping

blastidicin (10 µg/ml) in medium for up to 2 weeks. PKCδ-CRM expressing N27 cells were identified by immunostaining of the C-terminal V5 epitope.

### **Transient transfection of primary neuronal cultures**

Transient transfection of primary neuronal cultures was performed by electroporation. A Rat Neuron Nucleofector kit from Amaxa biosystems (Cologne, Germany) was employed. Briefly, about  $1-2 \times 10^6$  cells were resuspended with 100 µl nucleofector solution mixed with 2 µg plasmid (pLenti/PKCδ-CRM, pLenti/PKCδ-CF, or pLenti/PKCδ-RF) and transferred into a cuvette. The cuvette was then put in a nucleofector device (Amaxa biosystems, Cologne, Germany) for electroporation. After electroporation, cells were gently transferred to a 6-well plate and incubated at 37°C.

### **Immunocytochemistry**

Double immunostaining of TH and PKCδ, GAD and PKCδ, and TH and V5 was performed sequentially in primary neuronal cultures. Primary neuronal cultures grown on the poly-L-lysine and laminin coated cover slips were first fixed in 4% paraformaldehyde, then permeabilized and blocked with blocking reagent (0.4% BSA, 5% goat serum, and 0.2% Triton-X 100 in PBS) for 20 min. Cells were then incubated with one of the primary antibodies (mouse anti-TH, mouse anti-GAD, or rabbit anti-TH, 1:1000 in blocking reagent) overnight at 4°C and then washed 4x8 min with PBS. Immunoreactivity was visualized by incubation with Alexa 488-conjugated goat anti-rabbit secondary antibody or Cy3-conjugated goat anti-mouse secondary antibody (1:2000 in PBS) at RT for 90 min. After the wash, cells were incubated with second primary antibodies (rabbit anti-PKCδ or mouse anti-

V5) and the second secondary antibodies. After another 4x8 min PBS wash, Hoechst 33342 (final concentration of 10  $\mu\text{g/ml}$  in PBS) was added to stain the cell nuclei at RT for 3 min. Finally, cells were mounted on a slide with antifade mounting medium. The cells were observed under a TCS/NT confocal microscopy system (Leica, Bannockburn, IL). All images were processed in MetaMorph 5.07 from Universal imaging (Downingtown, PA).

### **Immunohistochemistry**

Control and MPTP-treated mice were perfused by the intracardiac route with 5% sucrose, followed by 4% paraformaldehyde in PBS. The mice were kept for 2 hr and then decapitated. The brains of mice were then removed and immersed for 48 hr in 4% paraformaldehyde for fixation. Nigral and striatal cortical sections (25  $\mu\text{m}$  in thickness) were then prepared with a cryostat. Double immunostaining of TH and PKC $\delta$  was then performed sequentially. The sections were rinsed with PBS containing 0.1% Triton-X (PBS-T), followed by incubation with mouse anti-TH antibody (1:1000) in PBS-T containing 10% goat serum overnight at 4°C with continuous shaking. The sections were washed three times with PBS and incubated with Cy3-conjugated goat anti-mouse secondary antibody (1:2000) at RT for 2 hr. The staining of PKC $\delta$  was then followed using the same procedure, but with the Alexa 488-conjugated goat anti-rabbit secondary antibody. All sections were washed and mounted on a slide. Mounted sections were observed under a TCS/NT confocal microscopy system (Leica, Bannockburn, IL). All images were processed in MetaMorph 5.07 from Universal Imaging (Downingtown, PA).

**Immunoprecipitation kinase assay**

PKC $\delta$  enzymatic activity was assayed using an immunoprecipitation kinase assay as previously described (Anantharam et al., 2002). Protein (100-200  $\mu$ g) extracted from the substantia nigra of control and MPTP-treated mice was immunoprecipitated overnight at 4°C using 2  $\mu$ g of anti-PKC $\delta$  antibody. The immunoprecipitates were then incubated with protein-A–sepharose for 1 hr at 4°C. The protein-A bound antigen-antibody complexes were then washed 3 times with lysis buffer, 3 times with kinase buffer (40 mM Tris, pH 7.4, 20 mM MgCl<sub>2</sub>, 20  $\mu$ M ATP, and 2.5 mM CaCl<sub>2</sub>), and resuspended in 20  $\mu$ l of kinase buffer. Reactions were started by adding 20  $\mu$ l of reaction buffer containing 0.4 mg Histone H1 and 5  $\mu$ Ci of [ $\gamma$ -<sup>32</sup>P] ATP (3,000 Ci/mM) to the immunoprecipitated samples and incubated for 10 min at 30°C. SDS gel loading buffer (2X) was then added to terminate the reaction, the samples were boiled for 5 min, and the products were separated on a 12% SDS-PAGE gel. The phosphorylated histone bands were detected using a Personal Molecular Imager (FX model, Bio-Rad) and quantified using Quantity One 4.2.0 software (Bio-Rad, Hercules, CA).

**Striatal dopamine and DOPAC measurement**

The mice were sacrificed the day after the last MPTP treatment. Both striata were rapidly dissected with the use of a brain slicer and tissue puncher on ice-chilled glass plates. The striata were frozen at -70°C immediately after dissection. For the measurement of dopamine and its metabolites, the striata were then thawed and resuspended in 0.1 M ice-chilled perchloric acid (PCA). The resuspensions were sonicated and centrifuged. Aliquots were taken for protein quantification with the Bradford assay kit. Other aliquots were used

for the measurement of dopamine and its metabolites by HPLC with electrochemical detection. Concentrations of dopamine and DOPAC are expressed as pmol/mg protein.

### **Quantification assay for DNA fragmentation**

DNA fragmentation was measured using a recently developed Cell Death Detection ELISA plus Assay Kit (Molecular Biochemicals, Indianapolis, IN). Briefly, cells were spun down at 200xg for 5 min and washed twice with 1X PBS. Cells were then incubated with a lysis buffer (supplied with the kit) at RT. After 30 min, samples were centrifuged and 20  $\mu$ l aliquots of the supernatant were then dispensed into streptavidin-coated 96 well microtiter plates followed by addition of 80  $\mu$ l of HRP-conjugated antibody cocktail, and incubated for 2 hr at RT with mild shaking. After incubation, unbound components were removed by washing with the incubation buffer supplied with the kit. The nucleosomes retained by the antibody cocktail in the immunocomplex were quantified spectrophotometrically with ABTS as an HRP substrate. Measurements were made at 405 nm and 490 nm using a SpectroMax 190 spectrophotometer (Molecular Devices, Sunnyvale, CA). The difference in absorbance between OD405 and OD490 nm was used to measure the actual DNA fragmentation level.

### **Data analysis**

Data analysis was performed using Prism 3.0 software (GraphPad Software, San Diego, CA). DNA fragmentation, QRT-PCR, the number of TH positive neurons and their neuronal processes, and dopamine content were first analyzed using one-way ANOVA. Bonferroni's post-test was then performed to compare all groups, and differences with

$p < 0.05$  were considered significant. To analyze the PKC $\delta$  kinase enzymatic activity results, the paired t-test was used.

## RESULTS

### **Selectively high expression of PKC $\delta$ protein in dopaminergic neurons of substantia nigra (SN)**

PKC $\delta$  has been shown to be proteolytically activated under oxidative stress conditions in dopaminergic neuronal cells; however, the expression level and subcellular localization of PKC $\delta$  have not been investigated in dopaminergic neurons. Double immunostaining of PKC $\delta$  with tyrosine hydroxylase (TH) or GABA decarboxylase (GAD) was first performed in rat primary mesencephalic neuronal cultures that contain a mixture of dopaminergic and GABAergic neurons. TH and GAD serve as markers for dopaminergic and GABAergic neurons, respectively. As shown in Figure 1Aa, clear immunoreactivity of PKC $\delta$  was seen in dopaminergic neurons identified by positive TH immunostaining; PKC $\delta$  was seen mostly in the cytoplasm and neuronal processes that co-localize with TH (Figure 1Ad). In contrast, only very weak immunoreactivity of PKC $\delta$  was observed in the cytoplasm and neuronal processes of GABAergic neurons identified by positive GAD immunostaining. This result suggests that PKC $\delta$  is more abundant in the dopaminergic neurons than in GABAergic neurons. To verify this observation *in vivo*, double immunostaining of PKC $\delta$  with TH or GAD was then performed in the substantia nigra (SN) and striatum sections of mouse brain. As shown in Figure 1B, immunoreactivity of PKC $\delta$  in the substantia nigra brain section is

consistently intense, appearing only in the dopaminergic neurons identified by positive TH staining and also co-localizing very well with TH in the cytoplasm. In the striatum section, although some PKC $\delta$  immunostaining signals were also seen in GABAergic neurons identified by positive GAD staining and nucleus staining, these signals were not quite distinct from the background. A survey of the expression level of different PKC isoforms in substantia nigra was further examined by immunoblot and was compared to that in cortex and striatum of the mouse brain. Based on the availability and quality of antibodies against different PKC isoforms, immunoblots of PKC $\alpha$ , PKC $\beta$ I, and PKC $\delta$  were made (Figure 1C). Consistent with the immunostaining results, the immunoblot of PKC $\delta$  also shows that the substantia nigra has the highest protein level of PKC $\delta$  as compared to the cortex and striatum. However, the PKC $\alpha$  protein level is almost the same in the three regions, and the PKC $\beta$ I protein level is lower in the substantia nigra region as compared to the cortex and striatum regions. The membrane was reprobated with  $\beta$ -actin antibody to ensure equal loading. Taken together, these results consistently demonstrate that nigral dopaminergic neurons in mice have a selectively higher expression of PKC $\delta$ .

### **Selectively high level of PKC $\delta$ mRNA in the substantia nigra**

To establish the correlation between the protein and mRNA levels of different PKC isoforms we next determined the mRNA levels of different PKC isoforms, including PKC $\delta$ , in the cortex (Ctx), striatum (St), and substantia nigra (SN) regions of mice brains, which were first carefully and precisely dissected. Total RNA was then prepared and converted into cDNA. For mouse PKC $\delta$ , PKC $\epsilon$ , and PKC $\theta$ , pre-designed TaqMan probes from Applied



Biosystems were employed for quantitative real time PCR (QRT-PCR). Because pre-designed TaqMan probes are not available for mouse PKC $\beta$ I and PKC $\zeta$ , the SYBR green dye based QRT-PCR method was used. 18s Ribosome RNA (18s rRNA) was used as an endogenous control to equalize the amount of RNA used in QRT-PCR. The real-time amplification plot of PKC $\delta$  from the Ctx, St, and SN is shown in Figure 2A. The Ct (threshold of cycle) value of amplification from SN cDNA is significantly lower than that in Ctx and St cDNA, indicating that the number of PKC $\delta$  mRNA copies in the SN is much higher than that in the Ctx and St. By using Ctx PKC $\delta$  Ct as the calibrator, the relative quantity of PKC $\delta$  mRNA among the three regions was calculated from the formula  $2^{-(\Delta C_t^{PKC\delta - \Delta C_t^{18s\ rRNA}})}$  and presented in Figure 2B. The number of PKC $\delta$  mRNA copies in the SN is 30-fold greater than that in the Ctx, and 2-fold greater than that in the St. Similar results were also found in rat: the number of PKC $\delta$  mRNA copies in the SN is about 5-fold more than that in the St and Ctx regions (Figure 4A). The relative quantity of several other PKC isoform mRNAs among the SN, Ctx, and St regions was also determined (Ctx as the calibrator). As shown in Figure 2C, the relative quantity of PKC $\beta$ I and PKC $\epsilon$  mRNA among the three regions is: SN < St < Ctx, while the relative quantity of PKC $\theta$  mRNA is: Ctx < SN < St. Both SN and St regions have similar levels of PKC $\zeta$  mRNA, which are higher than the level in the Ctx. We also attempted to determine the quantity of PKC $\alpha$  mRNA in the three regions. Since a pre-designed TaqMan probe for PKC $\alpha$  is unavailable, specific primers for PKC $\alpha$  were designed in order to use the SYBR green based QRT-PCR method; however, these primers failed to give good amplification and resulted in high background disturbance. Nevertheless, none of these PKC isoforms surveyed have more abundant mRNA in the SN

region, suggesting that PKC $\delta$  is a unique kinase in the PKC family with a selectively high level of mRNA in the SN region.

### **Proteolytic activation of PKC $\delta$ in nigral dopaminergic neurons of mice**

The classic Parkinsonian toxin MPP<sup>+</sup> has been shown to induce oxidative stress and caspase activation in numerous *in vitro* and *in vivo* models of PD (Hartmann et al., 2000; Lee et al., 2000; Hartmann et al., 2001; Jenner, 2003). Our previous studies further demonstrated that PKC $\delta$  is proteolytically activated in a caspase-3 dependent manner, followed by MPP<sup>+</sup>-induced oxidative stress, and contributes to MPP<sup>+</sup>-induced apoptotic death of dopaminergic neuronal cells (Kaul et al., 2003). To examine whether MPP<sup>+</sup> also induces proteolytic activation of PKC $\delta$  in nigral dopaminergic neurons *in vivo*, mice were administered 30 mg/kg MPTP for 5d and the substantia nigra region was dissected. Dissected SN was then homogenized and proteins were separated by 10% SDS-PAGE. Anti-PKC $\delta$  antibody from Santa Cruz Biotechnology (Santa Cruz, CA) that recognizes the C-terminal epitope of PKC $\delta$  was employed for the detection of both native and cleaved PKC $\delta$  fragments. As shown in Figure 3A, cleaved PKC $\delta$  fragments (41/38KDa) were detected from whole tissue lysates of the SN region from MPTP treated mice. To demonstrate that proteolytic cleavage of PKC $\delta$  occurs in dopaminergic neurons, the presence of tyrosine hydroxylase (TH) was also examined and a clear TH band was detected on the immunoblot. The membrane was also reprobbed with anti- $\beta$ -actin antibody to equalize the protein loaded on the gel. After observing the proteolytic cleavage of PKC $\delta$ , we next examined the PKC $\delta$  kinase activity following MPTP administration. PKC $\delta$  was immunoprecipitated from whole lysate of the SN region in

control and MPTP treated mice and was evaluated in an *in vitro* kinase assay. As shown in Figure 3B, MPTP administration increases PKC $\delta$  kinase activity to 220% in comparison to untreated control mice, indicating that PKC $\delta$  is indeed proteolytically activated in mice administered MPTP.

**Cleavage resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM) attenuates MPP<sup>+</sup>-induced proteolytic cleavage of PKC $\delta$  in N27 cells and protects N27 cells from MPP<sup>+</sup>-induced apoptotic death**

RNAi mediated genetic loss-of-function analysis of PKC $\delta$  has demonstrated a promotional role of PKC $\delta$  in MPP<sup>+</sup>-induced degeneration of dopaminergic neurons in rat primary mesencephalic neuronal cultures (Yang et al., 2004). To determine whether the proteolytic cleavage of PKC $\delta$  is essential for its promotional role in MPP<sup>+</sup>-induced degeneration of dopaminergic neurons, PKC $\delta$  cleavage was blocked by using the cleavage resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM), and MPP<sup>+</sup>-induced apoptotic death of dopaminergic neuronal (N27) cells was examined. Dopaminergic neuronal (N27) cells were derived from rat mesencephalic dopaminergic neurons and established as an *in vitro* model of PD (Adams et al., 1996; Prasad et al., 1998). The expression level of PKC $\delta$  in N27 cells is comparable to the selectively high expression level of PKC $\delta$  in the SN region of rodent brain; thus, N27 cells are a relevant and valid *in vitro* model of PD with regard to the expression level of PKC $\delta$ . The expression level of PKC $\delta$  in dopaminergic neuronal (N27) cells was determined by the TaqMan probe based QRT-PCR method, and relative abundance of PKC $\delta$  mRNA in N27 cells was compared to that in the Ctx, St, and SN regions of rat brain (Ctx as the

calibrator). As shown in Figure 4A, the relative amounts of PKC $\delta$  mRNA in the three regions of rat brain are similar to those observed in mouse brain regions, i.e., SN > St > Ctx. The number of PKC $\delta$  mRNA copies in N27 cells is comparable to that in the SN region and is also significantly higher than that in the Ctx and St regions of rat brain. A stable N27 cell line that overexpresses PKC $\delta$ -CRM was generated via the ViraPower<sup>TM</sup> lentiviral expression system from Invitrogen. PKC $\delta$ -CRM contains a point mutation (D327A) in its caspase-3 recognition and cleavage motif which abolishes the cleavage of PKC $\delta$  by activated caspase-3 (Ghayur et al., 1996). As shown in Figure 4B, PKC $\delta$  cleavage was induced in the control cells at the 36 hr time point following MPP<sup>+</sup> exposure; however, cleavage of PKC $\delta$  was significantly abolished at the 36 hr time point following MPP<sup>+</sup> exposure in the PKC $\delta$ -CRM stably expressing N27 cells. The membrane was reprobbed with anti-V5 antibody to show the expression of exogenous PKC $\delta$ -CRM in PKC $\delta$ -CRM stably expressing N27 cells. The detailed mechanism of the dominant-negative effect of PKC $\delta$ -CRM in MPP<sup>+</sup>-induced cleavage of endogenous PKC $\delta$  is still under investigation. Some preliminary results suggest that overexpressed PKC $\delta$ -CRM can down-regulate the expression of endogenous PKC $\delta$ , as shown by RT-PCR (data not shown). The overexpressed PKC $\delta$ -CRM might also inhibit the feedback loop between PKC $\delta$  and caspase-3, resulting in the inhibition of continuous activation of caspase-3. Alternatively, the overexpressed PKC $\delta$ -CRM may simply out compete endogenous PKC $\delta$  for activated caspase-3, thus leaving endogenous PKC $\delta$  intact.

We next examined whether inhibition of caspase-3 mediated proteolytic cleavage of endogenous PKC $\delta$  by PKC $\delta$ -CRM protects N27 cells against MPP<sup>+</sup>-induced apoptotic cell death. In control cells, MPP<sup>+</sup> exposure for 42 hr induced an approximate 110% increase in

the DNA fragmentation level compared to untreated control cells; however, only a 30% increase in the DNA fragmentation level was induced in the PKC $\delta$ -CRM stably expressing N27 cells following MPP<sup>+</sup> exposure for 42 hr in comparison to untreated control cells (Figure 4C). The overexpression of PKC $\delta$ -CRM did not induce any DNA fragmentation (data presented in another manuscript). These results clearly show that the caspase-3 mediated proteolytic cleavage of PKC $\delta$  following MPP<sup>+</sup> exposure is required for PKC $\delta$ 's pro-apoptotic function in MPP<sup>+</sup>-induced apoptotic death of dopaminergic neuronal cells.

#### **Cleavage resistant mutant of PKC $\delta$ (PKC $\delta$ -CRM) protects primary dopaminergic neurons from MPP<sup>+</sup>-induced degeneration**

We next tested whether PKC $\delta$ -CRM also protects primary dopaminergic neurons against MPP<sup>+</sup>-induced degeneration. Rat primary mesencephalic neuronal cultures were first transfected with pLenti/PKC $\delta$ -CRM by electroporation and then exposed to 10  $\mu$ M MPP<sup>+</sup> for 48 hr. Because of the presence of the V5 epitope in the C-terminal of pLenti/PCK $\delta$ -CRM, double immunostaining of TH and V5 was performed to identify dopaminergic neurons and the expression of exogenous PKC $\delta$ -CRM in dopaminergic neurons. The morphology of TH positive neurons among different groups is presented in Figure 5A. This particular dopaminergic neuron is intact and has long, multiple-branched neuronal processes in control cells, as revealed by TH immunoreactivity. Treatment with 10  $\mu$ M MPP<sup>+</sup> for 48 hr substantially decreased the neuronal processes and induced shrinkage of the cell body. However, the same MPP<sup>+</sup> treatment did not cause any significant degeneration of dopaminergic neurons in pLenti/PKC $\delta$ -CRM transfected primary neuronal cultures. The

morphology of this TH positive neuron is also intact with long, multiple-branched neuronal processes. The expression of PKC $\delta$ -CRM in TH positive neurons was revealed by V5 immunoreactivity (Figure 5B), and this particular TH positive neuron also has normal morphology following treatment with 10  $\mu$ M MPP<sup>+</sup> for 48 hr. Expressed PKC $\delta$ -CRM is primarily localized in the cytoplasm, where it co-localizes with TH (Figure 5B). This is consistent with the results in Figure 1.

The detection of clear V5 immunoreactivity in TH positive neurons indicates PKC $\delta$ -CRM was indeed transfected into dopaminergic neurons. The transfection efficiency of PKC $\delta$ -CRM into TH positive neurons is 55%, as calculated from the number of total TH positive neurons and the number of TH and V5 double positive neurons. The TH positive neurons and their neuronal processes were employed to evaluate the effect of PKC $\delta$ -CRM on MPP<sup>+</sup>-induced degeneration of dopaminergic neurons, since quantification of TH positive neurons is considered to be a reliable method of determining MPP<sup>+</sup>-induced dopaminergic toxicity in primary mesencephalic cultures (Choi et al., 1999; Callier et al., 2002). After counting the number of TH positive neurons and measuring their neuronal processes in multiple fields (about 5000 cells in each group), the effect of PKC $\delta$ -CRM on MPP<sup>+</sup>-induced degeneration of dopaminergic neurons was quantified and presented in Figure 5C&D. Treatment with 10  $\mu$ M MPP<sup>+</sup> for 48 hr substantially decreased the number of TH positive neurons by over 80% as compared to untreated control cells (Fig. 5C). However, MPP<sup>+</sup>-induced loss of TH<sup>+</sup> neurons was significantly reduced to 20% in PKC $\delta$ -CRM-transfected primary neuronal cultures, demonstrating a significant neuroprotective effect of PKC $\delta$ -CRM. PKC $\delta$ -CRM not only protects the number of TH positive neurons, but also protects the

neuronal processes of TH positive neurons from MPP<sup>+</sup>-induced degeneration. As shown in Figure 5D, 10  $\mu$ M MPP<sup>+</sup> exposure for 48 hr causes 83% loss of neuronal processes in TH positive neurons as compared to the control; however, only a 20% loss of neuronal processes in TH positive neurons was found in PKC $\delta$ -CRM-transfected primary neuronal cultures. Together, these results demonstrate that inhibition of endogenous PKC $\delta$  cleavage by PKC $\delta$ -CRM significantly protects dopaminergic neurons from MPP<sup>+</sup>-induced degeneration.

### **Catalytic fragment of PKC $\delta$ (PKC $\delta$ -CF) directly induces degeneration of primary dopaminergic neurons**

Proteolytic cleavage of PKC $\delta$  removes the pseudosubstrate bound to the catalytic site, leading to the persistent activation of the kinase (Emoto et al., 1995). The proteolytic activation of PKC $\delta$  has been associated with apoptotic death induced by various stimuli in different cells (Brodie and Blumberg, 2003; Kanthasamy et al., 2003). The exogenously introduced PKC $\delta$ -CF has also been shown to directly induce apoptosis in some cells (DeVries et al., 2002). However, whether PKC $\delta$ -CF directly induces the degeneration of dopaminergic neurons in primary neuronal cultures is not known. pLenti/PKC $\delta$ -CF expressing the catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF) was directly transfected into the rat primary neuronal cultures by electroporation. pLenti/PKC $\delta$ -RF, which expresses the regulatory fragment of PKC $\delta$  (PKC $\delta$ -RF), was also transfected into the primary neuronal culture to serve as control for PKC $\delta$ -CF. Double immunostaining of TH and V5 was performed at 48 hr post-transfection to evaluate the degeneration of dopaminergic neurons and examine the expression of PKC $\delta$ -CF or PKC $\delta$ -RF in primary dopaminergic neurons.

neuronal processes of TH positive neurons from MPP<sup>+</sup>-induced degeneration. As shown in Figure 5D, 10  $\mu$ M MPP<sup>+</sup> exposure for 48 hr causes 83% loss of neuronal processes in TH positive neurons as compared to the control; however, only a 20% loss of neuronal processes in TH positive neurons was found in PKC $\delta$ -CRM-transfected primary neuronal cultures. Together, these results demonstrate that inhibition of endogenous PKC $\delta$  cleavage by PKC $\delta$ -CRM significantly protects dopaminergic neurons from MPP<sup>+</sup>-induced degeneration.

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Representative TH positive neurons expressing either PKC $\delta$ -CF or PKC $\delta$ -RF were presented in Figure 6A. Neurons expressing PKC $\delta$ -RF have normal morphology and extended neuronal processes; however, TH positive neurons that express PKC $\delta$ -CF have a shrunken cell body and very short neuronal processes, similar to the morphology of the degenerated dopaminergic neuron induced by MPP<sup>+</sup> (Figure 5A). To quantify the effect of PKC $\delta$ -CF on the degeneration of dopaminergic neurons, the number of TH positive neurons was counted in multiple fields among different groups (about 5000 cells observed in each group). Quantitative analysis of the number of TH positive neurons in PKC $\delta$ -CF and PKC $\delta$ -RF transfected primary neuronal cultures is presented in Figure 6B. The number of TH positive neurons was only slightly less (10%) in PKC $\delta$ -RF transfected primary neuronal cultures than in control cells, while the number of TH positive neurons in PKC $\delta$ -CF transfected primary neuronal cultures was dramatically less (60%) than in control cells. These results clearly demonstrate that PKC $\delta$ -CF itself is toxic and directly induces degeneration of dopaminergic neurons in rat primary neuronal cultures.

## DISCUSSION

In the present study, we investigated the expression level of different PKC isoforms in the cortex, striatum, and substantia nigra regions of rodent brains and demonstrated that the substantia nigra region of rodent brains has a higher level of PKC $\delta$  protein and mRNA as compared to that in the cortex and striatum regions. To our knowledge, this is the first report investigating the expression level of PKC isoforms in the substantia nigral dopaminergic

neurons of rodent brains. Our results also demonstrate, for the first time, that administration of the Parkinsonian toxin MPTP to mice induces *in vivo* proteolytic activation of PKC $\delta$  in the substantia nigra region. By employing PKC $\delta$ <sup>-/-</sup> mice, the cleavage resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM), and the catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF), our studies clearly suggest that proteolytic activation of PKC $\delta$  is an essential downstream event in the degenerative process in nigral dopaminergic neurons in the MPTP mouse model of Parkinson's disease.

The Parkinsonian toxin MPTP has been shown to be a potent mitochondrial complex I inhibitor (Fritz et al., 1985; Singer et al., 1988; Marini et al., 1989). In the brain, MPTP is metabolized to its active form, MPP<sup>+</sup>, and selectively accumulates in dopaminergic neurons through the dopamine transporter (DAT) (Uhl et al., 1985; Mayer et al., 1986). The MPP<sup>+</sup>-induced inhibition of mitochondrial complex I leads to the massive production of reactive oxygen species (ROS) (Cassarino et al., 1997), which subsequently initiates a series of apoptotic events, including mitochondrial dysfunction, cytochrome C release, and activation of the major effector caspase, caspase-3, in dopaminergic neurons (Kaul et al., 2003; Vila and Przedborski, 2003). Recent *in vitro* studies further characterized that PKC $\delta$  is proteolytically activated by caspase-3 in dopaminergic neuronal cells exposed to MPP<sup>+</sup> (Kaul et al., 2003). PKC $\delta$  contains the caspase-3 cleavage motif located at the hinge region that connects the regulatory and catalytic fragments of PKC $\delta$ . The proteolytic cleavage of PKC $\delta$  by caspase-3 separates the inhibitory regulatory fragment from the catalytic fragment, thus persistently activating the kinase (Emoto et al., 1995; Reyland et al., 1999). The kinase active catalytic fragment of PKC $\delta$  itself is sufficient to induce cell death, as indicated by our previous study (manuscript under review) as well as several other studies (DeVries et al.,

2002; Ren et al., 2002; Basu, 2003). By employing the cleavage resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM) that abolishes the caspase-3 cleavage motif by point mutation D327A (DeVries et al., 2002)), we demonstrated that proteolytic cleavage of PKC $\delta$  is an essential downstream event in MPP<sup>+</sup>-induced degeneration of nigral dopaminergic neurons. In addition, we also showed that the exogenous expression of the kinase active catalytic fragment PKC $\delta$ -CF, but not the regulatory fragment PKC $\delta$ -RF, directly induces the degeneration of dopaminergic neurons.

Although the pathology of Parkinson's disease has been well characterized, we still do not know why nigral dopaminergic neurons are most severely degenerated in PD. Many studies have suggested that dopaminergic neurons are particularly susceptible to oxidative stress (Lotharius and Brundin, 2002), and the metabolism of the specific neurotransmitter dopamine generates many toxic free radicals, including dopamine-quinone species, superoxide radicals, and hydrogen peroxide in the cytosol of dopaminergic neurons (Graham, 1978). Redox active Fe<sup>2+</sup>, which contributes to the generation of hydroxyl radicals, was also selectively elevated in the SNc region of PD brains (Sofic et al., 1991; Jellinger, 2000), partially due to the enrichment of Fe<sup>2+</sup> by neuromelanin (NM) which is selectively localized in nigral dopaminergic neurons (Good et al., 1992; Zecca et al., 1994; Zecca et al., 2003). On the other hand, although genetic mutations of several genes, including  $\alpha$ -synuclein, Parkin, UCHL1, DJ-1, PINK1, and LRRK2, have been implicated in the pathogenesis of familial PD patients (Dawson and Dawson, 2003; Shen, 2004), it is not clear how nigral dopaminergic neurons are selectively affected by the loss of function of these genes.

Our studies showed that the oxidative stress sensitive pro-apoptotic kinase PKC $\delta$  is selectively abundant in nigral dopaminergic neurons. Because proteolytic cleavage of PKC $\delta$  is mediated by activated caspase-3, various apoptotic stresses, including oxidative stress, that trigger the mitochondrial dependent intrinsic pathway can activate caspase-3 and induce subsequent proteolytic cleavage of PKC $\delta$ . Thus, the selective abundance of PKC $\delta$  in nigral dopaminergic neurons could significantly increase cellular vulnerability due to the potentially easier and enhanced generation of pro-apoptotic cleaved activated fragments of PKC $\delta$ , and greatly facilitate oxidative stress-induced degeneration of nigral dopaminergic neurons. We also determined the expression level of other representative PKC isoforms, but found a relatively lower expression level of these isoforms, particularly PKC $\epsilon$  and PKC $\beta$ I, in nigral dopaminergic neurons. Interestingly, most studies indicate that PKC $\beta$ I and PKC $\epsilon$  are predominantly anti-apoptotic PKC kinases (Gutcher et al., 2003). The relatively lower expression level of anti-apoptotic PKC isoforms and the higher expression level of pro-apoptotic PKC $\delta$  in nigral dopaminergic neurons suggest that the expression level of these PKC isoforms potentially contributes to the susceptibility of nigral dopaminergic neurons in Parkinson's disease.

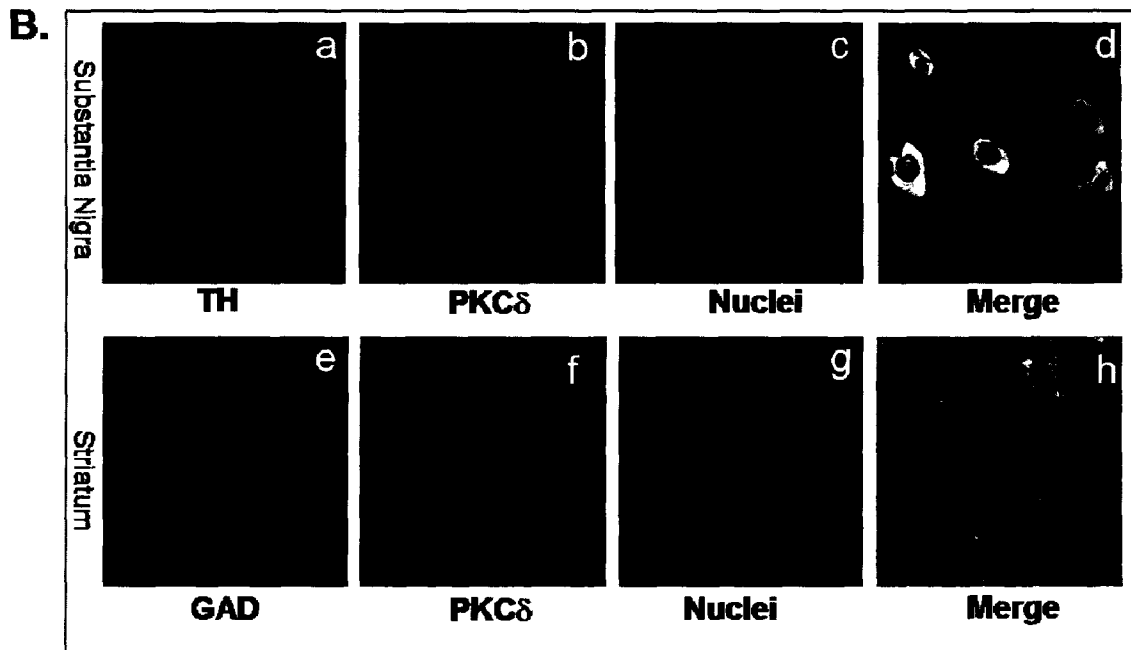
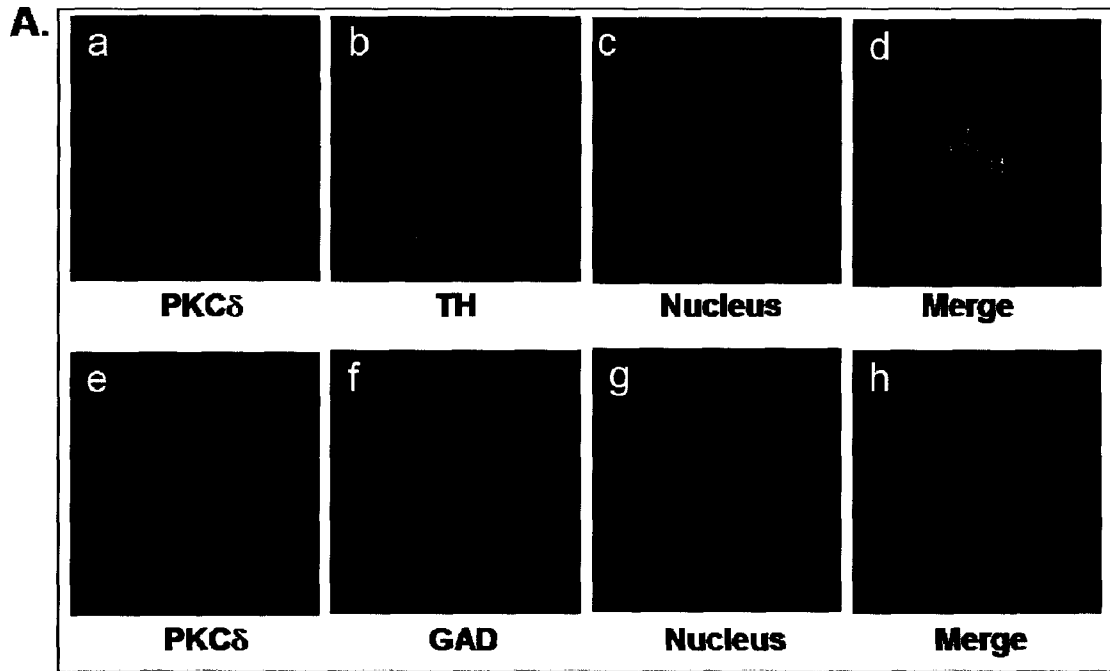
Interestingly, abundant levels of PKC $\delta$  were also found to co-localize with TH, the rate-limiting enzyme in dopamine synthesis. TH is a substrate of various serine/threonine protein kinases, including cAMP-dependent protein kinase A (PKA) (Lovenberg et al., 1975), cGMP-dependent protein kinase G (PKG) (Roskoski et al., 1987), protein kinase C (PKC) (Albert et al., 1984), Ca<sup>2+</sup>-calmodulin dependent protein kinase II (CaMKII) (Vulliet et al., 1984), extracellular signal-related kinase (ERK1/2) (Sutherland et al., 1993), and the recently

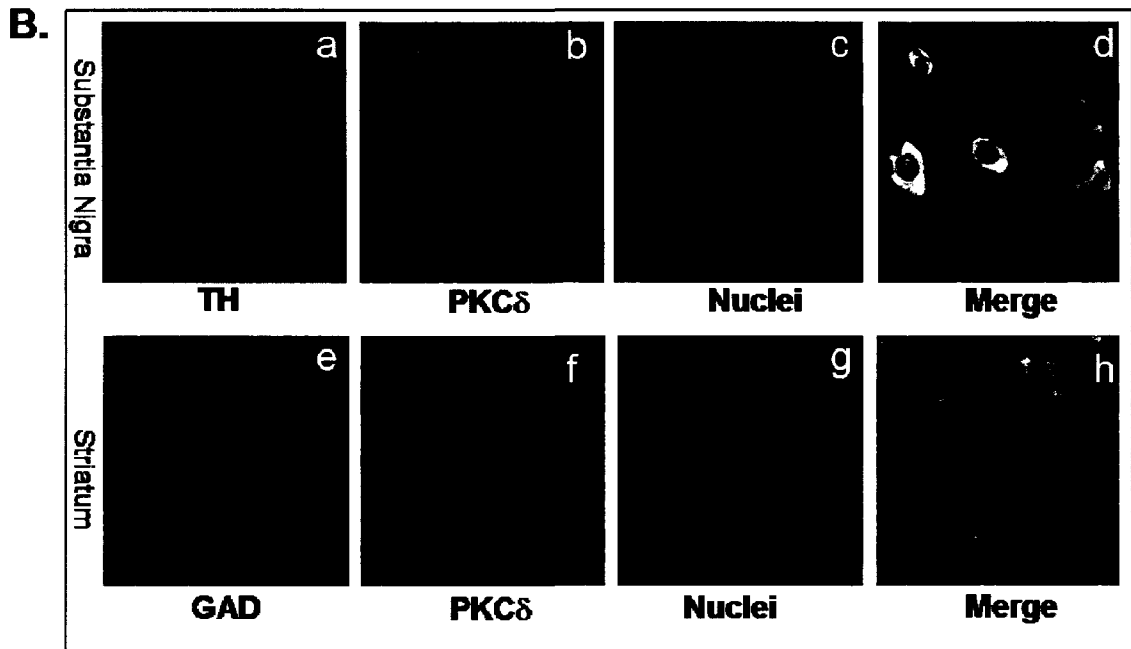
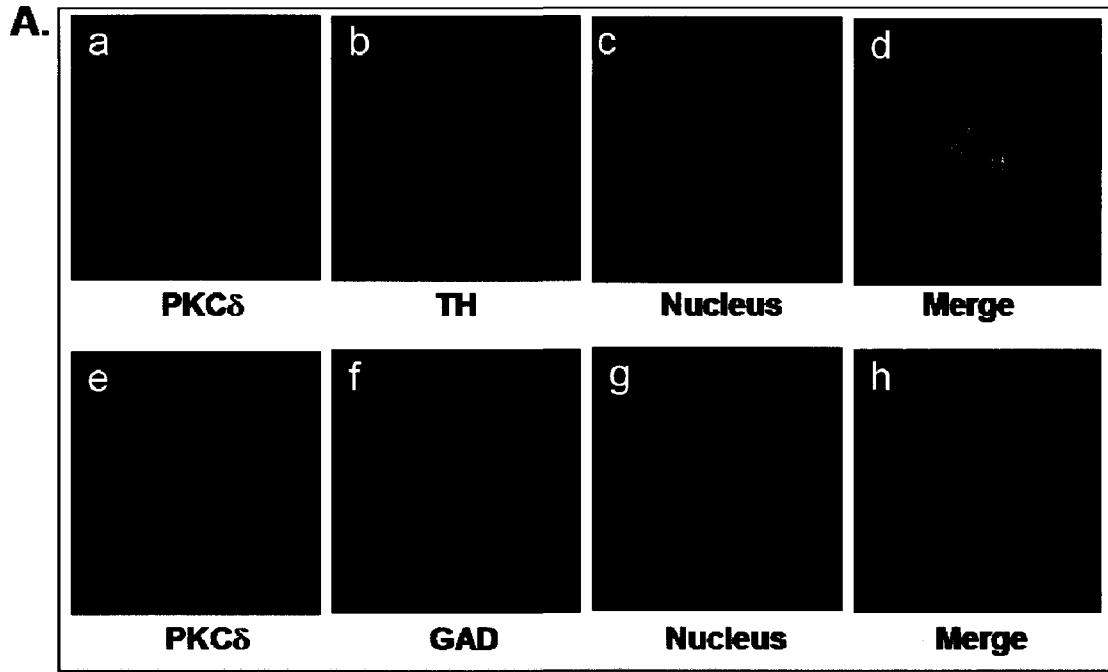
identified cyclin-dependent protein kinase 5 (Cdk5) (Moy and Tsai, 2004). Phosphorylation status of TH is closely associated with its activity and the synthesis of dopamine in dopaminergic neurons (Dunkley et al., 2004). Studies are underway to elucidate the interaction of PKC $\delta$  with TH and the potential regulatory role of PKC $\delta$  in TH phosphorylation and activity.

In summary, we demonstrate that MPTP administration induces *in vivo* proteolytic activation of PKC $\delta$  in nigral dopaminergic neurons, and proteolytic activation of PKC $\delta$  is an essential downstream event following caspase-3 activation in MPTP-induced degeneration of nigral dopaminergic neurons. Our studies suggest that the characterization of downstream apoptotic molecules in experimental models of PD is important to better understand the pathogenesis of this neurodegenerative disorder.

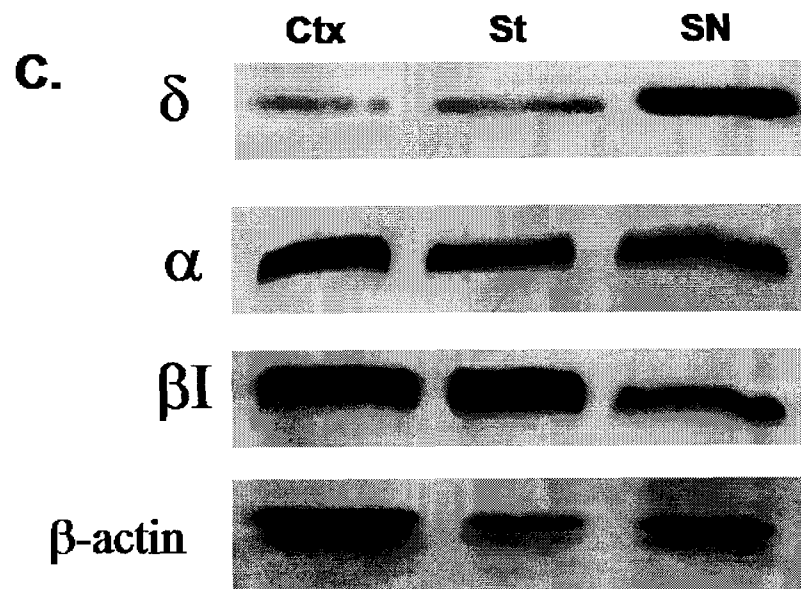
**Figure 1: Selectively high expression of PKC $\delta$  protein in nigral dopaminergic neurons**

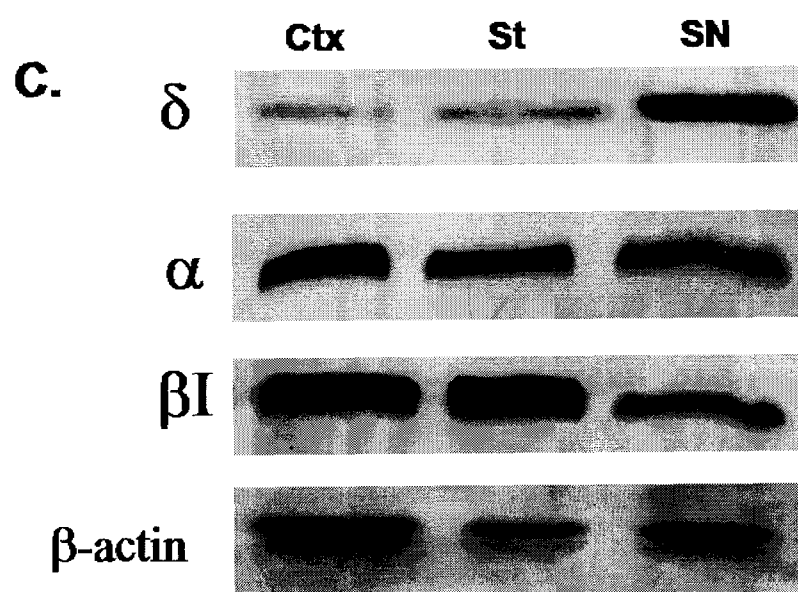
(A) Immunostaining of PKC $\delta$  in dopaminergic and GABAergic neurons in rat primary mesencephalic neuronal cultures. (B) Immunostaining of PKC $\delta$  in dopaminergic and GABAergic neurons in brain sections of mice substantia nigra (SN) and striatum (St). Double immunostaining of PKC $\delta$  with TH or GAD in primary neuronal cultures or brain sections was performed sequentially. Mouse anti-TH, mouse anti-GAD antibody (1:1000) and rabbit anti-PKC $\delta$  antibody (1:1000) were used. Stained cells and sections were observed under a TCS/NT confocal microscopy system (Leica, Bannockburn, IL). (C) Protein level of PKC isoforms in cortex (Ctx), substantia nigra (SN), and striatum (St) of mice brains. Whole tissue lysates were prepared after Ctx, SN, and St regions were carefully dissected and separated by 10% SDS-PAGE.





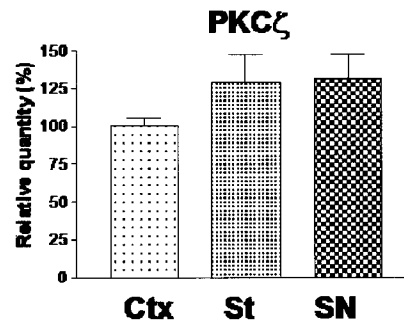
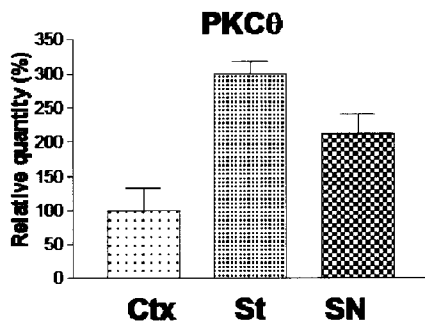
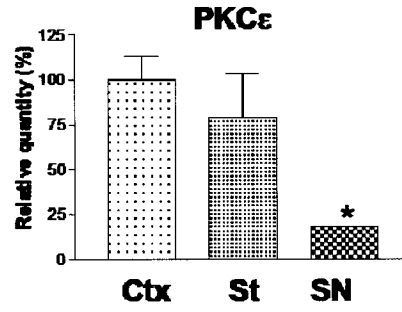
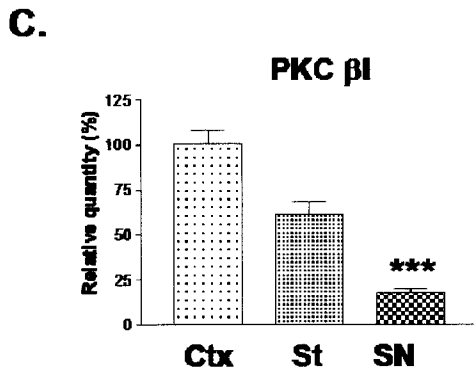
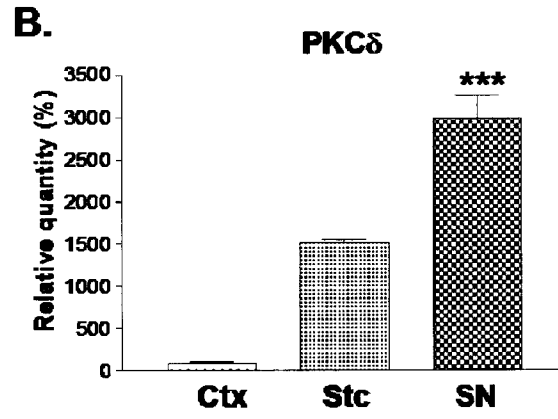
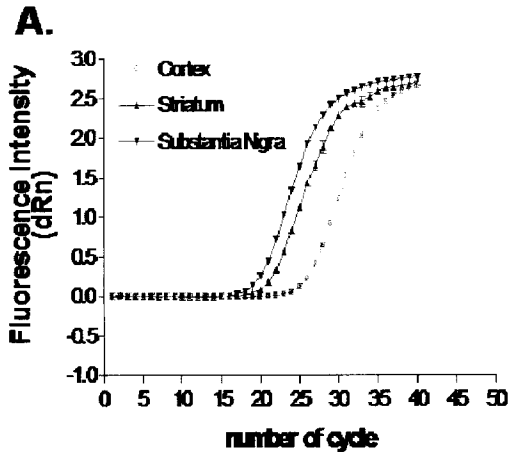






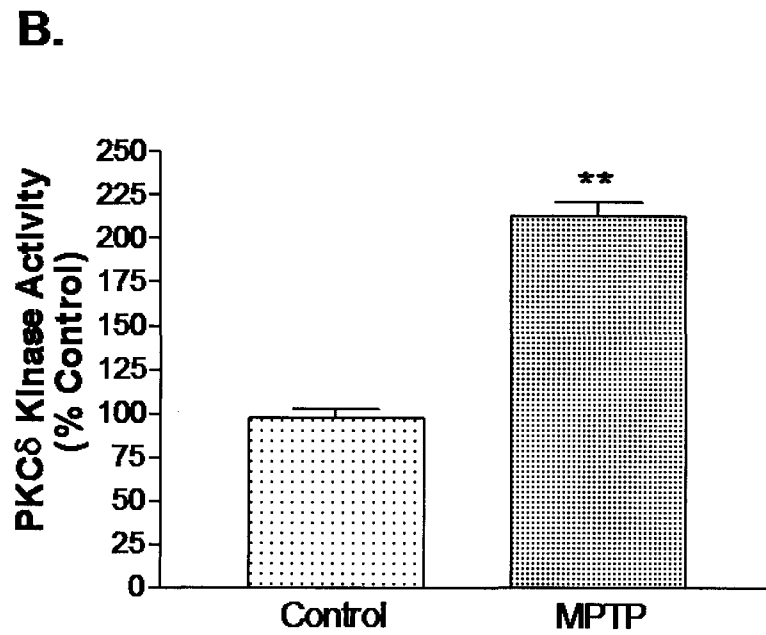
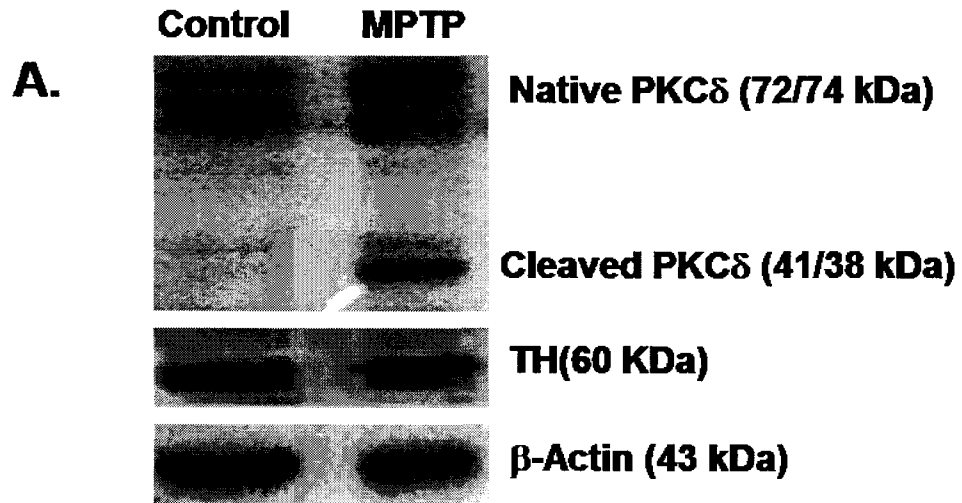
**Figure 2: Relative quantity of the mRNA level of PKC isoforms in different regions of mice brains**

(A) Amplification plot of PKC $\delta$  mRNA among SN (red), St (blue), and Ctx (green) regions of mice brains. (B) Relative PKC $\delta$  mRNA level among SN, St, and Ctx regions of mice brains. (C) Relative PKC $\beta$ I, PKC $\epsilon$ , PKC $\theta$ , and PKC $\zeta$  mRNA levels among SN, St, and Ctx regions of mice brains. Total RNA extracted from the SN, St, and Ctx regions of mice brains was converted into cDNA. For the QRT-PCR of PKC $\delta$ , PKC $\epsilon$ , and PKC $\theta$ , a TaqMan probe based method was used; for the QRT-PCR of PKC $\beta$ I and PKC $\zeta$ , a SYBR green based method was used. 18s Ribosome RNA (18s rRNA) was employed as an endogenous control to normalize the RNA used in QRT-PCR. The relative PKC isoform mRNA levels among the SN, St, and Ctx regions were calculated from the formula  $2^{-(\Delta C_t \text{ PKC} - \Delta C_t \text{ 18s rRNA})}$  and the Ct value in the cortex was always used as the calibrator. The data represent the mean  $\pm$  SEM from two separate experiments in triplicate (\*,  $p < 0.05$ ; \*\*\*,  $p < 0.001$ ; N=6).



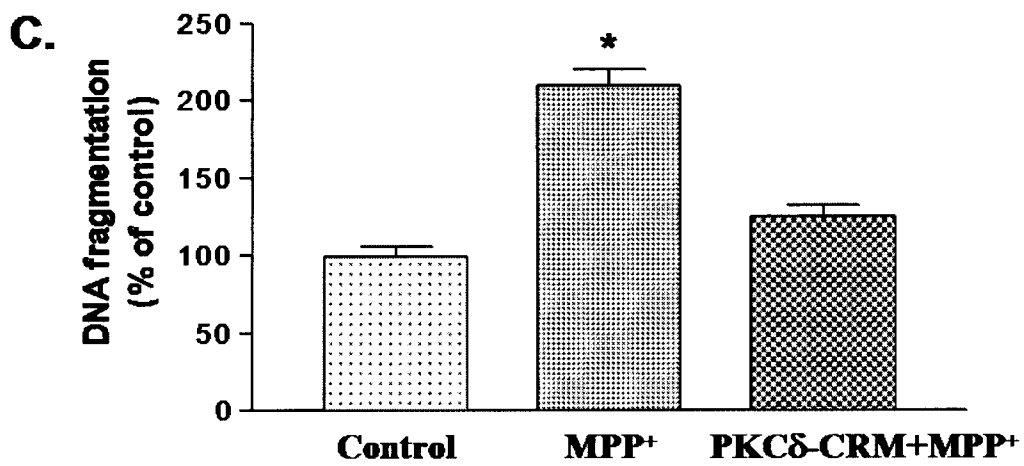
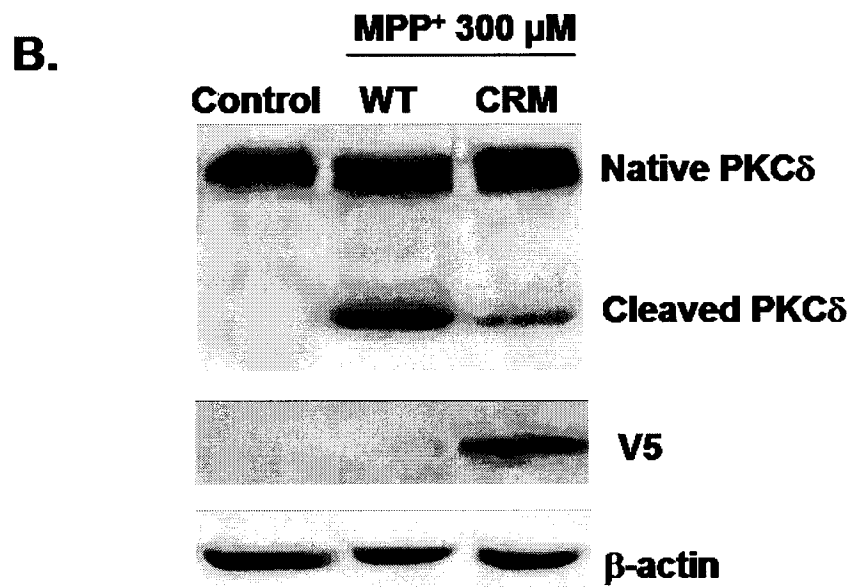
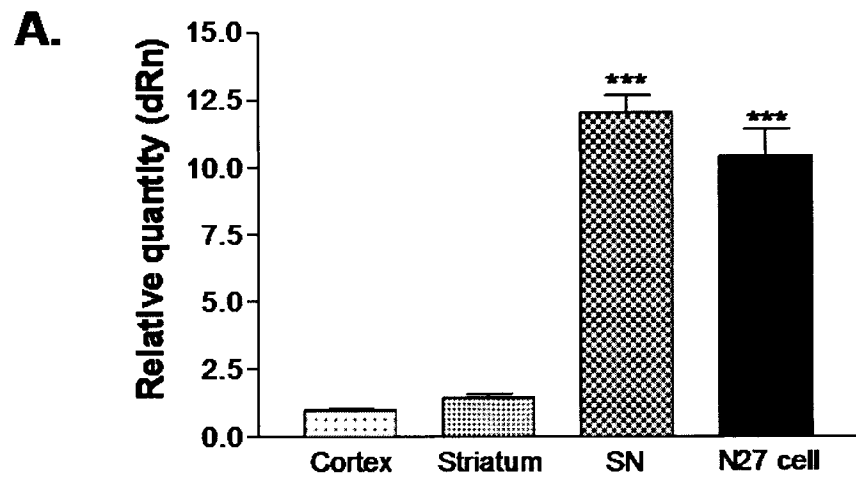
**Figure 3: MPTP administration induces proteolytic activation of PKC $\delta$  in the substantia nigra region of mice brains**

(A) Proteolytic cleavage of PKC $\delta$  in the substantia nigra region of mice brains following MPTP administration for 5d. (B) Increased PKC $\delta$  kinase activity in the substantia nigra region of mice brains following MPTP administration for 5d. MPTP was administered at a dose of 30 mg/kg intraperitoneally to mice (n=6) every day for five doses. Control mice (n=6) were treated with an equal volume of ddH<sub>2</sub>O. All animals were sacrificed the day after the last injection. The data represent the mean  $\pm$  SEM from two separate experiments in triplicate (\*\*, p<0.01; N=6).



**Figure 4: Cleavage resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM) protects N27 cells from MPP<sup>+</sup>-induced apoptotic death**

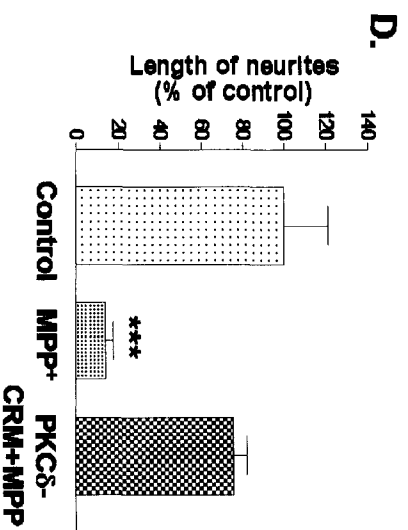
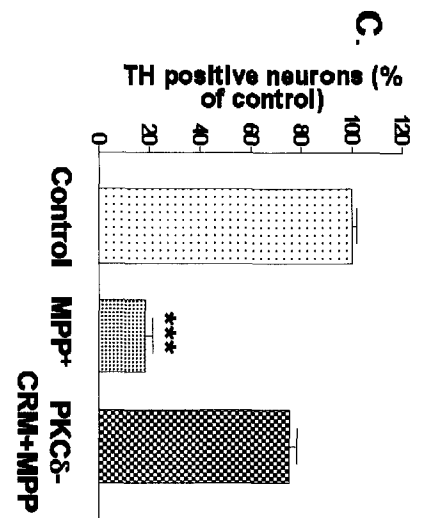
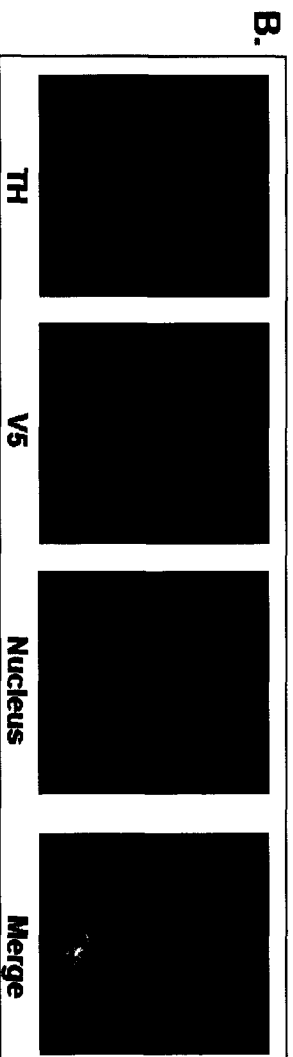
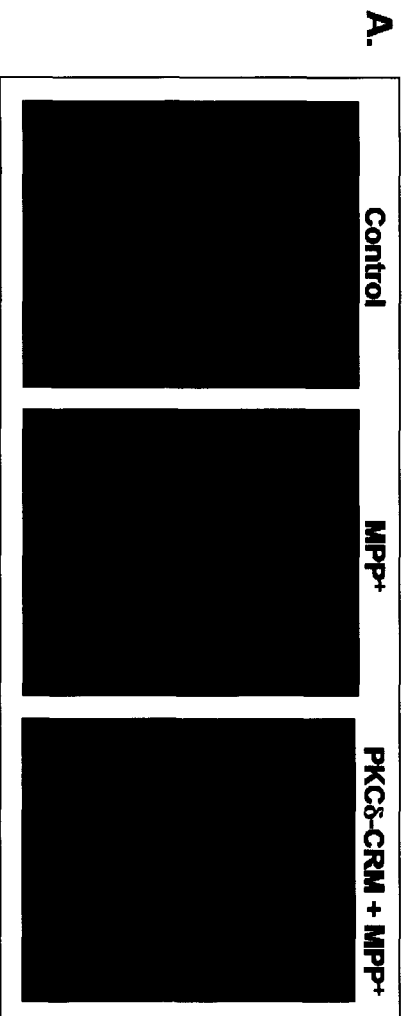
(A) Relative quantity of PKC $\delta$  mRNA in N27 cells and in the SN, St, and Ctx regions of rat brains. The TaqMan based QRT-PCR method (rat PKC $\delta$  expression assay kit) was employed and 18s rRNA was used as an endogenous control. For comparison of the relative PKC $\delta$  mRNA levels, the Ct value of the Ctx sample was used as the calibrator. (B) MPP<sup>+</sup>-induced PKC $\delta$  cleavage was abolished in PKC $\delta$ -CRM stably expressing cells. Control cells and PKC $\delta$ -CRM stably expressing cells were treated with 300  $\mu$ M MPP<sup>+</sup> for 36 hr. The cells were lysed and whole cell lysate was used for immunoblot analysis to detect the PKC $\delta$  cleavage. The membrane was reprobed with anti-V5 antibody (1:5000) to ensure the expression of PKC $\delta$ -CRM in the PKC $\delta$ -CRM stably expressing N27 cell line. (C) PKC $\delta$ -CRM protects against MPP<sup>+</sup>-induced apoptotic death in N27 cells. The data represent the mean  $\pm$  SEM from two separate experiments in triplicate (\*,  $p < 0.05$ ; \*\*\*,  $p < 0.001$ ; N=6).

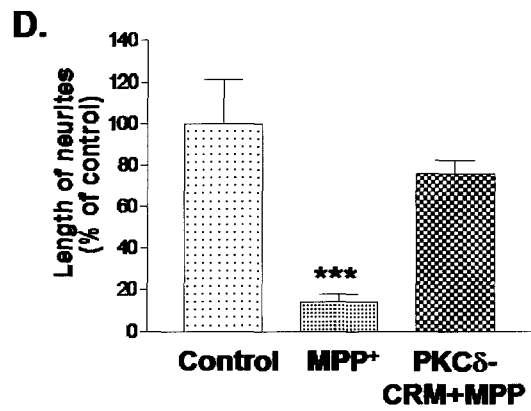
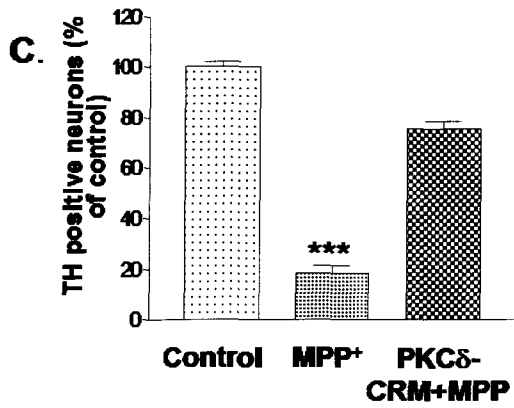
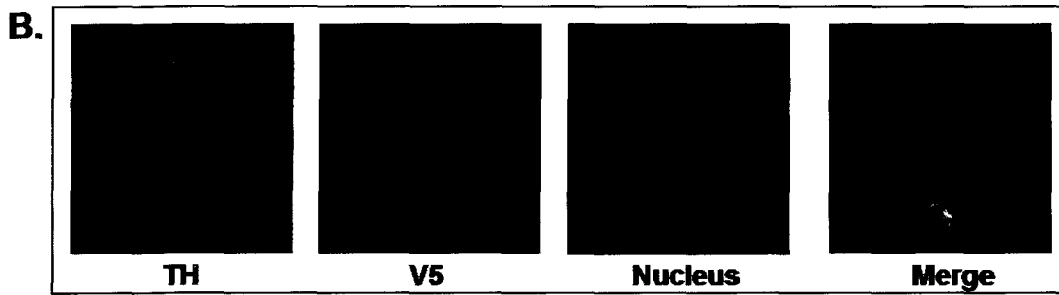
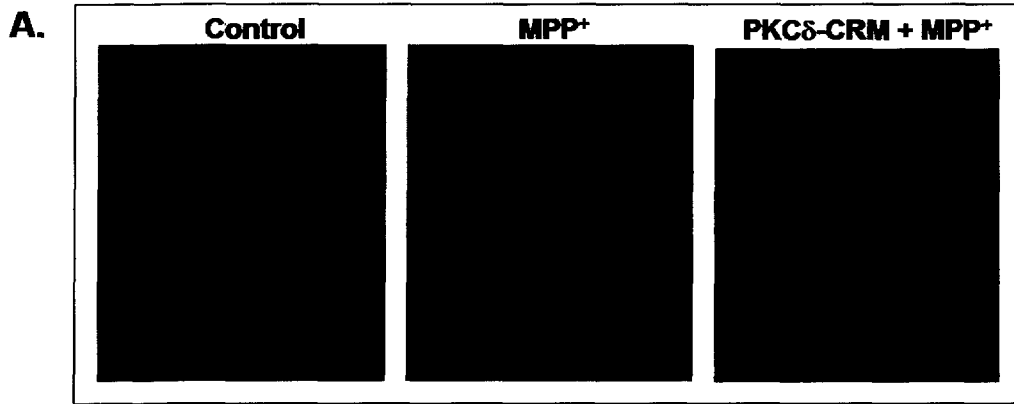


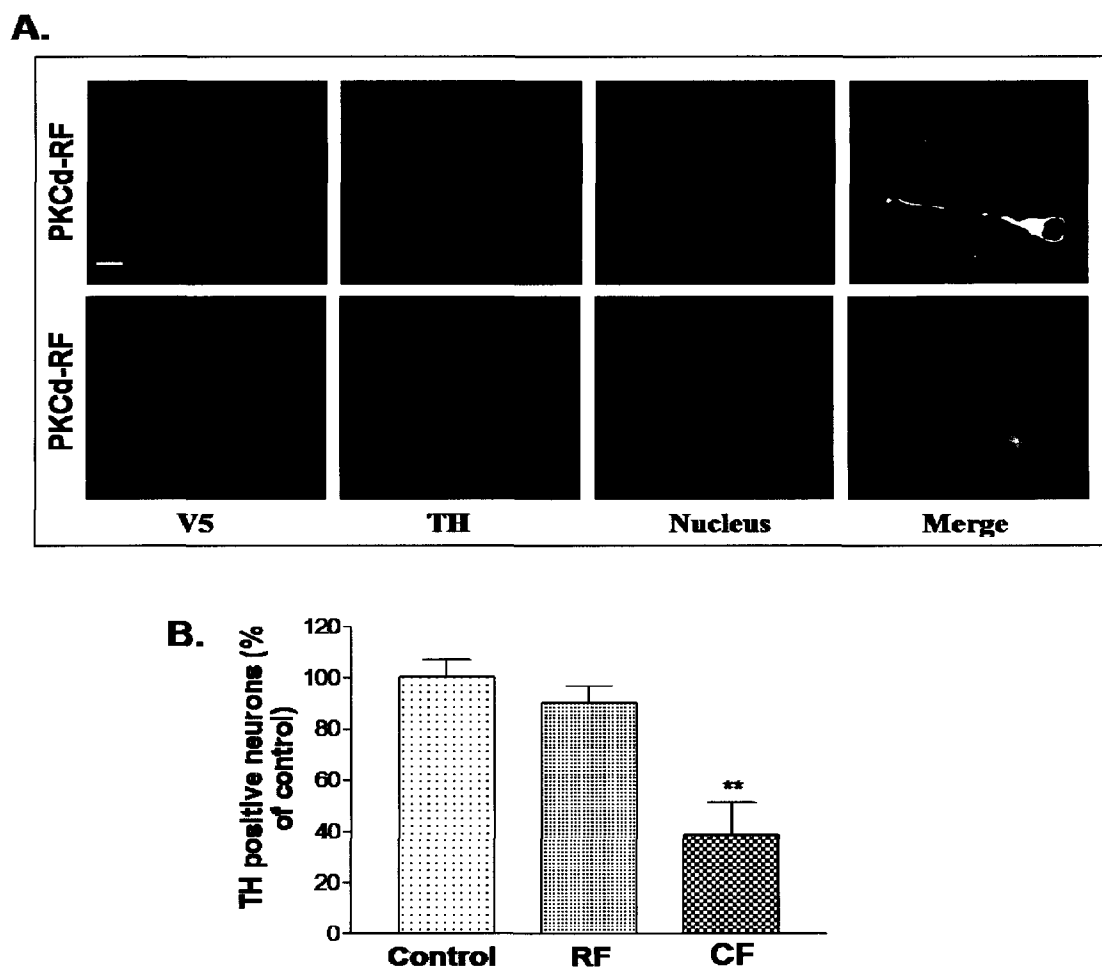


**Figure 5: Cleavage resistant mutant of PKC $\delta$  (PKC $\delta$ -CRM) protects primary dopaminergic neurons from MPP $^+$ -induced apoptotic death**

(A) Morphology of representative TH positive neurons from MPP $^+$ -treated groups with or without pre-transfection of PKC $\delta$ -CRM, and control group. Cells were observed under a Nikon inverted fluorescence microscope (Model TE-2000U). (B) Expression of PKC $\delta$ -CRM in the TH positive neurons of rat primary mesencephalic neuronal cultures. At 24 hr post-transfection of PKC $\delta$ -CRM, primary neuronal cultures were treated with 10  $\mu$ M MPP $^+$  for another 48 hr. Double immunostaining of TH (rabbit anti-TH antibody) and V5 (mouse anti-V5 antibody) was performed sequentially after treatment. Cells were observed under a TCS/NT confocal microscopy system (Leica, Bannockburn, IL). (C) Quantitative analysis of the number of TH positive neurons following PKC $\delta$ -CRM transfection and MPP $^+$  treatment. (D) Quantitative analysis of the neuronal processes of TH positive neurons following PKC $\delta$ -CRM transfection and MPP $^+$  treatment. After PKC $\delta$ -CRM transfection, cells were exposed to 10  $\mu$ M MPP $^+$  for 48 hr and then TH positive neurons were identified using anti-TH antibody exposure. The number of TH positive neurons was counted in multiple fields (total 5000 cells) and their neuronal processes were measured in MetaMorph 5.07. Data represent the mean  $\pm$  SEM from two separate experiments in triplicate (\*\*\*,  $p < 0.001$ ;  $N = 6$ ).







**Figure 6: Catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF) directly induces the degeneration of dopaminergic neurons in rat primary neuronal cultures**

(A) Morphology of representative TH positive neurons in PKC $\delta$ -RF or PKC $\delta$ -CF transfected primary neuronal cultures. (B) Quantitative analysis of the number of TH positive neurons following PKC $\delta$ -CF or PKC $\delta$ -RF transfection. Double immunostaining of TH (rabbit anti-TH antibody) and V5 (mouse anti-V5 antibody) was performed 48 hr post-transfection of PKC $\delta$ -CF or PKC $\delta$ -RF. Cells were observed under a TCS/NT confocal microscopy system (Leica, Bannockburn, IL). Data represent the mean  $\pm$  SEM from two separate experiments in triplicate (\*\*,  $p < 0.01$ ;  $N = 6$ ).

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## CHAPTER VI: GENERAL CONCLUSIONS

The major findings of my research described in the dissertation have already been discussed in the discussion sections of each chapter. The overall conclusions derived from these studies and integral mechanisms of PKC $\delta$  in neurotoxin-induced apoptotic death of dopaminergic neurons and relevance to the pathogenesis of Parkinson's disease (PD) will be discussed here.

### **Selectively high expression of oxidative stress sensitive kinase PKC $\delta$ contributes to the vulnerability of nigral dopaminergic neurons to neurotoxin-induced degeneration**

Nigral dopaminergic neurons are most severely degenerated in Parkinson's disease partially due to the presence of dopamine in these neurons (Carlsson and Fornstedt, 1991; Hirsch et al., 1997). Dopaminergic neurons are persistently exposed to oxidative stress because metabolism of free cytosolic dopamine dramatically increases the generation of ROS. DAT and VMAT2 regulate the level of free cytosolic dopamine, and therefore, have been implicated in the selective vulnerability of dopaminergic neurons (Gonzalez-Hernandez et al., 2004; Uhl, 1998). In addition, other molecules related to oxidative stress, including neuromelanin (NM) and redox active Fe $^{2+}$ , are also selectively rich or elevated in nigral dopaminergic neurons (Good et al., 1992; Lotharius and Brundin, 2002; Zecca et al., 2003). In this study, we demonstrated that oxidative stress sensitive kinase PKC $\delta$  is selectively abundant in nigral dopaminergic neurons and co-localizes with TH, the rate-limiting enzyme in dopamine synthesis. Ongoing studies in our laboratory have demonstrated that abundant PKC $\delta$  normally inhibits TH activity to regulate dopamine synthesis. However, abundant

PKC $\delta$  becomes sensitive to neurotoxin-induced oxidative stress and is cleaved by caspase-3 in dopaminergic neuronal cells and in mice. In dopaminergic neuronal cells, we demonstrated that caspase-3 mediated cleavage of PKC $\delta$  releases the catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF), which further translocates to the nucleus. The PKC $\delta$ -CF serves as effector and promotes apoptotic death of dopaminergic neuronal cells by mediating the ser14 phosphorylation of histone H2B.

Proteolytic cleavage of PKC $\delta$  apparently serves as a switch that converts the physiologically important PKC $\delta$  in the regulation of TH activity and dopamine synthesis to a pro-apoptotic kinase promoting degeneration of dopaminergic neurons. Because proteolytic cleavage of PKC $\delta$  is mediated by activated caspase-3, various apoptotic stresses, including oxidative stress, which triggers the mitochondrial-dependent intrinsic pathway and subsequent activation of caspase-3, can activate this switch. A certain extent of oxidative stress and other apoptotic stresses are always present in the central nervous system (Halliwell, 1992; Jenner, 2003). The selective abundance of PKC $\delta$  could significantly increase the vulnerability of dopaminergic neurons to the same level of insults due to the potentially easier and increased generation of pro-apoptotic cleaved activated fragments of PKC $\delta$ .

### **Regulation of the nuclear localization of PKC $\delta$ by regulatory fragments through position obstacle effects in tertiary structure**

The function of some serine/threonine protein kinases in cells is closely related to their nuclear/cytoplasmic localization. For example, p21-activated kinase 2 (PAK2) is mainly localized in the cytoplasm and promotes cell survival; however, cleaved PAK2p34 is

localized in the nucleus and promotes cell death (Jakobi, 2004). The nuclear/cytoplasmic localization is mainly regulated by a nucleus localization signal (NLS)/nucleus export signal (NES) mediated nuclear import/export (Kaffman and O'Shea, 1999). NLS but not NES has been identified in the C-terminal of the catalytic fragment of PKC $\delta$  (DeVries et al., 2004); however, PKC $\delta$  is primarily localized in the cytoplasm in various cell types, including dopaminergic neuronal cells. The regulation of the nuclear localization of PKC $\delta$  is unknown. In dopaminergic neuronal cells, we demonstrated that the N- and C-terminals of PKC $\delta$  are in close proximity in the tertiary structure by FRET. By employing the C1 or C2-like domain deletion mutant of PKC $\delta$  (PKC $\delta$ - $\Delta$ C1 or PKC $\delta$ - $\Delta$ C2), we showed that deletion of the C2-like domain, but not the C1 domain, induces strong nuclear localization of PKC $\delta$ . Meanwhile, nuclear translocation of activated cleaved fragments of PKC $\delta$  generated from caspase-3-mediated proteolytic cleavage in response to neurotoxin exposure has been observed, and the exogenously expressed catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF) also primarily localizes to the nucleus. Although sequence analysis of the C2-like domain reveals a possible leucine-rich nuclear export signal (NES), the C2-like domain is not sensitive to the nuclear export inhibitor leptomycin B (Fornerod et al., 1997), suggesting that this leucine-rich motif is not a functional NES. Moreover, the human immunodeficiency virus (HIV) Rev chimera protein was generated by fusing the C2-like domain in the N-terminal of a NES deleted form of Rev, the RNA binding protein of HIV, which is still primarily localized in the cytoplasm. Our studies suggest that the N-terminal C2-like domain regulates the subcellular localization of PKC $\delta$  by masking the C-terminal NLS through the position obstacle in the tertiary structure, but not by employing NES or interacting with anchoring proteins. Our model is consistent

with the previously proposed tertiary conformation of PKC $\delta$ ; the pseudosubstrate in the middle of the N-terminal regulatory fragment binds to the catalytic site of the C-terminal catalytic fragment.

The presence of NLS is not sufficient but necessary, as shown in our study, to localize PKC $\delta$  into the nucleus. NLS could be normally kept in an incompetent status and converted to competent status in response to certain stimuli. The subcellular localization of kinases is critical for their close proximity to their activator or substrates; thus, the maintenance and regulation of competent status of NLS is important for their functions. In addition, the intra-molecular regulation provides more flexibility for kinases to self-regulate subcellular localization and functions.

In summary, we surveyed the expression of different isoforms of PKC in rodent brains and determined that PKC $\delta$  has the highest expression in the SNc dopaminergic neurons in rodent brains. We also characterized the molecular mechanisms of PKC $\delta$  in neurotoxin-induced apoptotic death of dopaminergic neuronal cells. Under normal physiological conditions, the highly expressed PKC $\delta$  interacts with tyrosine hydroxylase (TH) in dopaminergic neurons. The close proximity of the C2-like domain to the nuclear localization signal (NLS) provides the position obstacle to inhibit the recognition of the nuclear import receptor to the NLS and retains PKC $\delta$  in the cytoplasm. However, under stressful conditions, abundant PKC $\delta$  was proteolytically cleaved by caspase-3 activated by neurotoxin-induced oxidative stress to release the activated cleaved fragments of PKC $\delta$ . The proteolytic cleavage of PCK $\delta$  by caspase-3 serves as a switch to convert it from non-apoptotic to pro-apoptotic kinase and makes highly expressed PKC $\delta$  a potential inherent

factor for the vulnerability of dopaminergic neurons. The removal of the regulatory fragment from the catalytic fragment by cleavage also exposes the NLS and induces the nuclear translocation of the activated cleaved fragments of PKC $\delta$ . In the nucleus, we further demonstrated that activated PKC $\delta$  mediated the Ser14 phosphorylation of histone H2B, and the catalytic fragment of PKC $\delta$  (PKC $\delta$ -CF) itself induced the apoptosis of dopaminergic neuronal cells.



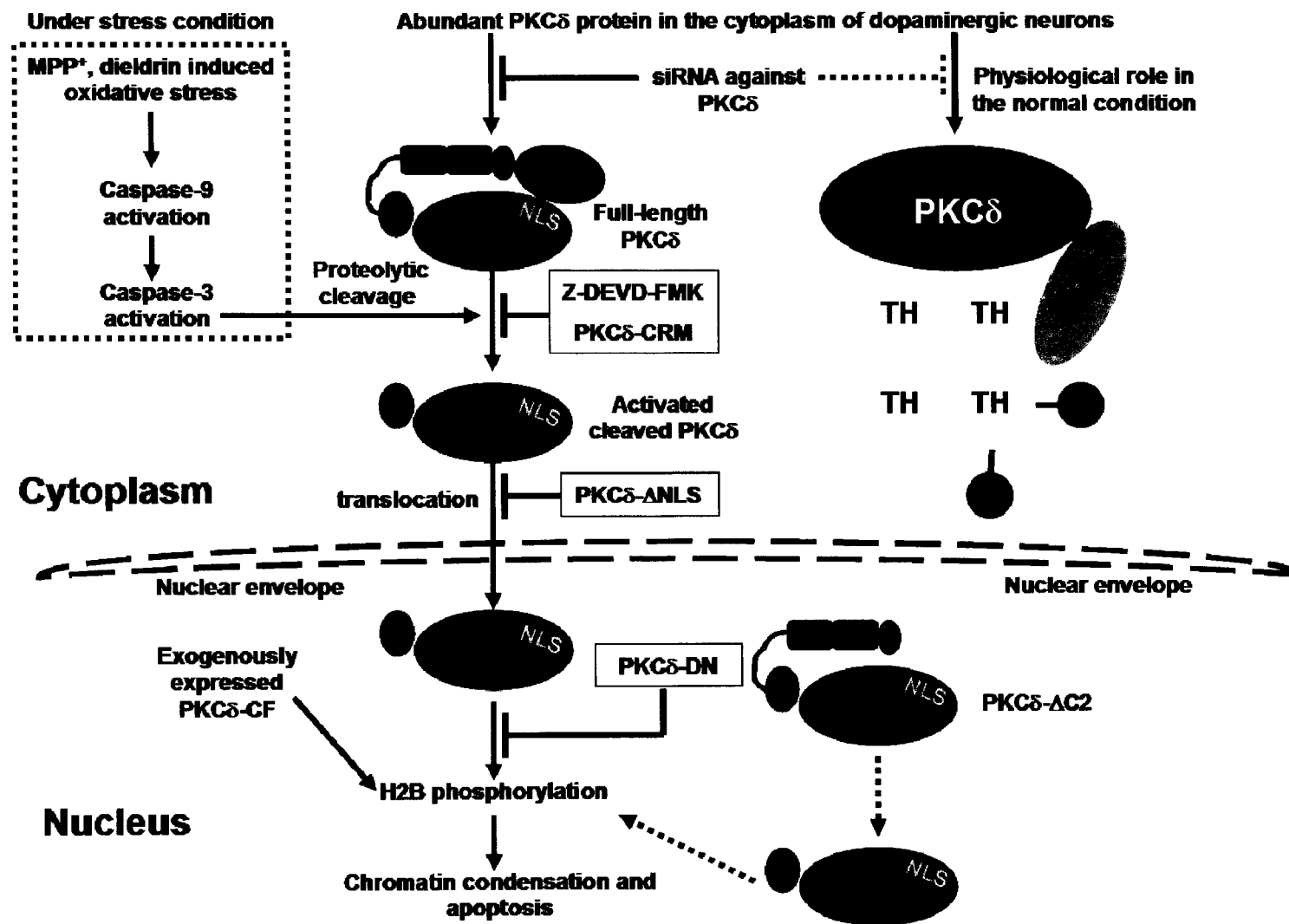


Figure 13. Integral mechanisms of PKCδ in neurotoxin-induced apoptotic death of dopaminergic neurons

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