



Published in final edited form as:

*Adv Biol Regul.* 2020 December ; 78: 100757. doi:10.1016/j.jbior.2020.100757.

## Functional proteomic analysis reveals roles for PKC $\delta$ in regulation of cell survival and cell death: Implications for cancer pathogenesis and therapy

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### Abstract

Protein Kinase C- $\delta$  (PKC $\delta$ ), regulates a broad group of biological functions and disease processes, including well-defined roles in immune function, cell survival and apoptosis. PKC $\delta$  primarily regulates apoptosis in normal tissues and non-transformed cells, and genetic disruption of the *PRKCD* gene in mice is protective in many diseases and tissue damage models. However pro-survival/pro-proliferative functions have also been described in some transformed cells and in mouse models of cancer. Recent evidence suggests that the contribution of PKC $\delta$  to specific cancers may depend in part on the oncogenic context of the tumor, consistent with its paradoxical role in cell survival and cell death. Here we will discuss what is currently known about biological functions of PKC $\delta$  and potential paradigms for PKC $\delta$  function in cancer. To further understand mechanisms of regulation by PKC $\delta$ , and to gain insight into the plasticity of PKC $\delta$  signaling, we have used functional proteomics to identify pathways that are dependent on PKC $\delta$ . Understanding how these distinct functions of PKC $\delta$  are regulated will be critical for the logical design of therapeutics to target this pathway.

### Keywords

Protein kinase C; functional proteomics; signal transduction; cancer; apoptosis; therapeutics

### 1. Introduction

Post-translational modification of proteins by phosphorylation contributes to the regulation of most, if not all, cellular functions (Cohen, 2002). Indeed, up to 30% of proteins are

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Declaration of interest: none

known to be phosphorylated by serine/threonine, tyrosine, or histidine kinases, and dephosphorylated by phosphatases that recognize these specific residues (Cohen, 2000). Changes in phosphorylation status are typically rapid but transient, enabling dynamic responses to the cellular environment through the regulation of protein activity, stability, and subcellular localization. As many protein kinases and phosphatases are widely expressed, rapid activation/inactivation of signaling complexes and cascades may help determine the specificity of cellular responses to a diverse set of stimuli.

Protein kinase regulation by cyclic nucleotide second messengers was first described by Fischer and Krebs in 1968 (Walsh et al., 1968). The identification of Protein Kinase C (PKC)<sup>1</sup> almost 10 years later expanded the paradigm to include Ca<sup>2+</sup> and lipids as kinase regulators and led to the identification of membrane lipids as signaling molecules (Inoue et al., 1977; Takai et al., 1977). Further studies have identified 10 PKC isoforms that can be subdivided into families based on their differential dependency on lipid second messengers and calcium for activation (Newton, 2001). The development of isoform specific *in vivo* and *in vitro* tools has revealed unique roles for this kinase family in the regulation of the DNA damage response and repair, immune function, neural plasticity, cell migration, proliferation, survival, apoptosis and metabolism (Antal et al., 2015; Reyland, M.E. and Jones, D. N., 2016). Surprisingly, these studies have shown that a given PKC isoform can participate in many different cellular pathways, allowing dynamic “re-wiring” in response to changes in the cellular environment.

Given their contribution to a wide variety of signaling cascades and biological functions, it is likely that PKC isoforms play important roles in a variety of human diseases, particularly in the context of cancer. Here we will discuss what is currently known about biological functions of PKC $\delta$  with an emphasis on how dysregulation of PKC $\delta$  may contribute to cancer. We will also discuss potential targets of PKC $\delta$  that we have recently identified using a functional proteomics approach, and address prospects for targeting PKC $\delta$  in human disease.

## 2. Insights into biological functions of PKC $\delta$ from *in vivo* studies

Studies in PKC $\delta$ <sup>-/-</sup> mice reveal prominent roles for this isoform in regulation of proliferation, immune function and apoptosis (Reyland, M.E. and Jones, D. N., 2016), while *in vitro* tools such as si/shRNA have identified PKC $\delta$ -dependent regulation of signaling pathways that contribute to these biological endpoints (Reyland, M.E. and Jones, D. N., 2016). PKC $\delta$ <sup>-/-</sup> mice appear to develop normally, although some developmental programs such as mammary gland development may be delayed (Allen-Petersen et al., 2010) and fertility is reduced (Ma et al., 2015). However, with age PKC $\delta$ <sup>-/-</sup> mice show significant defects in immune function and develop a lupus-like autoimmune disease (Mecklenbrauker et al., 2002; Miyamoto et al., 2002). Mechanistically, this has been linked to a defect in the establishment of B-cell tolerance and impaired clonal deletion of autoreactive B cells

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<sup>1</sup>**Abbreviations:** Protein Kinase C (PKC), Protein Kinase C- $\delta$  (PKC $\delta$ ), Ionizing Radiation (IR), Non-small Cell Lung Cancer (NSCLC), Tyrosine Kinase Inhibitor (TKI), Epidermal Growth Factor Receptor (EGFR), Extra-cellular regulated kinase (ERK), Mitogen Activated Protein Kinase (MAPK), DNA-damage- response (DDR), Ataxia Telangiectasia Mutated (ATM), Reverse Phase Protein Array (RPPA), Ingenuity Pathway Analysis (IPA).

(Banninger et al., 2011; Limnander et al., 2011; Mecklenbrauker et al., 2002; Miyamoto et al., 2002). Interestingly, the expression of a dominant negative form of PKC $\delta$  specifically in T cells can also induce a lupus-like autoimmune disease in mice (Gorelik et al., 2015), and in humans a similar phenotype has been described in a patient with a rare loss-of-function mutation in the *PRKCD* gene (Belot et al., 2013; Kuehn et al., 2013).

Many studies show that depletion of PKC $\delta$  can be protective in disease and tissue injury models in mice. This includes protection against diet-induced fatty liver disease (Greene et al., 2014), endotoxin induced lung injury (Chichger et al., 2012) and cytokine-stimulated death of pancreatic islet cells (Cantley et al., 2011). Inhibition of PKC $\delta$  also reduces amyloid- $\beta$  levels and Alzheimer disease associated-phenotypes in mice (Du et al., 2018) and protects dopaminergic neurons in a Parkinson disease model (Gordon et al., 2012; Jin et al., 2014). In addition, conditional knock-out of PKC $\delta$  in osteoclasts increases bone mass (Cremasco et al., 2012; Li et al., 2020). Mechanistically, many of these findings may be related to the well-known function of PKC $\delta$  in the regulation of cell death, including findings from our lab that demonstrate PKC $\delta^{-/-}$  mice are protected from ionizing radiation (IR)-induced apoptosis (Humphries et al., 2006).

While most studies suggest a pro-apoptotic function for PKC $\delta$  in normal tissues and non-transformed cells, PKC $\delta$  can clearly have pro-survival/pro-proliferative functions in some transformed cells and in mouse models of cancer. Indeed, depletion of PKC $\delta$  suppresses tumor formation in nearly all mouse models studied, providing firm evidence for a tumor-promoter function (Allen-Petersen et al., 2014; Mauro et al., 2010; Symonds et al., 2011). A more thorough understanding of the functional landscape of PKC $\delta$  is needed to shed light on the paradoxical and sometimes conflicting functions of PKC $\delta$  *in vivo*.

### 3. PKC $\delta$ and apoptosis

Dysregulation of apoptotic pathways contribute to tumor progression by increasing DNA instability and by promoting survival of tumor cells (Brown and Attardi, 2005; Zhivotovsky and Kroemer, 2004). Indeed, many anti-cancer therapeutics have been developed based on the principle of eliminating cancer cells through induction of apoptosis (Carneiro and El-Deiry, 2020; Jan and Chaudhry, 2019). Early studies from our lab and others established a requirement for PKC $\delta$  in response to a wide variety of cell damaging agents and under conditions where cell survival pathways are inhibited (Majumder et al., 2001; Matassa et al., 2001; Matassa et al., 2003). *In vivo*, salivary epithelial and smooth muscle cells isolated from PKC $\delta^{-/-}$  mice are resistant to apoptotic stimuli, and the salivary gland and thymus gland in PKC $\delta^{-/-}$  mice are protected from IR-induced damage (Allen-Petersen et al., 2010; Humphries et al., 2006; Leitges et al., 2001). A requirement for PKC $\delta$  for the induction of apoptosis by a wide variety of toxins suggests that it may be a global regulator of apoptosis. This perspective is supported by studies that show PKC $\delta$  depletion is protective in degenerative diseases where cell death contributes to pathogenesis, and in tissue injury models (Du et al., 2018; Gordon et al., 2012; Jin et al., 2014) (see section 2).

How PKC $\delta$  regulates apoptosis remains unclear, with evidence for both direct effects on the apoptotic machinery and indirect effects through integration with survival pathways and

pathways that regulate cellular responses to damage. Mechanistic studies from our lab show that PKC $\delta$  is required for loss of mitochondrial membrane potential in response to cell toxins and for downstream events including activation of caspase and DNA fragmentation (Matassa et al., 2001; Reyland et al., 1999). Activation of PKC $\delta$  is also important for apoptosis induced by death receptors, including TRAIL and TNF $\alpha$  (Gonzalez-Guerrico and Kazanietz, 2005; Gordon et al., 2012; Lee et al., 2018; Xu et al., 2012). For instance, phorbol ester-induced apoptosis in LNCaP prostate cancer cells requires PKC $\delta$  for secretion of death receptor ligands and transduction of apoptotic signals downstream of death receptors (Gonzalez-Guerrico and Kazanietz, 2005). Similarly, PKC $\delta$  can regulate death receptor expression in response to endoplasmic reticulum stress to induce apoptosis (Goncalves et al., 2018; Liu, C. et al., 2019).

Activation of PKC $\delta$  during apoptosis is tightly regulated by mechanisms that orchestrate translocation of PKC $\delta$  to specific subcellular areas in response to apoptotic stimuli. This can include the plasma membrane and other subcellular organelles, most notably the nucleus (Reyland, M.E. and Jones, D. N., 2016; Yoshida, 2008). Our laboratory has defined critical events that mediate nuclear accumulation of PKC $\delta$  in response to genotoxic damage including tyrosine phosphorylation and caspase cleavage (Reyland, M.E. and Jones, D. N., 2016). PKC $\delta$  has been also shown to localize to the mitochondria in response to apoptotic stimuli such as oxidative stress and ischemia (Li et al., 1999; Majumder et al., 2001; Majumder et al., 2000; Murriel et al., 2004; Qi and Mochly-Rosen, 2008), and to the Golgi in response to ceramide (Kajimoto et al., 2004). Knowledge of how PKC $\delta$  is activated by apoptotic stimuli has been exploited therapeutically to suppress tissue injury. For instance, the Mochly-Rosen lab has shown that peptides that inhibit PKC $\delta$  translocation to the plasma membrane can be used prior to an experimentally induced ischemic event in mice to significantly reduce damage and decrease apoptosis (Bright et al., 2004; Bright et al., 2007; Churchill and Mochly-Rosen, 2007; Churchill et al., 2009). These findings have also been reported in ischemia reperfusion-induced lung injury, in which inhibition of PKC $\delta$  using siRNA or a PKC $\delta$  inhibitor peptide reduces damage and apoptotic cell death (Kim et al., 2016). Likewise, we and others have shown that agents that inhibit the activation of PKC $\delta$  protect against IR-induced damage in mice (Wie et al., 2017) and cytotoxin-induced renal cell injury (Pabla et al., 2011). Similarly, splice variants of PKC $\delta$ , PKC $\delta$ IX and PKC $\delta$ II, which are caspase-3 resistant, have been shown to inhibit apoptosis and/or promote cell survival (Apostolatos et al., 2012; Patel et al., 2006; Patel et al., 2013).

### Regulation of apoptosis by PKC $\delta$

Potential substrates of PKC $\delta$  in apoptosis include heat shock proteins, kinases and phosphatases, cell cycle regulators, transcription factors, apoptotic regulators, DNA damage response (DDR) and DNA repair proteins (Reyland, M.E. and Jones, D. N., 2016). PKC $\delta$  has been shown to target Bcl-2 proteins, providing evidence for a direct effect on apoptotic pathways. For instance, PKC $\delta$  can induce apoptosis by facilitating dephosphorylation of the proapoptotic protein Bad (Murriel et al., 2004), and through enhancing activation of Bax and Bak (Choi et al., 2006). Several studies suggest that PKC $\delta$  can also regulate protein stability or degradation. For instance, PKC $\delta$  directly targets and down-regulates the anti-apoptotic protein Mcl-1 to trigger apoptosis (Sitailo et al., 2006), while it upregulates TAp63 to induce

apoptosis by increasing protein stability (Li et al., 2015). PKC $\delta$  has been shown to regulate mRNA 3' end processing of the BIK protein to induce apoptosis through a mechanism that requires PKC $\delta$  association with the Star-PAP processing complex (Li et al., 2012). Additional mechanisms of regulation by PKC $\delta$  may include binding to and sequestering proteins that either inhibit or promote apoptosis such as Smac, an antagonist of inhibitor-of-apoptosis-proteins (IAPs) (Holmgren et al., 2016; Masoumi et al., 2012).

Evidence supports an emerging role for PKC $\delta$  in activation of the DNA-damage- response (DDR) and DNA repair pathways. PKC $\delta$  can function upstream of the DNA damage sensors, nuclear DNA-PK and Ataxia Telangiectasia Mutated (ATM), suggesting a role for PKC $\delta$  in direct regulation of the DDR (Arango et al., 2012; Bharti et al., 1998; Soriano-Carot et al., 2014). In these studies blocking PKC $\delta$  activity inhibits the phosphorylation of ATM and histone H2AX, two key regulators of the DDR (Arango et al., 2012; Li et al., 2004). Other studies support a role for PKC $\delta$  in mediating G1 arrest through induction of p21 (Liu et al., 2007; Nakagawa et al., 2005; Perletti et al., 2005; Ryer et al., 2005; Saha et al., 2014; Yoshida et al., 2006), in S phase arrest (Santiago-Walker et al., 2005), and in the maintenance of the G2/M DNA damage checkpoint (LaGory et al., 2010). Recently, Liu et al. has illustrated an important role for PKC $\delta$  in the development of the first cell stage of mouse embryos through the phosphorylation Cdc25b on Ser96 to promote G2/M transition (Liu, Y. et al., 2019). Taken together, these studies suggest that inhibition of the DDR, and subsequently DNA repair, may be a mechanism through which PKC $\delta$  promotes rapid cell death when appropriate.

#### 4. PKC $\delta$ in Cancer

The ability of phorbol esters to promote tumors was described nearly 50 years ago (Baird and Boutwell, 1971). However, it was not until PKC was shown to be the major phorbol ester “receptor” in the cell that the contribution of PKC isoforms to human cancer was explored (Castagna et al., 1982; Kikkawa et al., 1983). Studies from the Newton lab indicate that functional genomic alterations of PKC $\delta$  are rare, and none have been definitively linked to cancer, supporting the paradigm that PKC $\delta$  is a cancer “supporter” and not a cancer “driver” (Antal et al., 2015). Thus, PKC $\delta$  activation, expression, localization and/or the oncogenic context may largely determine the function of this kinase in cancer. Data on expression of PKC $\delta$  in human tumors supports potential roles for PKC $\delta$  in both tumor suppression and tumor promotion. PKC $\delta$  expression is decreased in human squamous cell and bladder carcinomas, endometrial carcinoma, and colorectal cancer (D'Costa et al., 2006; Langzam et al., 2001; Reno et al., 2008; Su et al., 2020; Yadav et al., 2010), but increased in pancreatic cancer, breast cancer and non-small cell lung cancer (NSCLC) (Allen-Petersen et al., 2014; Evans et al., 2003; Symonds et al., 2011; Symonds et al., 2016). Our studies in K-ras mutant non-small cell lung cancer (NSCLC) cell lines suggest that PKC $\delta$  function may be dependent on oncogenic context and subcellular localization. PKC $\delta$  expression is increased in NSCLC cells that are dependent on K-ras for survival, and this correlates with increased nuclear abundance of PKC $\delta$  (Ohm et al., 2017). In these studies, NSCLC cells with high nuclear PKC $\delta$  are resistant to chemotherapy-induced apoptosis. Likewise, nuclear accumulation of PKC $\delta$  correlates with resistance to tyrosine kinase inhibitors (TKIs) (Lee et al., 2018).

## Evidence for PKC $\delta$ as a tumor promoter

Depletion of PKC $\delta$  suppresses tumor formation in nearly all mouse models studied, strongly supporting a tumor-promoter function for this kinase (Allen-Petersen et al., 2014; Mauro et al., 2010; Symonds et al., 2011). Furthermore, while PKC $\delta^{-/-}$  mice have a reduced life span, presumably due to autoimmune disease, we have found no evidence of an increased rate of spontaneous tumors in PKC $\delta^{-/-}$  mice up to 18 months of age (Reyland, et al. unpublished data). Our *in vivo* studies reveal that PKC $\delta$  functions as a tumor promoter in mouse models of mammary gland cancer, pancreatic cancer and lung cancer (Allen-Petersen et al., 2014; Mauro et al., 2010; Symonds et al., 2011). Using a urethane-induced lung cancer model in which nearly 100% of the tumors were determined to have K-ras mutations, we found that tumor incidence was dramatically reduced in urethane treated PKC $\delta^{-/-}$  mice compared to PKC $\delta^{+/+}$  mice and further, the tumors in PKC $\delta^{-/-}$  mice were significantly reduced in size (Symonds et al., 2011). In similar studies we showed that ErbB2/Her2neu induced mammary gland tumorigenesis is reduced in PKC $\delta^{-/-}$  mice, and that increased expression of PKC $\delta$  correlated with poor prognosis in a subset of human breast cancer tumors (Allen-Petersen et al., 2014; McKiernan et al., 2008). Likewise, data from Mauro et al. shows that overexpression of PKC $\delta$  in PANC-1 cells results in decreased tumor latency in a mouse xenograft model (Mauro et al., 2010).

Maintenance of cancer stem cells may contribute to the tumor promoter phenotype associated with PKC $\delta$ . PKC $\delta$  supports the survival of cancer stem cells from multiple types of human tumors (Berardi et al., 2016; Chen et al., 2014), promotes c-Kit activation in colon cancer cells (Park et al., 2013) and helps to maintain the phenotype of tumor initiating cells through a cytokine-mediated autocrine positive feedback loop (Kim et al., 2015). Notably, the PKC inhibitor, sotrastaurin, can regulate stem cell properties in gastric cancer cells and inhibit metastasis and chemoresistance in gastric cancer (Yuan et al., 2019). Possibly linked to stem cell homeostasis, PKC $\delta$  has been shown to contribute to cellular senescence as part of a complex that represses hTERT transcription (Yamashita et al., 2016). Other studies indicate that expression of hTERT in adipose-derived stem cells is regulated by the PKC $\delta$  splice variant, PKC $\delta$ VIII (Carter et al., 2013).

Additional mechanisms of tumor promotion by PKC $\delta$  may include regulation of cell migration and invasion (Allen-Petersen et al., 2014; Gan et al., 2012; Razorenova et al., 2011; Symonds et al., 2011; Zhao et al., 2009). Studies from the Cheresch lab demonstrate that integrin  $\alpha_v\beta_3$  is increased during metastasis and promotes cancer stem cell survival and resistance to EGFR inhibitors (Seguin et al., 2014). Our lab and others have shown that PKC $\delta$  modulates integrin  $\alpha_v\beta_3$  regulated survival pathways (Putnam et al., 2009; Symonds et al., 2016). In our studies, depletion of PKC $\delta$  resulted in decreased expression of integrin  $\alpha_v\beta_3$ , reduced ERK activation, and decreased anchorage independent growth (Symonds et al., 2016). Similar results have been shown in somatotropinomas and NSCLC cells, suggesting a potential mechanism for regulation of tumor progression and metastasis (Lei et al., 2018; Symonds et al., 2011).

A tumor promoter function for PKC $\delta$  seems incongruent with its central role in apoptosis. How then is the tumor promoter function of PKC $\delta$  specified in cancer cells? An interesting idea is that PKC $\delta$  function in cancer may be dictated by the specific oncogenic context. This

has been explored largely in cells with activated K-ras, but the concept is also supported by studies that indicate a role for PKC $\delta$  in drug resistant K-ras NSCLC (Lee et al., 2018; Wilson et al., 2015). PKC $\delta$  has been validated as a synthetic lethal target in multiple cancers with aberrant activation of Ras signaling (Chen et al., 2011; Xia et al., 2009; Xia et al., 2007). Studies by Xia et al. show that PKC $\delta$  is required for the survival of cells engineered to overexpress activated K-ras, and that depletion of PKC $\delta$  in these cells induces apoptosis (Xia et al., 2009; Xia et al., 2007). We have explored this further using a panel of 17 NSCLC cells lines that represent two subpopulations of *KRAS* mutant NSCLC cells that differ in their functional dependence on K-ras (Collisson et al., 2011; Singh et al., 2009). Our studies show that functional dependency on K-ras is highly correlated with a pro-survival, pro-tumorigenic role for PKC $\delta$ , while in *KRAS* mutant lung cancers that are no longer functionally dependent on K-ras, PKC $\delta$  regulates the apoptotic response to chemotherapeutic agents (Ohm et al., 2017; Symonds et al., 2011). PKC $\delta$  functions downstream of K-ras in this model, as depletion of PKC $\delta$  does not suppress K-ras activation (Symonds et al., 2011). Our cumulative studies show that K-ras dependent NSCLC cells are dependent on PKC $\delta$  for many tumor associated phenotypes including *in vivo* tumor formation, cell migration and invasion, and anchorage independent growth (Ohm et al., 2017; Symonds et al., 2011; Symonds et al., 2016). Mechanistically, the requirement for PKC $\delta$  for the activation of extracellular-regulated-kinase (ERK) is a central theme that defines functional K-ras dependency in NSCLC cells. We have proposed that this is an example of “non-oncogene addiction” where cancer cells can become dependent on proteins that are non-essential for the survival of normal cells (Luo et al., 2009; Symonds et al., 2016). Taken together, these studies suggest that inhibition of PKC $\delta$  might be useful in certain subsets of cancer patients, particularly those who have developed resistance to TKIs and inhibitors that target Raf/MEK/ERK signaling. A variety of approaches to targeting PKC $\delta$  have been explored as discussed in section 7.

### Evidence for PKC $\delta$ as a tumor suppressor

The pro-apoptotic role of PKC $\delta$  has led to the suggestion that it may act as a tumor suppressor (Reyland, M.E. and Jones, D. N., 2016). Support for this hypothesis is mostly based on *in vitro* studies that show suppression of proliferation by PKC $\delta$  in a variety of cancer cell lines. For instance, PKC $\delta$  can suppress proliferation of colon cancer cells (Hernández-Maqueda et al., 2013) through inhibition of Wnt signaling and hepatocellular carcinoma cells through regulation of Hedgehog signaling (Cai et al., 2009). Similarly, as discussed above, PKC $\delta$  can inhibit cell cycle progression and promote cell cycle arrest (LaGory et al., 2010; Nakagawa et al., 2005; Santiago-Walker et al., 2005). PKC $\delta$  regulation of apoptosis in prostate cancer cells through p38 MAPK is likewise tumor-suppressive (Fujii et al., 2000; Tanaka, Y. et al., 2003). While these *in vitro* studies are consistent with PKC $\delta$  functioning as a tumor suppressor, *in vivo* support for this hypothesis is limited. Early studies in transgenic mice that overexpress PKC $\delta$  showed resistance to chemically induced skin cancer (Reddig et al., 1999) but not UV radiation-induced skin cancer (Aziz et al., 2006). PKC $\delta$  may also be important for IR-induced inhibition of tumor growth downstream of PLOD3 (Baek et al., 2019). However, Cheng et al. have described a role for caspase-3/ PKC $\delta$ /Akt/VEGF-A signaling in mediating repopulation of tumor cells following irradiation, which suggests PKC $\delta$  may function as a tumor promoter in this context (Cheng

et al., 2019). Given the considerable *in vitro* data supporting pro-apoptotic and antiproliferative functions of PKC $\delta$ , a more thorough analysis of potential tumor suppressor functions *in vivo* is warranted. In particular, studies that address a tumor suppressor function for PKC $\delta$  in the context of a wider variety of genetic drivers are needed to fully understand the potential roles for PKC $\delta$  in tumorigenesis.

### Perspective

While the preponderance of *in vivo* and *in vitro* studies indicate a tumor promoter function for PKC $\delta$ , these studies have limitations and also raise important questions. For instance, almost all studies that have examined a pro-tumorigenic role PKC $\delta$  have used models that are dependent on ErbB2/Her2 or K-ras signaling. These studies show that dependency on PKC $\delta$  is highly correlated with functional dependency on K-ras (Ohm et al., 2017; Symonds et al., 2011; Symonds et al., 2016) or on activated K-ras (Xia et al., 2009; Xia et al., 2007). Whether the tumor-promoter function of PKC $\delta$  can be extrapolated to other oncogenic contexts will need to be determined by examination of a wider group of cancers with different oncogenic drivers. Additional studies are also needed to tease out potential contributions of the pro-apoptotic function of PKC $\delta$  in cancer. For instance, our studies on K-ras mutant NSCLC cells do not address whether the PKC $\delta$  pro-apoptotic phenotype seen in some K-ras “independent” NSCLC cells is tumor-suppressive (Ohm et al., 2017; Symonds et al., 2011; Symonds et al., 2016). Such questions may be relevant to emerging roles for PKC $\delta$  in drug resistance (Lee et al., 2018; Wilson et al., 2015).

Finally, while evasion of apoptosis is a hallmark of cancer, based on the lack of compelling evidence that PKC $\delta$  can act as a tumor suppressor, it is possible that the pro-apoptotic function of PKC $\delta$  may not contribute significantly to tumorigenesis. Indeed, support for a pro-apoptotic function for PKC $\delta$  comes primarily from studies in non-cancer cells, including studies in PKC $\delta$ <sup>-/-</sup> mice which show a clear lymphoproliferative phenotype (Banninger et al., 2011; Limnander et al., 2011; Mecklenbrauker et al., 2002; Miyamoto et al., 2002). In these models, loss of PKC $\delta$  protects against tissue damage/injury *in vivo*, and clonal deletion of autoreactive B cells, at least in part through suppression of apoptosis (see section 2). PKC $\delta$  may have unique functions in cancer cells that support tumor progression. This raises interesting questions about the plasticity of signaling by PKC $\delta$  and the contribution of oncogenic context to re-wiring of PKC $\delta$  in some cancer cells. Understanding if PKC $\delta$  can function both as a tumor promoter and a tumor suppressor, and what determines PKC $\delta$  function in a particular cell and tissue context will be essential for advancing this kinase as a drug target in cancer.

## 6. Functional proteomic analyses reveals unique roles for PKC $\delta$

Given the ubiquitous expression of PKC $\delta$ , and its contribution to many cellular processes, deciphering how its unique functions are specified is challenging. In some cases, manipulation of PKC $\delta$  expression and activity in cell lines has identified PKC $\delta$ -regulated signaling cascades that contribute to these biological endpoints (Li et al., 2020; Symonds et al., 2016; Wermuth et al., 2011). Several studies have approached this question using mRNA microarray analysis to determine changes in transcript abundance. For example, our lab has



compared mRNA expression in K-ras mutant NSCLC cell lines with and without depletion of PKC $\delta$  (Symonds et al., 2016). KEGG analysis of this data showed that depletion of PKC $\delta$  decreased transcripts for proteins involved in cancer gene signaling, in particular the regulation of extracellular matrix and focal adhesion pathways (Symonds et al., 2016). In contrast, mRNA transcripts for proteins involved in metabolic processes such as glutathione metabolism, amino acid metabolism and nitrogen metabolism were increased (Symonds et al., 2016). Li *et al.* recently used RNA-seq to identify gene alterations in an inducible PKC $\delta$  knockout murine osteoclast model, and found sex-specific and PKC $\delta$ -dependent differences in collagen binding and peptidase regulation (Li et al., 2020). Contrary to our analysis, their studies showed that genes involved in focal adhesion and ECM–receptor interaction were upregulated, while many of the downregulated genes were involved in cell differentiation.

While gene expression profiling via high throughput analysis of RNA transcripts can be highly informative, transcript abundance does not necessarily correlate with protein expression (de Sousa Abreu et al., 2009; Vogel and Marcotte, 2012). Furthermore, pathway activation/inactivation is frequently regulated by post-translational modifications of proteins, rather than protein expression. Functional proteomic analysis enables profiling of changes in protein expression and post-translational modifications, such as phosphorylation, with the goal of identifying differentially regulated signal transduction pathways (Monti et al., 2019). Reverse Phase Protein Array (RPPA) uses a pre-specified set of antibodies to detect protein abundance in cell or tissue lysates (Petricoin et al., 2019). As the RPPA panel contains antibodies to many post-translationally modified proteins, dynamic changes in signaling pathways can also be detected. To explore PKC $\delta$  regulation of the functional proteome, we assayed protein abundance in biological triplicates of two sets of ParC5 cells that stably express unique PKC $\delta$  targeted shRNAs or their paired controls (shScr/sh $\delta$ 561 and shNT/sh $\delta$ 110). Analysis was done by the MD Anderson Functional Proteomics Core ([www.mdanderson.org](http://www.mdanderson.org)) using an RPPA platform consisting of antibodies to 371 proteins, including 100 antibodies that recognize proteins with specific post-translational modifications (the majority being anti-phosphorylation antibodies). ParC5 cells are a well-differentiated cell line derived from rat parotid acinar cells (Quissell et al., 1998). We have used these cells extensively to study DNA damage-induced apoptosis as they closely phenocopy physiologic models such as primary salivary acinar cells and mouse models of salivary gland function (Reyland, M.E. and Jones, D. N., 2016). In addition, analysis of changes in gene expression upon depletion of PKC $\delta$  in ParC5 cells (this manuscript) and several non-K-ras dependent NSCLC cell lines indicates that many common pathways are regulated (Symonds et al., 2016). Therefore, data from ParC5 cells may be generally extrapolatable to some subsets of cancer cells, particularly those that are not dependent on K-ras signaling (Ohm et al., 2017; Symonds et al., 2011; Symonds et al., 2016).

### Changes in protein expression and post-translational modifications

We first analyzed changes in the abundance of total proteins and post-translationally modified proteins using normalized values provided by the MD Anderson Functional Proteomics Core. Z-score transformation was then performed for the antibody signals found to be significantly altered ( $p < 0.1$ ) in both shRNA pairs (shScr versus sh $\delta$ 561 and shNT versus sh $\delta$ 110). Z-scores greater than 2 or less than -2 indicate significant upregulation or

downregulation of the specific protein, respectively. The heatmap shown in Figure 1A depicts the Z-scores for the 54 proteins regulated in both pairs of PKC $\delta$  shRNA depleted cells, grouped into those that are up- or down-regulated. Antibodies that detect proteins with specific post-translational modifications revealed changes in the abundance of 21 phosphoproteins, with 8 increased and 13 decreased. The 19 proteins and protein modifications that were found to be up regulated include proteins that participate in processes previously shown to be regulated by PKC $\delta$ , including the DNA damage response, cell cycle checkpoint activation and DNA repair (e.g. TIGAR, CDK1 pT14/T15 and DNA ligase IV) and receptor signaling (e.g. PLC-gamma and PLC-gamma pS1248, LRP6 pS1490). Our analysis also suggest PKC $\delta$  regulation of other processes including glucose metabolism and nutrient sensing (e.g. S6 and phospho-S6, GYS1 and phospho-GYS1 and eEF2). Thirty-five proteins and protein modifications were shown to be down regulated upon depletion of PKC $\delta$ . This group includes proteins involved in the DNA damage response and cell cycle arrest (e.g. CDKN2A (p14/p16), RAD17 pS645, ATM and ATM pS1981 and DAPK2), proliferation and signaling pathway integration (e.g. Notch 1 cleaved, STAT3 and STAT3 pY705, Jun and Jun pS73) and mitochondrial function and the antioxidant response (e.g. SOD1, PDHA1, T-FAM). Down-regulated proteins also include receptor and non-receptor tyrosine kinases (e.g. EphA2/EphA2 pY588/S897, Her3/Her3 pY1289, Syk, Src/Src pY416/pY527) and tyrosine phosphatases (e.g. SHP2/SHP2 pY542). Finally, the downregulation of PKC $\alpha$  and PKC $\beta$ -II expression and phosphorylation suggests coordinated activation/expression of some PKC isoforms. Our lab has previously shown that PKC $\alpha$  is protective against PKC $\delta$ -induced apoptosis, offering a possible explanation for why PKC $\alpha$  may be reduced in the absence of PKC $\delta$  (Matassa et al., 2003).

Remarkably, while many phosphorylation events appear to be regulated by PKC $\delta$ , the most dramatically altered post-translation modification observed in was total protein polyADP-ribosylation (PARylation). Protein PARylation was reduced 3.3-fold in sh $\delta$ 110 cells, and 2.1-fold in sh $\delta$ 561 cells relative to their controls. Protein PARylation is a reversible modification that is associated with cellular stress responses and is responsible for the regulation of chromatin organization, DNA repair, DNA replication, transcription as well as other processes (Schuhwerk et al., 2017; Wei and Yu, 2016). Based on our RPPA data, the decrease in PARylation observed is not a result of an increase in Poly(ADP-Ribose) Glycohydrolase, the enzyme responsible for removing PARylations (data not shown), or Poly(ADP-Ribose) polymerase.

The protein alterations identified by RPPA (Figure 1A) agree well with data from our lab and others that demonstrates a suppression of apoptosis with depletion or inhibition of PKC $\delta$  (Allen-Petersen et al., 2010; Humphries et al., 2008; Leitges et al., 2001). Importantly, our studies also suggest new targets of PKC $\delta$  that may contribute to the anti-apoptotic phenotype observed with PKC $\delta$  depletion. For example, we have shown that ERK activation by PKC $\delta$  is required for DNA damage-induced apoptosis (Ohm et al., 2019). Both phosphorylated and total astrocytic phosphoprotein PEA-15 (PEA-15) are increased with PKC $\delta$  depletion (Figure 1A). In its unphosphorylated state PEA-15 binds and sequesters ERK1/2 in the cytoplasm, inhibiting ERK nuclear translocation and activation of proliferative signaling (Greig and Nixon, 2014). Phosphorylation of PEA-15 on Ser116 results in the release and nuclear translocation of ERK1/2 coincidental with the recruitment

of PEA-15 pS116 to the apoptotic death-initiation signaling complex (DISC) and inhibition of apoptosis (Formstecher et al., 2001; Renganathan et al., 2005). Similarly, our data shows increased expression of the p53 regulated protein, TIGAR (Figure 1A), which increases glucose metabolism via the pentose phosphate pathway. This was also a pathway identified in our previous analysis of NSCLC cells (Symonds et al., 2016). Activation of the pentose phosphate pathway by TIGAR has been shown to be anti-apoptotic by reducing oxidative stress and increasing DNA repair (Bensaad et al., 2006; Fico et al., 2004; Yu et al., 2015). Finally, Glycogen Synthase 1 (GYS1), another metabolism associated anti-apoptotic protein (Bhanot et al., 2015; Pelletier et al., 2012), and DNA Ligase IV, a component of the non-homologous end joining DNA repair pathway were also shown to be upregulated. It is worth remembering that these proteins and phosphoproteins are increased in cells depleted of PKC $\delta$ , and thus suggests that regulation by PKC $\delta$  must be both negative and indirect.

### Ingenuity Pathway Analysis

To integrate specific changes in protein expression with changes in cell signaling pathways, we performed Ingenuity Pathway Analysis (IPA). Figure 1B shows the distribution of the 142 genes that were significantly ( $p < 0.05$ ) altered in the RPPA. From the RPPA, there were 30 and 84 uniquely altered genes in sh $\delta$ 110 and sh $\delta$ 561 compared to their controls, respectively, with 28 genes that were common between them. Because of the small number of genes that were significantly altered in both shPKC $\delta$  pairs (overlap in Venn diagram, Figure 1B), IPA was performed on significantly altered genes in each individual shRNA pair (shScr versus sh $\delta$ 561 and shNT versus sh $\delta$ 110). Figure 1C shows the top 33 pathways common to both shPKC $\delta$  knockdown pairs that were most significantly altered ( $p < 0.005$ ,  $[-\log(p\text{-value}) > 2.3]$ ). Additionally, seven pathways that were very highly significant in one shRNA pair ( $p < 0.00001$ ,  $[-\log(p\text{-value}) > 5]$ ) and strongly significant in the other ( $p < 0.01$ ,  $[-\log(p\text{-value}) > 1.9]$ ) are also included.

Given the relatively small number of genes, we were not able to determine whether the identified pathways were up- and down-regulated. However, in some cases directionality can be inferred from the protein alterations identified in the RPPA (Figure 1A). Pathways identified by IPA validate a role for PKC $\delta$  in growth factor signaling, the DNA damage response and cell cycle regulation as well as apoptosis, the primary phenotype observed with PKC $\delta$  depletion. Importantly, the DNA damage checkpoints at both G1/S and G2M and the p53 signaling pathway were all found to be altered. PKC $\delta$  has been previously shown to be involved in G1/S progression, which was found to activate cell-cycle checkpoints and p53 (Santiago-Walker et al., 2005). In this regard, PKC $\delta$  regulation of G1/S progression has been shown to be pro-apoptotic (Santiago-Walker et al., 2005), which concurs with an anti-apoptotic phenotype with PKC $\delta$  depletion. The IPA analysis also shows an enrichment of energy/metabolism pathways, which included AMPK Signaling, Insulin Receptor Signaling, mTOR Signaling and Sirtuin Signaling. These pathways correlate well with previous studies as well as our unpublished data, where PKC $\delta$  has been shown to be involved in mitochondrial respiration (Mayr et al., 2004a; Mayr et al., 2004b), as well as our data that shows depletion of PKC $\delta$  alters amino acid metabolism and modulates the pentose phosphate pathway in NSCLC cells (Symonds et al., 2016). mTOR signaling is associated with increases in anabolism and cell proliferation and decreases in catabolism and apoptosis

(Laplante and Sabatini, 2012). Increased phosphorylation of S6K, an mTOR substrate, suggests that mTOR signaling is increased, which concurs with the anti-apoptotic phenotype observed with PKC $\delta$  knockout. Sirtuin signaling opposes mTOR activity (Ghosh et al., 2010), thus based on the increase in mTOR activity, Sirtuin signaling is likely decreased, but this will need to be validated. Together, these changes suggest an increased proliferative state or decreased apoptosis. Ingenuity pathway analysis also demonstrates additional alterations in growth factor and proliferative signaling pathways that are impacted by the depletion of PKC $\delta$ , highlighting the important role of this kinase in cellular survival and the anti-apoptotic phenotype.

Our analyses provide confirmation of the numerous known PKC $\delta$  regulated cellular processes, but also suggest numerous opportunities for further investigation. For instance, it is noteworthy that while few gene expression changes overlap between the shRNA pairs, many of the same pathways identified by IPA are shared, suggesting that there are multiple ways to meet a common goal. This plasticity in signaling pathways may be similar to what has been identified in some cancer cells (Luo et al., 2009; Pagliarini et al., 2015; Quintanal-Villalonga et al., 2020). Overall, the protein expression and post-translational modifications observed in the RPPA and the pathway analysis in PKC $\delta$  depleted cells follow the general theme of upregulation of DNA damage response and a decrease in apoptosis. These analyses provide data for generation of new hypotheses regarding additional mechanisms that may drive pro-apoptotic and pro-proliferative phenotypes associated with PKC $\delta$ . For instance, our data shows that depletion of PKC $\delta$  activates ERK signaling via increased expression and phosphorylation of PEA-15 at S116 (Figure 1A). Likewise, upregulation of TIGAR is associated with protection from apoptosis (Bensaad et al., 2006). The identification of PKC $\delta$  as a regulator of these pathways may have implications for targeting drug resistant tumors that are reliant on PKC $\delta$  (Lee et al., 2018; Wilson et al., 2015).

## 7. Therapeutic Strategies for Targeting PKC $\delta$

Given its role in regulating many aspects of cell signaling, numerous efforts have been made to target PKC $\delta$  activity. However, this is a challenging task, in part because the high degree of structural and sequence similarity between the different PKC isoforms results in a lack of specificity for a particular isoform. This is particularly true for reagents that target the catalytic domain, which often show inhibition of multiple kinases. Indeed, multiple compounds that were originally described as selective PKC inhibitors were in fact highly promiscuous and inhibited kinases or functioned via mechanisms that did not depend on kinase activity (Soltoff, 2007; Wu-Zhang and Newton, 2013). Unfortunately, a number of studies continue to use these compounds as selective PKC inhibitors.

In targeting PKC it is important to consider the specific role that the kinase plays in cellular signaling. Studies from the Newton lab suggest that a number of naturally occurring mutations of multiple PKC isoforms identified in cancer patients are loss of function and can promote tumorigenesis when tested in mouse models (Antal et al., 2015; Newton and Brognard, 2017). As a result, they suggest that, for cancer, therapeutic strategies should focus on rescuing rather than inhibiting PKC dependent signaling. However, as reviewed above, there is evidence that in some cancers PKCs promote tumorigenesis, and in these

cases and in other diseases it may be more appropriate to inhibit PKC isotype function. Further, different isoforms of PKC can have opposing effects within the same tissue. For example, in ischemia reperfusion, PKC $\delta$  and PKC $\epsilon$  have opposing effects. The pharmacological agents developed over the years to target PKC activity have been extensively reviewed elsewhere (Budasz et al., 2007; Churchill et al., 2009; Cunningham et al., 2017; Das et al., 2016; Deka and Trivedi, 2019; Mackay and Twelves, 2007; Mochly-Rosen et al., 2012; Wu-Zhang and Newton, 2013). We have previously reviewed therapeutic approaches that target PKC $\delta$  (Reyland, M.E. and Jones, D. N., 2016). Here we highlight recent developments in targeting PKC $\delta$  for disease intervention.

### Targeting the Regulatory Domains

The bryostatins are a family of macrolide lactones from the marine organism *Bugula neritina* (Pettit et al., 1970; Pettit et al., 1982). In common with phorbol esters, these compounds bind with high affinity to the C1 domains of PKC (de Vries et al., 1988; Kraft et al., 1986; Wender et al., 1988) and can lock PKC in an open conformation that ultimately leads to its down regulation (reviewed in (Antal et al., 2015; Newton, 2018; Newton and Brognard, 2017)). Recently it has been shown that bryostatins also target other C1 domain containing proteins including Munc13 family members (Blanco et al., 2019). Early on, it was recognized that while bryostatin-1 could target multiple isoforms of PKC to induce membrane translocation and down regulation, it showed differential effects on PKC $\delta$ . At low concentrations bryostatin-1 down-regulated PKC $\delta$ , similar to phorbol esters, but at high concentrations it protected against TPA induced down regulation (Szallasi et al., 1994a; Szallasi et al., 1994b). Additional studies showed that bryostatin-1 functions to inhibit PKC $\delta$  dependent apoptosis by preventing translocation of PKC $\delta$  to the plasma membrane, and the PKC $\delta$  dependent release of TNF $\alpha$  (Tanaka, Yuichi et al., 2003; von Burstin et al., 2010). These findings have been supported by further studies including with other bryostatin analogs that show differential effects on specific isoforms of PKC (Kedei et al., 2013; Kedei et al., 2011a; Kedei et al., 2011b). Therefore, there is a wealth of interest in discovering new bryostatin analogs for the manipulation of PKC activity in an isoform specific manner.

Bryostatin-1 showed significant efficacy against multiple cancer cell lines and early promise in clinical trials (Ajani et al., 2006; Barr et al., 2009; Ku et al., 2008; Propper et al., 1998; Zonder et al., 2001). However, adverse side effects or lack of significant outcomes has limited bryostatin development. Recently, bryostatin-1 has been investigated for use in chimeric antigen receptor T-cell (CART) therapy targeting CD22 in the treatment of leukemia and lymphoma (Ramakrishna et al., 2019). Resistance to CD22 CART therapies is associated with reduced antigen presentation on the tumor cell surface (Fry et al., 2018; Nguyen et al., 2016; Ramakrishna et al., 2019). Bryostatin-1 treatment of these resistant tumors leads to increased CD22 surface expression in both cells and ex vivo models of acute and chronic lymphocytic leukemias (ALL and CLL), and non-Hodgkin's lymphoma (al-Katib et al., 1993a; al-Katib et al., 1993b; Biberacher et al., 2012; Ramakrishna et al., 2019) and also *in vivo* in human clinical trials (Varterasian et al., 1998; Varterasian et al., 2000). In CLL this appears to depend on the down regulation of PKC $\beta$  II (Biberacher et al., 2012). However, in ALL bryostatin may function through mechanisms that are related to broader changes in plasma membrane trafficking, as treatment with either enzastaurin targeting

PKC $\beta$  or the pan PKC inhibitor, staurosporine did not upregulate CD22 levels (Ramakrishna et al., 2019). The development of bryostatins as potential therapeutic agents has been severely limited by their availability, and synthetic routes to bryostatins have been challenging. More efficient approaches to the synthesis of bryostatin-1 derivatives have recently been reported that make available large quantities for clinical studies and the exploration of novel derivatives with improved selectivity (Hardman et al., 2020; Wender et al., 2017).

Anthracycline antibiotics typified by doxorubicin are among the most effective and widely used anti-cancer compounds. These compounds generally bind to DNA and inhibit topoisomerase II (Gewirtz, 1999). Surprisingly, N-Benzyladriamycin-14-valerate (AD 198), a less toxic derivative of doxorubicin, was found to function by targeting PKC $\delta$  through its C1b domain to stimulate mitochondrial dependent apoptosis (Barrett et al., 2002; Roaten et al., 2002). Additionally, AD198 was found to protect against doxorubicin induced cardiac damage through activation of PKC $\epsilon$  in cardiomyocytes (Cai et al., 2010). An improved derivative pivarubicin (AD 445) has recently been developed, which is more effective than doxorubicin in orthotopic mouse models of triple negative breast cancer, producing reduced growth rates and tumor regression in response to a single dose (Barrett et al., 2002; Roaten et al., 2002). Pivarubicin activity is dependent on activation of PKC $\delta$  and is also cardioprotective.

Ingenol mebutate (PEP005) is a phorbol ester derivative that received approval in the US and Europe for the treatment of actinic keratosis (Lebwohl et al., 2012), the precursor of squamous cell carcinoma (SCC), the second most common form of skin cancer. Multiple studies indicate that PEP005 acts primarily through its effects on PKC $\delta$  (Benhadji et al., 2008; Freiburger et al., 2015; Hampson et al., 2005; Serova et al., 2008). However, recent data suggests that patients treated with PEP005 actually show higher incidences of SCC, which has prompted its withdrawal from the European market (Mohd Mustapa et al., 2020). PEP005 was recently identified in high throughput screens to reverse the suppression of T-cell activity by inhibitory receptors (T-cell exhaustion) that are targeted in checkpoint inhibitor therapies e.g. against PD-1 or PD-L1 (Marro et al., 2019). This activity of PEP005 was dependent on PKC signaling, in this case most probably PKC $\theta$ , however the involvement of other PKC isotypes remains to be determined.

### Targeting Kinase Activity

Uveal melanomas (UM) harboring mutations in the G proteins GNAQ or GNA11 (Chua et al., 2017; Van Raamsdonk et al., 2009; Van Raamsdonk et al., 2010) show hyperactivation of PKC-dependent MAPK signaling. These melanomas frequently overexpress the proteins mouse double minute (MDM)2 and MDMX12, which are inhibitors of p53, which itself is not mutated in UM (de Lange et al., 2012). Recent studies have shown that specifically depleting PKC $\delta$  inhibits UM growth and this is enhanced by reactivation of p53 dependent signaling by reducing/inhibiting MDM2/MDMX12-p53 interactions including by the use of nutlins (Carita et al., 2016; Heijkants et al., 2018), or by inhibition of mTORC1 downstream of p53 (Carita et al., 2016). Clinical trials with pan-PKC inhibitors in combination with inhibitors of MAPK signaling, showed promising effects but limiting toxicity (Carita et al.,

2016). Clinical trials of the novel drug IDE196 (formerly known as LXS196), a pan PKC inhibitor with IC<sub>50</sub> in the low nM to pM range that targets binding of ATP, showed early promise (Kapiteijn et al., 2019) for the treatment of metastatic UM, and follow up trials against other solid tumors harboring mutations in GNAQ or GNA11 or PKC-fusions are ongoing (NCT03947385).

PKC $\delta$  has recently been shown to play a central role in regulating the resistance of EGFR mutant NSCLC tumors to treatment with TKIs (Lee et al., 2018). TKI resistance in these tumors can occur through multiple mechanisms (Camidge et al., 2014; Minari et al., 2016), which appear to converge on the activity of PKC $\delta$ , as inhibition of PKC $\delta$  either pharmacologically or with shRNA restored gefitinib sensitivity. Co-treatment of tumors with EGFR inhibitors Osimertinib (AZD9291) and the PKC inhibitor sotrastaurin (AEB071) led to regression of tumor volume (Lee et al., 2018). In these tumors, PKC $\delta$  resistance requires nuclear localization as nuclear exclusion re-sensitizes cells to gefitinib treatment. We have previously shown that nuclear localization requires the activity of both importin- $\alpha$  and HSP90 to recognize a bipartite nuclear localization signal (Adwan et al., 2011; DeVries et al., 2002). The importance of this sequence was confirmed by Lee et al (Lee et al., 2018) and may help to explain the limited success of HSP90 inhibitors in treatment of NSCLC with EGFR mutants (Chatterjee et al., 2016). In a similar manner we demonstrated that K-ras-dependent NSCLC cells have increased nuclear localization of PKC $\delta$  and have reduced sensitivity to chemotherapeutic agents (Ohm et al., 2017), reinforcing the concept that co-inhibition of PKC $\delta$  represents a potential viable therapeutic avenue for treatment of NSCLC.

### **Inhibiting signaling pathways upstream of PKC $\delta$ activation**

Head and neck cancer patients typically undergo radiation therapy and surgery, sometimes with additional chemotherapy (Gregoire et al., 2015). Although the goal of radiation treatment is to eradicate the tumor, most patients also suffer debilitating damage to the surrounding non-tumor tissues, which can impact their quality of life and in some cases, limit the duration of therapy (Jensen et al., 2019). As tyrosine phosphorylation plays an important role in activating the pro-apoptotic function of PKC $\delta$  in IR-treated tissues, we explored utilizing TKIs, including dasatinib and imatinib, with activity against c-Abl and/or c-Src for radioprotection of the salivary gland *in vivo* (Wie et al., 2014; Wie et al., 2017). We showed that TKIs could successfully inhibit PKC $\delta$  activation and provide robust and durable radioprotection of salivary gland function in a mouse head and neck IR model without impacting cancer therapy (Wie et al., 2017). Other studies have also supported this approach; Arany et al. have shown that depletion of PKC $\delta$  in the salivary gland using siRNA coupled nanoparticles can protect against IR-induced loss of salivary gland function (Arany et al., 2013; Arany et al., 2012), while Pabla et al. report that loss of PKC $\delta$  leads to reduced damage to the kidneys of mice treated with cisplatin for gastrointestinal cancer (Pabla et al., 2011). Together these studies provide a rationale for targeting pathways required for PKC $\delta$  activation for radio and chemo-protection of non-tumor tissues.

## 8. Conclusions

The ubiquitous expression of PKC $\delta$  suggests that it plays an essential role(s) in cell function. This is supported by numerous studies demonstrating a role for PKC $\delta$  in processes as diverse as apoptosis and tumorigenesis. With few examples of functional genetic alterations in PKC $\delta$ , regulation of the expression, subcellular localization or the activation may be the primary way PKC $\delta$  contributes to human diseases, including cancer. This suggests considerable plasticity in how PKC $\delta$  interfaces with cell signaling pathways. In the current studies we have expanded our knowledge of known PKC $\delta$  regulated pathways using functional proteomics. RPPA analysis of PKC $\delta$  depleted cells concurs with previous published data, demonstrating a role in MAPK/ERK signaling cascades, the regulation of apoptosis and the DNA damage response. In addition, it suggests a potential role for PKC $\delta$  in cellular energy and metabolism. Our studies provide new hypotheses regarding PKC $\delta$  function and suggest potential targets for therapeutic intervention in cancer.

## Acknowledgements

We gratefully acknowledge the Bioinformatics Core at the University of Colorado Cancer Center, particularly the contribution of Dr. Andrew Goodspeed. We are also grateful for assistance by Ms. Olivia McGinn in performing the Ingenuity Pathway Analysis.

## Funding

This work was supported by the National Institutes of Health [grant numbers R01DE015648, R01DE027517, T32CA190216, T32CA174648, F32DE029116].

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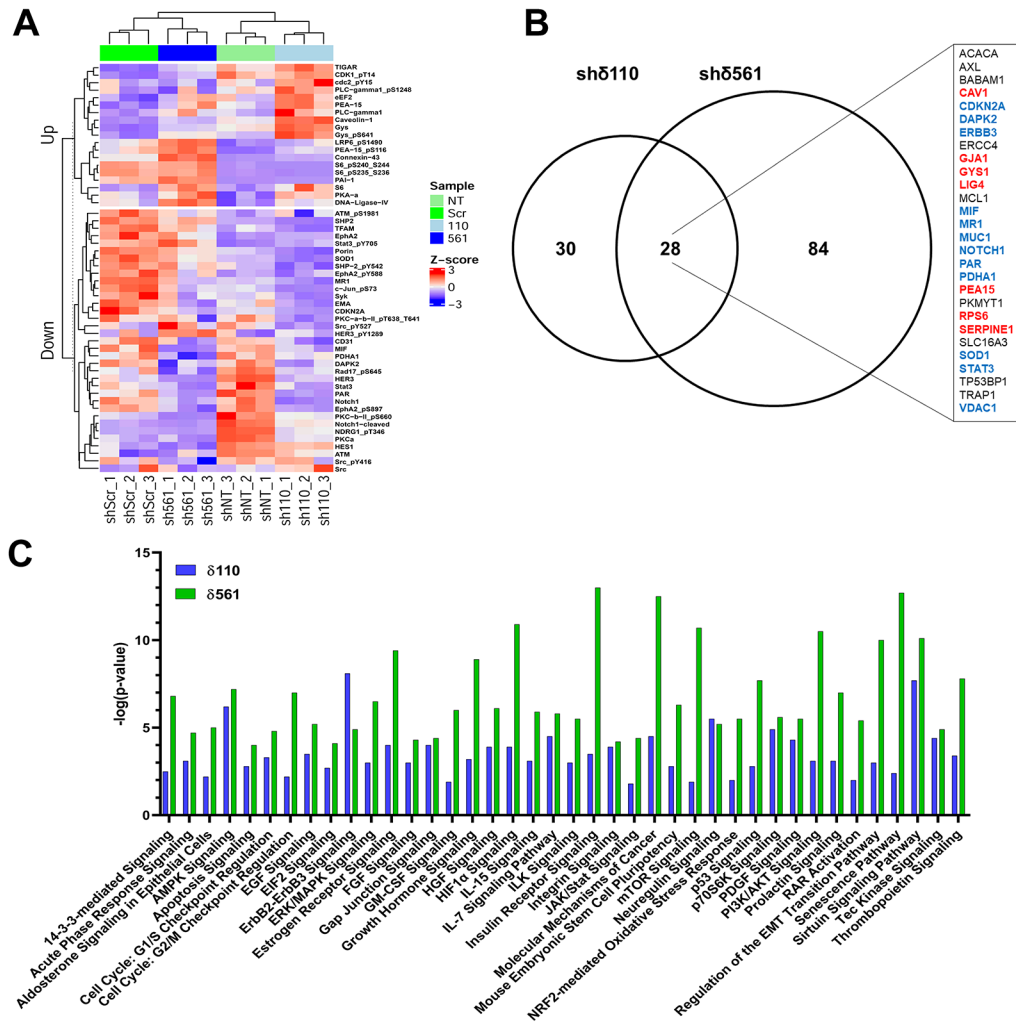


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**Figure 1.** Protein abundance in biological triplicates of two sets of ParC5 cells that stably express unique PKCδ targeted shRNAs or their paired controls (shScr/sh561 and shNT/sh110) was analyzed in triplicate at the RPPA Core at MD Anderson Cancer Center (Houston, TX). **A)** Proteins with an antibody changed in the same direction ( $p < 0.1$ ) in both shRNA constructs were plotted as a heatmap using the ComplexHeatmap R package (Gu et al., 2016) following z-score transformation. **B)** Shown is the number of genes ( $p < 0.05$ ) regulated in each shRNA as well as those that are found in both shRNA cell lines. The inset shows those genes regulated in both shRNAs with increased expression (red), decreased expression (blue) or both increased and decreased expression (black). **C)** Each gene expression comparison ( $p < 0.05$ ) (sh561 vs shScr and sh110 vs shNT) was analyzed using Ingenuity Pathway Analysis software (QIAGEN, inc., Hilden, Germany) to identify biological networks and functional pathways. Shown are the top 33 pathways common to both shPKCδ knockdown pairs that were most significantly altered ( $p < 0.005$ ,  $[-\log(p\text{-value}) > 2.3]$ ). Additionally, seven pathways that were very highly significant in one shRNA

pair ( $p < 0.00001$ ,  $[-\log(p\text{-value}) > 5]$ ) and strongly significant in the other ( $p < 0.01$ ,  $[-\log(p\text{-value}) > 1.9]$ ) are included.

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