

PKC θ is a Key Regulator of T-cell Behavior and a Drug Target for T cell-mediated Diseases

Noah Isakov*

The Shraga Segal Department of Microbiology, Immunology and Genetics, Faculty of Health Sciences and the Cancer Research Center, Ben Gurion University of the Negev, Beer Sheva, Israel

Abstract

The protein kinase C-theta (PKC θ) isoform is a member of the calcium-independent novel PKC subfamily of serine/threonine kinases. It is an essential regulatory enzyme in mature T lymphocytes, where it plays a key role in coupling the activated TCR and the CD28 costimulatory receptor to their downstream signaling pathways. TCR/CD28 engagement induces the translocation of PKC θ to the center of the immunological synapse where it undergoes posttranslational modifications and becomes fully active. The activated PKC θ then initiates signaling pathways leading to the activation of transcription factors, including NF- κ B, AP-1 and NF-AT that are essential for the survival, activation and differentiation of T cells. While PKC θ ablation was found to impair a wide range of *in vitro* responses of T cells, *in vivo* studies in Prkcd^{-/-} mice revealed that distinct T cell subpopulations differ in their requirements for PKC θ and that PKC θ has a selective role in different immune responses. Thus, PKC θ participates in cellular mechanisms leading to excessive inflammatory responses, autoimmunity, and graft vs host (GvH) disease, but is dispensable for beneficial immune responses against viruses and during graft vs leukemia responses. These studies suggest that PKC θ may serve as a potential drug target for catalytic and allosteric inhibitors in selected T cell-mediated diseases, and that fine-tuning of PKC θ -dependent functions may help prevent autoimmunity and GvH, without impairing the ability of T cells to eradicate viral-infected and transformed cells.

Keywords: Protein kinase C theta; PKC θ ; PKC; T cell receptor; TCR; Signal transduction

Introduction

Protein phosphorylation is a ubiquitous posttranslational process mediated by kinases and serves to regulate the activation state of numerous proteins. Many kinases possess the ability to integrate signals from specific surface receptors and play important roles in regulatory networks and signal transduction pathways that control cell activation and differentiation. One important family of kinases that transduce signals from a large number of cell surface receptors is the protein kinase C (PKC), originally discovered by Nishizuka and colleagues [1]. The first PKC family members identified were found to be sensitive to diacylglycerol (DAG) and calcium (Ca²⁺) ions, two products of phospholipase C-mediated hydrolysis of the membrane phospholipid, phosphatidylinositol 4,5-bisphosphate (PIP₂) [2-4]. These two second messengers transduce signals from a plethora of activated receptors where the hydrophobic DAG associates with the cell membrane, while the second product of the PIP₂ hydrolysis, the hydrophilic inositol 1,4,5-trisphosphate (IP₃) binds IP₃-receptors in the endoplasmic reticulum (ER) and triggers the release of free Ca²⁺ ions into the cytoplasm [5-7]. The utilization of phorbol esters, which mimic the activity of DAG, together with Ca²⁺ ionophores, demonstrated that PKC plays an essential role in the induction of T lymphocyte proliferation [8,9] and reactivation of effector cytotoxic T cells [10,11].

The PKC Family of Serine/Threonine Kinases

The PKC family includes nine structurally and functionally related isoforms that are encoded by distinct genes and are divided into three subfamilies based on the structure homology of their regulatory domains and their respective cofactor requirements [12,13]. Additional PKC isoforms are products of alternative splicing of the PKC β [14] and PKC δ genes [15-17]. Members of the first subfamily, which include the conventional PKC (cPKC) isoforms, PKC α , β , and γ , are regulated via two DAG-binding C1 domains organized in tandem near the cPKC amino terminus [18-20], and an adjacent Ca²⁺ and phospholipid-

binding C2 domain [19,21]. Members of the second subfamily include the novel PKC (nPKC) isoforms, PKC δ , ϵ , η , θ , which are DAG-dependent, but Ca²⁺- and phospholipid-independent for their activity. Members of the third subfamily include atypical PKC (aPKC), PKC ζ and $\lambda/1$ that require neither Ca²⁺ nor DAG for their activity. The PKC enzymes are involved in metabolic processes in different cell types and are implicated in signal transduction networks that convert different environmental cues into cellular actions [22]. Individual PKC isoforms are differentially expressed in tissues and cell types, and six of these isoforms, including PKC α , δ , ϵ , η , θ and ζ are expressed at varying amounts in T cells [23]. Immunological studies using different genetic models and pharmacological drugs indicated that distinct PKC isoforms are required for different aspects of the activation and effector function of T cells. It is assumed therefore that distinct PKC isoforms may serve as drug targets in different T cell-mediated adaptive immune responses [24].

PKC θ

PKC θ is a member of the novel PKC subfamily, initially isolated from T cells, skeletal muscle and platelets [25-27]. Additional studies demonstrated that PKC θ exhibits a relatively restricted pattern of expression, with high levels in T lymphocytes [23,25], platelets [27-30]

***Corresponding author:** Dr. Noah Isakov, The Shraga Segal Department of Microbiology, Immunology and Genetics, Faculty of Health Sciences, Ben Gurion University of the Negev, P.O.B. 653, Beer Sheva 84105, Israel, Tel: 97286477267; Fax: 97286477626; E-mail: noah@bgu.ac.il

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and skeletal muscle [26,27], and lower or undetectable levels in other tissues tested. For reasons that are not clear yet, it is highly expressed in gastrointestinal stromal tumors, but not in other mesenchymal or epithelial tumors [31-34].

Engagement of the TCR and the CD28 coreceptor on most T cells results in PKC θ translocation to the center of the immunological synapse (IS) [35,36]. Full activation of the enzyme requires the integration of TCR and CD28 costimulatory signals [37-39] and additional steps of posttranslational modification that increase the PKC θ catalytic activity [40]. These include the inducible phosphorylation of PKC θ at multiple sites on serine, threonine and tyrosine residues. Phosphorylation is mediated by several upstream kinases (including autophosphorylation) that affect the enzyme's topology, open the ATP binding site and activation loop, and convert PKC θ into a catalytically potent enzyme [41]. The most recent kinase described that phosphorylates the IS-residing PKC θ is the germinal center kinase (GSK)-like kinase (GLK) [42]. Similar to PKC θ , the GLK translocates to the IS of TCR-engaged T cells where it directly interacts with PKC θ and phosphorylates threonine 538 in its activation loop, thereby enabling better access of substrates to the enzyme's activation segment.

The IS-residing, enzymatically active PKC θ initiates a series of signaling events leading to activation of transcription factors, including nuclear factor- κ B (NF- κ B), activating protein-1 (AP-1) and nuclear factor of activated T cells (NF-AT), which are critical for T cell proliferation and differentiation [43-48]. These three types of transcription factors are primary physiological targets of PKC θ [43,49], although regulation of the NF-AT requires cooperation of PKC θ with calcineurin, a Ca²⁺-dependent serine/threonine phosphatase that regulates the nuclear translocation of the cytoplasmic NF-AT by dephosphorylating a critical residue that masks a nuclear localization sequence [43,49]. The three PKC θ -regulated transcription factors have corresponding binding sites on the IL-2 gene promoter, and all three transcription factors are essential for the induction of an optimal IL-2 response [50].

The translocation of PKC θ to the center of the IS is not a universal phenomenon in activated T cells, as demonstrated by Dustin and colleagues using an isolated population of regulatory T cells (Treg) [51,52]. Their findings indicated that although TCR/CD28 triggering of Treg resulted in IS formation, PKC θ translocates to the opposite cell pole, away from the IS, and negatively regulates their suppressive function, although the precise mechanism of action and mode of regulation of PKC θ in Treg is not yet clear.

Studies by Rao and colleagues further demonstrated that under certain activation conditions, PKC θ has the ability to translocate to the nucleus and physically interact with chromatin. Together with other nuclear enzymes, PKC θ molecules form active complexes that bind regulatory DNA regions and control the expression of selected microRNAs and specific T cell inducible genes [53].

The exact mechanisms by which the membrane-bound PKC θ delivers signals to the nucleus have not been fully resolved, but studies provided information on a number of effector molecules that operate along these pathways in activated T cells. These studies demonstrated that the regulation of NF- κ B by PKC θ involves the multisubunit inhibitor of κ B (I κ B) kinase (IKK) complex [44,46,47,54,55]. Another important upstream regulator of the NF- κ B signaling pathway is the I κ B α , which can directly associate with the cytosolic NF- κ B of resting T cells, and by masking its nuclear localization signal (NLS), prevent NF- κ B translocation to the nucleus [56-58]. On the other hand, IKK-

mediated phosphorylation of I κ B α signals the protein for degradation [59], and by exposing the NF- κ B NLS, it promotes NF- κ B translocation to the nucleus where transcriptional upregulation of NF- κ B-dependent genes occur. The current dogma, that PKC θ regulates NF- κ B activity through its effect on IKK-I κ B α , is further substantiated by *in vivo* studies demonstrating that T cells from PKC θ -deficient (*Prkcd*^{-/-}) mice fail to respond to TCR stimulation with degradation of I κ B α [45].

PKC θ Binding Proteins and Substrates

One of the most prominent target proteins that links PKC θ to IKK is the PKC θ substrate protein, caspase activation and recruitment domain (CARD) and membrane-associated guanylate kinase (MAGUK) domain-containing protein-1 (CARMA1) [60-63]. This scaffold protein is primarily expressed in lymphocytes [64,65] and its phosphorylation by PKC θ in TCR/CD28-stimulated T cells, promotes CARMA1 association with two additional effector molecules: the B-cell lymphoma/leukemia 10 (Bcl10), and the mucosa-associated lymphoid tissue 1 (MALT1) [66,67]. The resulting trimolecular complex recruits to the IS [68-70] where the three partners cooperate in delivering signals leading to maximal activation of NF- κ B [61,71].

Besides its effects on transcriptional regulation, PKC θ is also involved in the regulation of many other cellular functions. Some functions require the direct or indirect association of PKC θ with upstream kinases, which may affect the enzyme's conformation, activity or subcellular distribution (i.e., Lck [72]), while other functions are dependent on PKC θ interaction with downstream kinases, which serve as intermediate PKC θ -coupled signal transducers (i.e., Ste20-related upstream mitogen-activated protein kinase (SPAK) [49]). Additional molecules that serve as substrates for PKC θ regulate distinct cellular functions, such as cytoskeletal reorganization (i.e., Cbl, 14-3-3 τ and moesin [73-75]) and signal transduction (i.e., phosphoinositide-dependent-kinase-1 (PDK1) [76], insulin receptor substrate 1 (IRS-1) [77], Ras-related protein (Rap) guanine nucleotide exchange factor-2 (RapGEF2) [78], and hexamethylene bis-acetamide-inducible protein 1 (HEXIM1) [79]). Other proteins that associate with PKC θ include Fyn [80], AKT [54], PICOT [81] and the HIV nef protein [82], although the functional consequences of these interactions require further analyses.

A recent study suggests that the C2-like domain of PKC θ functions as a phosphotyrosine-binding (PTB) module that is also involved in regulating the PKC θ catalytic activity [83]. This study demonstrated that the PKC θ C2-like domain can interact with a CUB domain-containing protein 1 (CDCP1; also termed CD318)-derived tyrosine phosphorylated peptide with a relatively high affinity, and that binding increases the potency of the PKC θ catalytic activity. Furthermore, mutating the PTB sequence in a way that prevented binding of the tyrosine phosphorylated CDCP1, abrogated PKC θ activity and inhibited the TCR/CD28-mediated activation of a PKC θ reporter gene in T cells.

PKC θ in distinct T cell subsets

Following the discovery that PKC θ is expressed in T cells [50,84] studies have focused on the potential biological functions of this enzyme and provided substantial evidence to support a critical role in diverse intracellular signaling pathways that regulate T cell activation, proliferation, differentiation and apoptosis [45,48,85]. Despite its important functions in mature T cells, studies in *Prkcd*^{-/-} mice demonstrated that PKC θ is dispensable for thymocyte maturation and differentiation [45], suggesting a redundancy with other thymocyte-residing PKC isoforms [86].

Additional *in vivo* studies performed in *Prkcd*^{-/-} mice demonstrated that distinct T cell subpopulations differ in their requirements for PKC θ , a phenomenon that is dependent on the type of antigen and the immune response elicited. The current dogma suggests a requirement for PKC θ in Th2-type immune responses to allergens or helminth infection [87,88] and Th17-type immune responses leading to the development of experimental autoimmune encephalomyelitis (EAE), an inflammatory disease of the central nervous system that is widely used as a model of Multiple Sclerosis [85,89-92]. PKC θ is also required for the induction of experimental autoimmune myocarditis [91], Ag-induced arthritis [93], and systemic lupus erythematosus [42].

In contrast, ablation of PKC θ does not impair mouse resistance to *Leishmania major* infection, mediated primarily by Th1 cells [87,94], or CTL-mediated protection from viral infection, which may reflect compensatory activities mediated by innate immunity mechanisms [91,95-98].

Furthermore, PKC θ was found to be required for the induction of allograft rejection and graft-versus-host (GvH) and alloreactive T cell-mediated immune responses, [98,99], while being dispensable for graft-versus-leukemia responses in allogeneic bone marrow transplanted mice [98].

Although many of the effects induced by PKC θ ablation on the quality and intensity of immune responses are due to impaired TCR/CD28-coupled signaling pathways in the effector T cells (T_{eff}), some of these effects could reflect changes in the activity of regulatory T cells (T_{reg}) that under normal conditions downregulate specific functions of T_{eff}. Recent findings supported this assumption by showing that PKC θ mediates a negative feedback on T_{reg} functions [51]. In these studies activation of T_{reg} led to PKC θ sequestration away from the IS, while inhibition of PKC θ increased the suppressive activity of T_{reg} [51,52]. Furthermore, T_{reg} development in the thymus of *Prkcd*^{-/-} mice was abnormal, resulting in reduced numbers of T_{reg} cells in the periphery [51,52,100], although the activity of the mature PKC θ -deficient T_{reg} was not affected [101].

The Immunological Synapse and PKC θ

The immunological synapse, also known as the supramolecular activation cluster (SMAC), is a temporally and spatially regulated plasma membrane structure formed at the interface between an antigen-presenting cell (APC) and a responding T cell, and is the site at which early T cell activation signaling events occur [102]. It is formed upon the recognition by the TCR of a cognate antigenic peptide-MHC on the surface of APC, when both cell types respond by redistributing their receptors, cytoskeletal proteins and intracellular signaling molecules to the contact area, which rearranges as a platform for effective signaling [103,104].

The IS is characterized by specific microclustering of selected receptors and effector molecules [105], and is composed of three concentric rings, each containing a relatively high concentration of a typical combination of molecules. The central-SMAC (c-SMAC) is characterized by a high content of TCR and PKC θ [35,36], in addition to costimulatory receptors (CD28, CD2, CD4, and CD8) and Src family tyrosine kinases (Lck and Fyn) [106]. Recent studies utilizing a high-resolution total internal reflection fluorescence (TIRF) microscopy observed two structurally and functionally distinct cSMAC compartments: 1. A central TCR^{high} compartment, where TCR-associated signaling complexes are internalized and degraded and the entire signaling process is being terminated [107]. 2. An outer TCR^{low}

compartment enriched in PKC θ and CD28 where the two proteins are colocalized [38]. Coimmunoprecipitation studies confirmed that PKC θ and CD28 colocalization is a consequence of a physical interaction between the two proteins [38]. The second concentric ring of the IS, the peripheral-SMAC (pSMAC) possesses high concentrations of adhesion molecules (lymphocyte function-associated antigen-1 (LFA-1)) and the cytoskeletal elements (talin) [35], while the third outermost ring, the distal-SMAC (dSMAC), is characterized by its high content of CD43 and CD45 surface receptors [108,109].

Mechanism of Recruitment of PKC θ to the IS

Early investigations demonstrated that TCR engagement, which polarizes PKC θ and induces its recruitment to the IS, is greatly augmented by colligation of the CD28 stimulatory receptor [37-39]. More recent studies demonstrated a physical interaction between PKC θ and CD28 in PMA-stimulated T cells [38], findings that were further substantiated and set up the basis for the understanding of the mechanism by which the two protein interact [110]. These studies revealed that TCR/CD28 costimulation induces transient binding of PKC θ to the cytoplasmic tail of CD28.

Amino acid sequence comparison between PKC θ and PKC δ , the closest relative of PKC θ , indicated the existence of a lowest sequence homology between the two proteins in the V3 (hinge) domain (Figure 1), which corresponds to amino acids ~291-378 of human PKC θ . Since PKC δ , in contrast to PKC θ , does not translocate to the IS of TCR/CD28 activated T cells [36], the findings suggested a potential role for the PKC θ -V3 domain in targeting the enzyme to the IS.

To analyze this hypothesis, a V3-deletion mutant of PKC θ (PKC θ - Δ V3) or a PKC θ exchange mutant, in which the native V3 domain was replaced by the PKC δ V3 domain, were ectopically expressed in T cells, and tested for their ability to associate with CD28. The results demonstrated that, in contrast to the wild type PKC θ , the two mutants failed to coimmunoprecipitate with CD28 [110]. Furthermore, the two genetically modified PKC θ proteins failed to translocate to the IS and to activate PKC θ -dependent reporter genes, such as the CD28 response element (RE/AP). On the other hand, an overexpressed isolated V3 domain of PKC θ localized to the center of the IS of TCR/CD28 stimulated T cells and associated with CD28. In a complementary line of studies, T cells recovered from mouse bone marrow (BM)

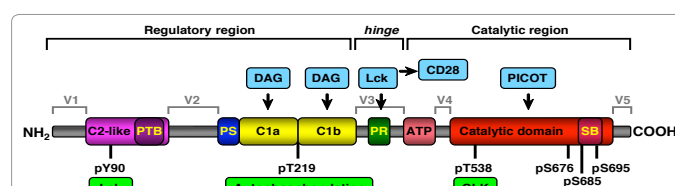


Figure 1: Structure of the human PKC θ protein.

Individual domains in the PKC θ regulatory and catalytic regions are indicated by rectangles with different colors. Molecules that bind PKC θ and are mentioned in the text are indicated above the enzyme (in light blue rectangles) and arrows point to specific PKC θ domains that mediate these interactions. PICOT is a representative of a growing number of proteins that were found to physically interact with PKC θ . Black lines represent phosphorylation sites and the type of amino acid residue that undergoes phosphorylation and its position is indicated below the black line. Kinases that are known to phosphorylate specific amino acids on PKC θ are indicated in a green box below the relevant phosphosite.

V: Variable domain; C: Constant domain; PTB: Phosphotyrosine Binding module; PS: Pseudosubstrate region; PR: Proline-Rich motif; SB: Substrate Binding region; DAG: Diacylglycerol; GLK: Germinal center kinase (GSK)-like kinase; PICOT: PKC-Interacting Cosine of Thioredoxin; Lck: Lymphoid cell kinase.

Most of the existing small molecule PKC inhibitors have toxic side effects because of their lack of absolute specificity, which reflects the relatively high conservation of catalytic domains within PKC family members. Furthermore, since most catalytic kinase inhibitors are ATP competitors, they need to be used at relatively high and potentially toxic concentrations in order to effectively compete with ATP, whose intracellular concentration is ~1 mM. As a result, current studies are aimed at the development of allosteric inhibitors that interact with regions on the kinase molecule, which are outside of the catalytic site, and are therefore likely to be more selective to individual PKC isoforms and exhibit less non-specific toxic effects [113]. The studies by Kong et al., revealed a new potential approach for attenuating PKC θ -dependent functions utilizing allosteric compounds based on the critical PR motif in the PKC θ -V3 domain that block PKC θ binding to CD28 [110]. Since this interaction is essential for PKC θ recruitment to the IS and for the induction of PKC θ -dependent downstream signaling, this new approach could serve as a basis for the development of new therapeutic agents that would selectively suppress undesired T cell-mediated inflammation and autoimmunity or prevent allograft rejection, while preserving desired immunity, such as antiviral responses.

Concluding Remarks

Past studies have established the requirement for PKC θ in the regulation of many fundamental processes in T cell biology (Figure 2). More recent findings indicated that pharmacological inhibitors of PKC θ might represent beneficial therapeutic modalities for blocking pathological T cell mediated immune responses, without interfering with anti-viral and anti-cancer immunity. Furthermore, since PKC θ is a positive regulator of T cell surveillance, its selective inhibition may help eradicate leukemic T cells by increasing their sensitivity to apoptosis. The development of new small molecule inhibitors and allosteric inhibitors of PKC θ provides promises for future ability to manipulate PKC θ in different disease conditions. Precautions must be taken prior to the clinical application of such inhibitors, in order to evaluate their potential *in vivo* effects on other PKC θ -positive cell types, and potential iatrogenic effects on PKC θ -negative tissues.

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