Protein Kinase C (PKC): Activation Mechanisms and Cellular Functions

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The isotype of protein kinase C (PKC) is a member of the atypical PKC subfamily and has been widely implicated in the regulation of cellular functions. Increasing evidence from studies using *in vitro* **and** *in vivo* **systems points to PKC as a key regulator of critical intracellular signaling pathways induced by various extracellular stimuli. The major activation pathway of PKC depends on phosphatidylinositol (PI)-3,4,5** trisphosphate (PIP₃), which is mainly produced by PI-3 kinase. 3'-PI-dependent pro**tein kinase 1, which binds with high affinity to PIP3, phosphorylates and activates PKC. Many studies demonstrated the involvement of PKC in the mitogen-activated protein kinase cascade, transcriptional factor NFB activation, ribosomal S6-protein kinase signaling, and cell polarity. An important molecular event in a cell is the association of PKC with other signaling molecules, as well as scaffold proteins, to form large complexes that regulate their pathways. The understanding of the mechanisms underlying PKC-mediated control of intracellular signaling is beginning to provide important insights into the roles of PKC in various cells.**

Key words: PDK1, PI3K, PIP3, PKC, ZIP/p62.

Structure of PKC

Protein kinase $C\zeta$ (PKC ζ) was originally discovered as a unique PKC isotype (*[1](#page-4-0)*). To date in mammals, it is classified into the atypical PKC (aPKC) subfamily, based on its structural similarity to PKC-/ [human PKC (*[2](#page-4-1)*) and mouse $\mathrm{PKC}\lambda \left(3\right)$ $\mathrm{PKC}\lambda \left(3\right)$ $\mathrm{PKC}\lambda \left(3\right)$ are orthologs]. The a $\mathrm{PKC}s$ and other PKC isotypes, namely, conventional PKC (cPKC) α , βI , βII, and γ, and novel PKC (nPKC) δ, ε, η, and θ, form the PKC family belonging to an extended group of Ser/Thr protein kinases, AGC (cAMP-dependent protein kinase (PKA), cGMP-dependent protein kinase (PKG), and PKC) (*[4](#page-4-3)*).

PKC ζ , as well as PKC λ ¹, consists of four functional domains and motifs, including a PB1 domain in the Nterminus, a pseudosubstrate (PS) sequence, a C1 domain of a single Cys-rich zinc-finger motif, and a kinase domain in the C-terminus (Fig. [1\)](#page-6-0). The PB1 domain recognizes OPCA (OPR/PC/AID) motifs of other proteins, such as PAR-6, ZIP/p62 and MEK5 (*[5](#page-4-4)*) (see below). The PS is a short stretch of amino acids which resembles a substrate sequence except for Ala occupying the position of Ser or Thr as a phospho-group acceptor, and is assumed to block the substrate-binding cavity of the kinase domain as an autoinhibition mechanism. The C1 domains of aPKC isotypes are different in terms of a repeat structure from those of cPKCs and nPKCs that contain two repeated zinc-finger motifs, C1A and C1B, both of which are essential for interaction with and activation by a second messenger diacylglycerol (DG) and phorbol-diester tumor promoters. Although the C1 domains of aPKCs are similar to those of C1A, aPKCs do not respond to DG and phorbol-diesters (*[6](#page-4-5)*). The kinase domain of PKC, as well as other members of the AGC group, includes an ATP-binding region, an activation loop, a turn motif, and a hydrophobic motif. The ATPbinding region contains a Lys residue, Lys-281, which is crucial for its kinase activity. A mutant whose Lys-281 is substituted for other amino acids is usually used as a kinase-defective dominant-negative form of PKC ζ (PKC ζ kn). The activation loop and turn motif contain important Thr residues, namely Thr-410 and Thr-560, respectively, which are phosphorylated upon activation. Recent studies reveal dynamic interactions of PKC ζ with other proteins.

Activation mechanisms

The mechanisms of PKC activation mainly consist of two events, release of the PS from the substrate-binding cavity and phosphorylations of the kinase domain (*[7](#page-4-6)*). Upon liberation from the PS-dependent autoinhibition, some lipids play important roles. cPKCs and nPKCs interact with membrane lipids, such as phosphatidylserine, and lipid metabolites such as DG, which presumably induce the release of PSs from active sites resulting in phosphorylation of their substrate proteins.

PKC ζ is also activated by lipid components, such as phosphatidylinositols (PIs) (*[8](#page-4-7)*), phosphatidic acid (*[9](#page-4-8)*), arachidonic acid (*[10](#page-4-9)*), and ceramide (*[10](#page-4-9)*). Among these lipids, PI-3,4,5-trisphosphate (PIP_3) has been the focus of much interest with regards to its regulation of aPKCs in various cells. Nakanishi *et al.* reported that enzymatically synthesized PIP_3 stimulates autophosphorylation of $PKC\zeta$ purified from bovine kidney, whose phosphorylation is one of the requirements for protein kinase activation, suggesting that aPKCs can be regulated by PI-3 kinase (PI3K), which produces PIP_3 from PI-4,5-bisphos-

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Fig. 1. **Schematic representation of domain structure of PKC.** PKC consists of a PB1 domain in the N-terminus, a pseudosubstrate (PS), a C1 domain, and a Ser/Thr kinase domain in the Cterminus. The kinase domain includes an ATP-binding region, an activation loop, a turn motif, and a hydrophobic motif. In the ATP-binding region, Lys-281 is essential for kinase activity. Thr-410 in the activation loop is phosphorylated by PDK1 which binds to the hydrophobic motif. Thr-560 in the turn motif is the autophosphorylation site and its phosphorylation is also crucial for the activation.

phate in response to various growth factors (*[8](#page-4-7)*). In rat 3Y1 cells stimulated by epidermal growth factor (EGF) or platelet-derived growth factor, overexpression of p110, a catalytic subunit of PI3K, enhances PKC λ ¹ activity ([11](#page-4-10)). To date, there are many lines of evidence on activations of PKC ζ and PKC λ h by PI3K in living cells, *e.g*., adipocytes (12) (12) (12) and monocytes (13) (13) (13) . How does PIP_3 interact with aPKCs?

 $PIP₃$ directly binds to pleckstrin homology (PH) domain–containing protein kinases, *e.g.*, protein kinase B (PKB; also known as Akt) and 3-PI–dependent protein kinase 1 (PDK1). The PH domain of PDK1 has a higher affinity for PIP_3 than that of PKB/Akt ([14](#page-5-2)). PDK1 is activated by binding PIP_3 through its PH domain, and attaches to the hydrophobic motifs of AGC kinases, so that they are phosphorylated at a Thr residue in each activation loop (*[15](#page-5-3)*) (Fig. [2\)](#page-6-0). The hydrophobic motifs of aPKCs include a short sequence, Phe-Glu-Gly-Phe-Glu-Tyr, which is very similar to that of PDK1-binding sites of PKC-related protein kinases, Phe-X (any amino acid)-X-Phe-Asp-Tyr ([16](#page-5-4)) (Fig. [1](#page-6-0)). In the activation loop of PKC ζ , Thr-410 is phosphorylated by PDK1 (*[17](#page-5-5)*, *[18](#page-5-6)*). In embryonic stem cells lacking PDK1 as a result of genetic manipulation, PKC ζ is not phosphorylated at Thr-410, markedly suggesting that $PKC\zeta$ is a physiological substrate of PDK1 (*[19](#page-5-7)*). Although a T410A mutant of PKC, whose Thr-410 is substituted for Ala, loses enzymatic activity, a Glu-mutant T410E, probably mimicking a

Fig. 2. **Schematic representation** of PIP₃ **and PDK1 in PKC activation.** The p85 subunit of PI3K interacts with the phosphorylated Tyr residues of receptor-Tyr kinases (RTKs) in responses to their ligands, and activates the p110 catalytic subunit, thereby producing PIP₃. PDK1 binds to PIP₃ via its PH domain, and becomes activated. The PDK1 interacts with PKC ζ and phosphorylates the kinase domain (KD) at Thr-410, which induces Thr-560 phosphorylation. The PKC ζ simultaneously and directly interacts with PIP_3 , which releases PSdependent autoinhibition. Both contributions of $PIP₃$ and PDK1 are necessary for the complete and stable activation of PKC.

phosphorylated Thr, retains its activity (*[17](#page-5-5)*, *[20](#page-5-8)*). These findings suggest that Thr-410 phosphorylation is essential for PKC ζ activation.

Following the Thr-410 phosphorylation, $PKC\zeta$ presumably exposes the kinase domain for further phosphorylation. Thr-560 in the turn motif of $PKC\zeta$ is a key residue for activation (18) (18) (18) , since in PKC α and PKC β II, phosphorylations of Thr-638 and Thr-641, respectively, corresponding to Thr-560 in PKC ζ are required for their catalytic functions and for locking these kinases in a catalytically competent state (*[21](#page-5-9)*, *[22](#page-5-10)*). The T410E active mutant of PKC ζ shows autophosphorylation but two Thr-560 mutants, T560A and T560E, do not in labeling experiments *in vitro*, indicating that Thr-560 is the sole autophosphorylation site in PKC ζ ([23](#page-5-11)). In living cells, whether Thr-560 of $PKC\zeta$ is phosphorylated by itself, by another $PKC\zeta$ intermolecularly, or by other protein kinases including other PKC isotypes, remains to be resolved.

Does PIP_3 activate aPKCs only through PDK1 activation? There are no discernible effects of PIP_3 on truncated PKC ζ and PKC λ h, both of which lack the PS sequence, whereas PIP_3 induces dose-dependent increases in the activity of a T410E/T560E PKC ζ double mutant; therefore, this mutant cannot phosphorylate the kinase domain (23) (23) (23) . This suggests that PIP_3 -induced activations of aPKCs are at least partly dependent on the presence of the PS sequences in their N-termini, and that these

apparent dependencies are most readily explained by their liberation from PS-dependent autoinhibition. Although no PIP_3 -binding region in PKC ζ has been identified, collectively, PIP_3 contributes to $\text{PKC}\zeta$ activation in two ways: direct modulation by the PS-dependent autoinhibition and indirect modulation by phosphorylation of the kinase domain through PDK1. Both contributions may be necessary for the complete and stable activation of PKC.

Furthermore, specific protein–protein interactions affect PKC activities. Several proteins interact with and inhibit aPKCs. Prostate apoptosis response–4 (Par-4) interacts with the C1 motifs of aPKCs and inhibits their activities (*[24](#page-5-12)*). A product of *Caenorhabditis elegans* partitioning defective gene-3 (PAR-3) (also known as ASIP, aPKC-specific interacting-protein, a mammalian homolog of PAR-3) binds the kinase domains of aPKCs and inhibits their activities (*[25](#page-5-13)*, *[26](#page-5-14)*). An OPCA motif–containing protein, PAR-6 (a product of partitioning defective gene– 6) binds to the PB1 domains of aPKCs (*[27](#page-5-15)*). Furthermore, PAR-6, PAR-3, and aPKC form a ternary complex (*[25](#page-5-13)*[,](#page-5-15) [27](#page-5-15)). In the complex, PAR-6 suppresses $PKC\lambda/1$ activity, which is released by the further association of an active form of Cdc42 (*[28](#page-5-16)*). In addition, several interacting proteins provide specificities of functional timing and location of aPKCs (see below).

Signaling and functions

Mitogen-activated protein kinase (MAPK) cascade. Many studies have shown that $PKC\zeta$ is involved in the MAPK cascade in various cells (*[29](#page-5-17)*–*[32](#page-5-18)*). In monkey COS cells stimulated by serum or tumor necrosis factor α (TNF α), an active mutant of rat PKC ζ or *Xenopus* PKC λ (previously known as an amphibian $PKC\zeta$) activates MAPK-kinase MEK1 and a MAPK ERK1, but a PKC ζ -kn mutant does not (*[29](#page-5-17)*). In thyroid cells, overexpression of wild-type $PKC\zeta$ activates $ERK1$ and $ERK2$, and increases transcriptional activity of Elk-1, a well-established target of ERK1 and ERK2, whereas thyroid-stimulating hormone does not (31) (31) (31) . What is the target of PKC ζ in the MAPK cascade? Interestingly, overexpression of an active form of PKC, which lacks PS, also activates MEK1 but not Raf1 in COS cells (*[31](#page-5-19)*). In human alveolar macrophages, lipopolysaccharide (LPS) activates MEK1, ERK1 and ERK2 but not Raf1 (*[32](#page-5-18)*). At this point, endogenous $PKC\zeta$ is activated and induced to associate with MEK1. Moreover, the myristoylated PKC ζ -PS peptide, which inhibits PKC, blocks these LPS effects (*[32](#page-5-18)*). These findings suggest that $PKC\zeta$ functions as a MEK1 kinase, independent of the Raf1 pathway. However, it is still unclear whether $PKC\zeta$ phosphorylates MEK1 directly or indirectly (*[31](#page-5-19)*, *[32](#page-5-18)*). Thus, to understand the functions of $PKC\zeta$ in the MAPK cascade, it is important to clarify this point.

On the other hand, $PKC\zeta$ was reported to function as an adapter in the MEK5-ERK5 pathway, which is another MAPK cascade critically involved in mitogenic activation by EGF (*[33](#page-5-20)*). In response to EGF, endogenous PKC ζ binds to MEK5 at its OPCA motif and increases ERK5 activity in the human transformed-cell line HEK293 (*[33](#page-5-20)*). Conversely, overexpression of the MEK5- OPCA peptide or the PKC-PB1-domain peptide, both of

which interfere with PKC ζ -MEK5 interaction, inhibits the ERK5 activity (*[33](#page-5-20)*). Importantly, overexpression of PKC ζ -kn can also increase this EGF-induced ERK5 activity, suggesting that $PKC\zeta$ functions only as an adapter (33) (33) (33) . Furthermore, PKC ζ binds to and activates PKB_Y/Akt3 by phosphorylation at the C-terminal Ser of PKB_{γ}/Akt₃ ([34](#page-5-21)). Interestingly, the phosphorylation does not depend on the PKC_{ζ} activity, but probably depends on an as yet unidentified type of PDK, PDK2 (*[34](#page-5-21)*). Although a novel and interesting function of $PKC\zeta$ as an adapter independent of its enzymatic activity is proposed in the above studies, further studies focusing on this issue in various signaling molecules are required.

From receptor signaling complexes to activation of NFB transcriptional factor. In signaling for cell growth and survival, extracellular ligands, $e.g., TNF\alpha$, interleukin-1 (IL-1), and nerve growth factor (NGF), play their roles most likely through regulations of signaling pathways from their receptor complexes to their target gene expressions mediated by transcription factors, such as nuclear factor κ B (NF κ B) (Fig. [3](#page-6-0)). PKC ζ -kn blocks responses of $NFRB$ to these stimuli, indicating that $PKC\zeta$ is critically involved in $NFRB$ activation in signal transductions of TNF α and IL-1 ([35](#page-5-22), [36](#page-5-23)). An important issue concerning the involvement of $PKC\zeta$ in these signaling pathways is its interactions with those receptor-signaling complexes. In this regard, OPCA motif–containing ZIP (zeta-interacting protein) homologs provide a mechanis-tic clue ([37](#page-5-24)-[39](#page-5-25)). Puls *et al.* first showed that PKCζ binds to rat ZIP in a yeast two-hybrid system (*[37](#page-5-24)*). Since ZIP homologs including human 62-kDa Lck-binding protein (p62) (*[40](#page-5-26)*) have been cloned using different methods (*[39](#page-5-25)*), we use the term ZIP/p62 in this article. Furthermore, two alternative-spliced forms, ZIP2 and ZIP_B, were reported $(41, 42)$ $(41, 42)$ $(41, 42)$ $(41, 42)$ $(41, 42)$. ZIP/p62 contains a TRAF6 (TNF α receptor-associated factor 6)-binding site (*[43](#page-5-29)*), whereas ZIP2 deletes this site.

ZIP/p62 links PKC ζ or PKC λ / ι to the TNF α receptor signaling complex including TRAF2 and receptor-interacting protein (RIP) (*[35](#page-5-22)*). In human carcinoma HeLa cells and HEK293 cells, ZIP/p62 selectively interacts with RIP, but not with TRAF2 (*[35](#page-5-22)*). Furthermore, ZIP/p62 links PKC ζ to IL-1 and NGF receptor complexes including TRAF6 (*[36](#page-5-23)*, *[43](#page-5-29)*). In these cases, ZIP/p62 only functions as an adapter or a scaffolding. However, ZIP/p62 antagonizes Par-4-induced PKC ζ inhibition and apoptosis of human osteosarcoma U2OS cells induced by TNF α ([44](#page-5-30)). This suggests that ZIP/p62 also plays a critical role in the regulation of PKC ζ activity in addition to its adapter function (*[44](#page-5-30)*). Although the activation mechanisms of PKC ζ containing ZIP/p62 are not understood, conformational changes may render PKC ζ accessible to their substrates and thereby inducing NF_KB activation.

Functions of NF_KB including DNA binding, transactivation, and nuclear translocation are blocked by its cellular inhibitor protein I_KB. An essential component of the N F κ B pathway is the I κ B kinase (IKK) complex, which $phosphorylates$ I_KB and triggers its degradation to release NF_KB from its cytosolic state and then to translocate it into the nucleus (45) (45) (45) . PKC ζ phosphorylates the IKK_{β} subunit *in vitro*, possibly through their direct inter-action ([46](#page-5-32)). In HEK293 cells, PKC₅ interacts with IKK_B through each catalytic domain in a TNF α -stimulation-

Fig. 3. **Schematic representation of involvement of PKC in** signaling pathways from receptor complexes of TNFa, IL-1, and NGF to NF_KB activation. ZIP/p62 links PKC₂ to RIP in $\text{TNF}\alpha$ receptor (TNFR) complex and to TRAF6 in complexes of IL-1 receptor (IL-1R) and NGF receptor (NGFR). The PKC ζ phosphorylates and activates IKK, which induces IKB degradation, thereby inducing nuclear translocation, DNA-binding, and transactivation of NF_KB.

dependent manner, thereby activating $IKK\beta$ ([46](#page-5-32)). In the lungs of PKC ζ -deficient mice, TNF α -induced IKK activation is depressed (47) (47) (47) . These findings indicate that $PKC\zeta$ is involved in the IKK signaling complex.

Collectively, aPKCs transduce signals from the receptors of TNF α , IL-1, and NGF to the activation sites of NF_KB *in vivo*. Furthermore, they may be involved in a variety of signaling pathways from receptor complexes to expressions of their target genes by activation of transcription factors.

p70S6 kinase signaling cascade. p70 ribosomal S6 protein kinase (p70S6K), which is phosphorylated and activated in response to mitogenic stimuli, modulates translation of a subset of mRNAs that encode ribosomal proteins and translation elongation factors. Akimoto *et* al. first reported that PKC λ ¹ directly associates with p70S6K, and that dominant negative forms of this kinase suppress the serum-induced activation of p70S6K in liv-ing cells ([48](#page-6-1)). In coexpression experiments, PKC ζ -kn antagonizes p70S6K activation by EGF, PDK1 and PI3K, and p70S6K associates with PDK1 as well as with PKC *in vivo* in a growth-factor-independent manner (*[49](#page-6-2)*). This suggests the existence of a multimeric PI3K-p70S6K signaling complex. Then, does PKC ζ modulate p70S6K activity in this complex? p70S6K is one of the AGCkinases, and phosphorylations of its Thr-229 and Thr-389 in the activation loop and the hydrophobic motif, respectively, are important for activity. Myristoylated PKC, a constitutive active form of PKC, synergistically enhances PDK1-induced phosphorylations, as well as simply increases phosphorylations, of these residues, which induces prolonged activation of p70S6K (*[50](#page-6-3)*). Thus collectively, aPKCs apparently play crucial roles in p70S6K activation. However, recombinant aPKCs do not directly phosphorylate p70S6K *in vitro* (*[48](#page-6-1)*, *[50](#page-6-3)*). The myristoylated PKC₅ does not occlude EGF-dependent activation of p70S6K (*[49](#page-6-2)*). Moreover, the myristoylated PKC can only enhance Thr-389 phosphorylation in the catalytically competent p70S6K (*[50](#page-6-3)*). These would suggest that aPKCs alone are not sufficient for the complete activation of p70S6K. Multiple signals, such as mammalian target of rapamycin (mTOR) and PKB/Akt, are required for p70S6K activation. Thus, aPKCs may play a tuning role in translation together with other regulators.

Cell polarity. Cell polarity is fundamental not only for cell functions but also for development and tissue maintenance. Recent studies have revealed the importance of the ternary complex of PAR-3, PAR-6, and PKC or PKC- in cell polarity (*[25](#page-5-13)*, *[27](#page-5-15)*, *[51](#page-6-4)*). The PAR-3/ASIP-PAR-6-PKC λ complex controls formation of tight junctions in MDCK cells, an epithelial cell line derived from the dog kidney (*[52](#page-6-5)*). PKCζ-kn, as well as PKCλ-kn, disrupts localization of ZO-1, a component of the tight junction, and probably interferes with the establishment of cell polarity (*[52](#page-6-5)*). Overexpression of the regulatory domain (amino acids $1-126$) of PKC ζ causes a similar defect in the tight junction assembly, whereas a mutant containing two Asp residues (Asp-62 and Asp-66) within the PB1 domain does not (*[53](#page-6-6)*). These findings suggest that both of the kinase activity and interactions *via* the PB1 domain are necessary for PKC ζ to control cell polarity.

In addition to epithelial cells, $PKC\zeta$ also controls polarity in migrating astrocytes. Scratching a confluent monolayer of rat primary astrocytes leads to their polarization at the leading edge, so that the microtubule organization center (MTOC) and the Golgi apparatus reorganize to face the new free space, and directed cell protrusion and migration specifically occur perpendicu-lar to the scratch ([54](#page-6-7)). Overexpressions of PKCζ, PKCζkn and PAR-6 inhibit MTOC and Golgi apparatus polarization without affecting the direction of protrusion (*[54](#page-6-7)*). Collectively, the ternary complex of PAR-3/ASIP-PAR-6 aPKC plays an essential role in polarization of some cell types.

A neuron is a typical polarized cell. A Leu-zipper motif–containing protein FEZ1 (fasciculation and elongation protein; zygin/zeta-1) interacts with PKC ζ at the Nterminal region including the PB1 domain, but does not contain any OPCA motif (*[55](#page-6-8)*). FEZ1 is a human homolog of the *C. elegans* locomotory-defect gene product UNC-76 that is necessary for axonal bundling and elongation within axonal bundles (*[56](#page-6-9)*). Coexpression of FEZ1 and an active form of PKC ζ stimulates dendritic neurite elongation of rat pheochromocytoma PC12 cells, whereas expression of FEZ1 alone does not affect the cells (*[55](#page-6-8)*). FEZ1 is phosphorylated by $PKC\zeta$ and then translocated from the cytoplasmic membrane to the cytoplasm (*[55](#page-6-8)*). Furthermore, a protein localized in the postsynaptic density and dendritic raft, PSD-Zip70, is a closely related homolog of FEZ1 (*[57](#page-6-10)*). Although evidence on cellular functions and phosphorylation is limited, interaction of PKC ζ with FEZ1/PSD-Zip70 may play an important role in neurite elongation and maintenance of the postsynaptic structure.

Furthermore, a tumor suppressor gene at 8p22 (*LZTS1*), a frequently altered chromosome region in many malignant tumors, including esophageal, prostate, and breast cancer, encodes FEZ1 (*[58](#page-6-11)*, *[59](#page-6-12)*). FEZ1 is associated with microtubule components in human epithelial cells (59) (59) (59) . Combined with these findings, PKC ζ through its

interaction with FEZ1/PSD-Zip70 might be also involved in mechanisms underlying human carcinogenesis.

Long-term potentiation (LTP). In the brain, not only a 75-kDa protein of the native PKC, but also a smaller 51-kDa protein is detected by immunoblotting (*[60](#page-6-13)*). The amount of this 51-kDa protein referred to as PKM ζ increases in hippocampal CA1 pyramidal cells during LTP maintenance (*[60](#page-6-13)*, *[61](#page-6-14)*). PKM is a catalytic domain released from PKC by proteolysis. Injection of a predicted recombinant PKM ζ increases the AMPA (α amino-3-hydroxy-5-methylisoxazole-4-propionic acid) receptor–mediated excitatory postsynaptic current amplitude of neurons, and this PKM ζ -mediated increase in the current completely occludes LTP (*[62](#page-6-15)*). Low concentrations of chelerythrine and a myristoylated PKC-PS peptide, both of which inhibit PKC, also impair LTP maintenance (*[62](#page-6-15)*). Furthermore, a transgenic fly that overexpresses PKM cenhances memory after massed training (*[63](#page-6-16)*). Chelerythrine and the induction of a dominant-negative form of $PKM\zeta$ inhibit memory without affecting learning in wild-type flies (*[63](#page-6-16)*). These findings interestingly imply that PKM ζ is both necessary and sufficient for maintenance of LTP and memory (*[62](#page-6-15)*, *[63](#page-6-16)*). However, the importance of $PKM\zeta$ in LTP is not clear because the inhibition of memory by the kinase-negative form of PKM ζ may reflect its dominant-negative effects. Although chelerythrine also inhibits memory, its specificity to PKM ζ remains unclear. Thus, the loss of function of PKM ζ needs to be examined to confirm its importance in LTP maintenance.

Another possibility of production of a kinase-domain protein of PKC ζ has emerged. A PKC ζ -related (PKC ζ) cDNA includes a short alternative sequence upstream of the region encoding PS ([64](#page-6-17), [65](#page-6-18)). Although PKC ζ cDNA was previously assumed to be derived from a splicing intermediate of $PKC\zeta$ mRNA, the alternative sequence of rat PKC ζ ' cDNA presents as a single exon (exon 1') at about 50 kb upstream of exon 5 encoding PS in the PKC gene, $Prkcz$ ([66](#page-6-19)). The PKC ζ ^r mRNA is expressed in a human prostate cancer cell line, and the sequence upstream of exon 1' has promoter activity in the cells (*[66](#page-6-19)*). From the mRNA sequence, a protein of the kinase domain with a molecular weight of 46,600 is deduced (65) (65) (65) , whose size is interestingly similar to that of PKM ζ . From the viewpoint of brain-specific expression, PKM might be a variant form of $PKC\zeta$ alternatively transcribed from exon 1' of the PKC ζ gene, rather than that produced by proteolysis. Further studies are needed to clarify this point and to elucidate the molecular mechanisms underlying LTP maintenance by PKM.

Perspectives

What are the differences in physiological functions between PKCζ and PKCλ/ι? Although there is a report on differences in nucleocytoplasmic translocation between PKC₅ and PKC λ ¹ ([67](#page-6-20)), obvious functional differences have not been revealed in *in vitro* experiments. However, clear differences may be observed *in vivo*. PKC ζ -deficient mice normally develop and are apparently normal, but exhibit phenotypic features of mildly impaired maturation of B cells and a reduced number of Peyer's patches $(47, 68)$ $(47, 68)$ $(47, 68)$ $(47, 68)$ $(47, 68)$, whereas PKC λ ¹-deficient mice die at the embry-

onic stage (see accompanying article on $\text{PKC}\lambda\prime$ ı by Suzuki *et al.*). Fly DaPKC (*Drosophila* aPKC) and nematode PKC-3 (aPKC of *C. elegans*) are key molecules at each stage of development, and their deficiencies cause death at the embryonic stage (*[69](#page-6-22)*, *[70](#page-6-23)*). On the basis of primary structures, DaPKC and PKC-3 are more related to PKC λ /ı than to PKC. Thus, in mammals, the developmental control must be dependent on $PKC\lambda/1$ rather than on PKC₄. What then is the main role of PKC₄? Does it only compensate the roles of PKC λ / ι ? Many questions remain unanswered.

Although not discussed in this article, there are other important aspects on cellular functions of PKC, such as regulation of glucose-transporter vesicles (*[71](#page-6-24)*). Including these aspects, many lines of evidence documenting the role of PKC ζ in various cellular functions are accumulating. We can approximately account for the diverse physiological functions of $PKC\zeta$ at the cellular and biological levels independently. However, it is largely unclear how the functions of PKC ζ at the cellular level contribute to the maintenance of homeostasis *in vivo*. Therefore, future studies should be aimed at integration of functions of PKC *in vitro* and *in vivo*.

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