# Lambda-Interacting Protein, a Novel Protein That Specifically Interacts with the Zinc Finger Domain of the Atypical Protein Kinase C Isotype  $\lambda$ / $\iota$  and Stimulates Its Kinase Activity In Vitro and In Vivo

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**The members of the atypical subfamily of protein kinase C (PKC) show dramatic structural and functional differences from other PKC isotypes. Thus, in contrast to the classical or novel PKCs, they are not activated by diacylglycerol or phorbol esters. However, the atypical PKCs are the target of important lipid second messengers such as ceramide, phosphatidic acid, and 3**\***-phosphoinositides. The catalytic and pseudosubstrate sequences in the two atypical PKCs (**l**/**i**PKC and** z**PKC) are identical but are significantly different from those of conventional or novel PKCs. It has been shown that microinjection of a peptide with the sequence of the pseudosubstrate of the atypical PKC isotypes but not of** a**PKC or** «**PKC dramatically inhibited maturation and NF-**k**B activation in** *Xenopus* **oocytes, as well as reinitiation of DNA synthesis in quiescent mouse fibroblasts. This indicates that either or both atypical isoforms are important in cell signalling. Besides the pseudosub**strate, the major differences in the sequence between  $\lambda$ /**iPKC** and  $\zeta$ PKC are located in the regulatory domain. **Therefore, any functional divergence between the two types of atypical PKCs will presumably reside in that region. We report here the molecular characterization of lambda-interacting protein (LIP), a novel protein that** specifically interacts with the zinc finger of  $\lambda$ /**iPKC** but not  $\zeta$ PKC. We show in this paper that this interaction is detected not only in vitro but also in vivo, that LIP activates  $\lambda/\iota PKC$  but not  $\zeta PKC$  in vitro and in vivo, and **that this interaction is functionally relevant. Thus, expression of LIP leads to the transactivation of a** k**B-dependent promoter in a manner that is dependent on** l**/**i**PKC. To our knowledge, this is the first report on the cloning and characterization of a protein activator of a PKC that binds to the zinc finger domain, which** has so far been considered a site for binding of lipid modulators. The fact that LIP binds to  $\lambda$ /*iPKC* but not **to the highly related** z**PKC isoform suggests that the specificity of the activation of the members of the different PKC subfamilies will most probably be accounted for by proteins like LIP rather than by lipid activators.**

The atypical subgroup of the protein kinase C (PKC) family of isozymes is composed of two members:  $\lambda / \mu$ PKC and  $\zeta$ PKC  $(1, 33, 38)$ . *IPKC* is the human homolog of the mouse  $\lambda P K C$ , and both show a high degree of homology in the catalytic as well as in the regulatory domain with  $\zeta$ PKC from different species (32). Of great interest is the fact that both the structure and the mechanism of regulation of the two atypical PKCs by lipid activators differ from those of the other members of their family. Thus, they do not contain the  $Ca^{2+}$ -binding region, and they have only a single zinc finger-like motif, which in other PKC isoforms has been shown to be double and responsible for the activation by diacylglycerol and phorbol esters (32). Consequently, the atypical PKCs cannot be regulated by  $Ca^{2+}$ , and are insensitive to phorbol esters and diacylglycerol (1, 33, 38, 42). However, native  $\zeta$ PKC is activated by critical lipid second messengers like phosphatidic acid (31) and phosphatidylinositol 3,4,5-P3 (30). Phosphatidic acid is produced as consequence of the activation of phosphatidylcholine-phospholipase D or the concerted action of phosphatidylcholine-phospholipase C and diacylglycerol kinase (12). Both phospholipases have been implicated in cell proliferation and tumor transformation (12, 20, 22, 43). Phosphatidylinositol  $3,4,5$ - $P_3$  is the product of the phosphoinositide-3 kinase, which constitutes a decisive step

during mitogenic signal transduction (41). On the other hand, ceramide that is generated following the activation of sphingomyelin hydrolysis by inflammatory cytokines, such as interleukin-1 or tumor necrosis factor alpha (TNF- $\alpha$ ) (13, 18), has been shown to bind and activate  $\zeta$ PKC (24, 28). Taken together, all these observations pinpoint to zPKC as a target of important lipid second messengers and suggest its role in cell signalling.

Molecular cloning of an atypical PKC isotype from *Xenopus laevis* with the regulatory domain of rat  $\zeta PKC$  as a probe produced a cDNA encoding a protein highly homologous to rat zPKC, which was the only atypical isotype known at that time (10, 33). The cloned *X. laevis* atypical PKC displays an overall 72% identity at the amino acid level to  $\zeta$ PKC, which becomes 84% in the catalytic domain (10, 33). This led to the identification of that gene product as the *X. laevis*  $\zeta PKC$  (10). The more recent description of  $\lambda$ / $\mu$ PKC (1, 38) allowed the comparison of the *X. laevis* enzyme with all known atypical subspecies. On the basis of alignment of their sequences, the cloned *X. laevis* atypical PKC shows the highest degree of homology with  $\lambda / \mu$ KC, with an overall 90% identity at the amino acid level. Therefore, the cloned *X. laevis* enzyme is actually  $\lambda/\mu$ PKC (10). Interestingly, the pseudosubstrate sequence is identical in both atypical isotypes but is significantly different from that of conventional or novel PKCs (1, 32, 38). Microinjection of a peptide with the sequence of the pseudosubstrate of the atypical PKC isotypes but not of  $\alpha$ PKC or εPKC, dramatically inhibited maturation (10) and NF-kB (11)

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activation in *X. laevis* oocytes, as well as the reinitiation of DNA synthesis in quiescent mouse fibroblasts (3). This indicates that either or both atypical isoforms are important in mitogenic activation. Besides the pseudosubstrate, the major differences in the sequence between  $\lambda/\mu$ PKC and  $\zeta$ PKC are located in the regulatory domain. Therefore, any functional divergence between the two types of atypical PKCs will presumably reside in that region. We reasoned that proteins that interact with the regulatory domain of  $\lambda / \nu P K C$  but not with zPKC could be potential and specific regulators of its enzymatic activity both in vitro and in vivo and that their molecular characterization would help to dissect specific pathways regulating the different atypical isotypes.

## **MATERIALS AND METHODS**

**Yeast strains and media.** The genotype of the *Saccharomyces cerevisiae* reporter strain Y190, used for the two-hybrid screening, is *MAT*a *leu2-3*,*112 ura3-52 trp1-901 his3-*D*200 ade2-101 gal4* D*gal80 URA3*::*GAL-lacZ LYS*::*GAL-HIS3 cyh*<sup>r</sup> . The genotype of SFY526, used to test interactions between GAL4-BD and GAL4-AD fusions, is *MAT***a** *ura3-52 his 3-200 ade 2-101 lys2-801 trp1-901 leu 2-3*,*112 canr gal4-542 gal80-538 URA3*::*GAL1-lacZ* (Clontech Laboratories, Inc.). Strains were grown under standard conditions in rich or synthetic medium with appropriate supplements at  $30^{\circ}$ C (39).

**Two-hybrid screening and cDNA isolation.** For the yeast two-hybrid screening, pYTH9 $\lambda$ /<sub>U</sub>PKC<sup>REG</sup> was cotransformed with the human placenta cDNA Matchmaker library in the pGAD10 vector (Clontech Laboratories, Inc.) into the Y190 yeast strain, as described previously (14, 37), and the transformants were plated to synthetic medium lacking histidine, leucine, and tryptophan but containing 20 mM 3-amino-1,2,4-triazole. The plates were incubated at 30°C for 5 days. His<sup>+</sup> colonies were assayed for  $\beta$ -galactosidase activity by a filter assay as described below. To obtain a cDNA for the full-length lambda-interacting protein (LIP) coding sequence, a human placenta 5'-RACE-Ready cDNA (Clontech Laboratories, Inc.) was used as the template in PCR with primers RACE1 (5'-GCG AATTCTCTGAGTAGACATATCCTGG-3') and anchor (5'-CTGGTTCGGC CCACCTCTGAAGGTTCCAGAATCGATAG-3'). The conditions of the PCR were 30 cycles of 94°C for 45 s, 60°C for 45 s, and 72°C for 2 min, with a final extension time of 7 min at 72°C. For the second 5'-RACE reaction, primers RACE2 (5'-CTGAATTCTCATGCTGGTTAGGATAGCAG-3') and anchor were used. Oligonucleotides were synthesized by Isogen Biosciences. DNA sequencing was done by the dideoxynucleotide chain termination method.

b**-Galactosidase filter assays.** Yeast strains were patched to synthetic medium lacking leucine and tryptophan, incubated for 3 days at  $30^{\circ}$ C, and transferred to a nitrocellulose filter (5). The filter was placed on aluminum foil atop a sea of liquid nitrogen for 20 s and then immersed in liquid nitrogen for 1 to 2 s. The filter was allowed to come to room temperature and then placed on top of Whatman no. 1 paper that had been prewetted in Z buffer containing 0.75 mg of 5-bromo-4-chloro-3-indolyl-β-D-galactoside (X-Gal) per ml (25). The filters were incubated for 3 h at  $30^{\circ}$ C. Blue coloration is indicative of  $\beta$ -galactosidase activity.

Plasmids. pYTH9 $\lambda$ /<sub>L</sub>PKC was constructed from full-length *X. laevis*  $\zeta$ PKC derived by PCR (oligonucleotides 5'-GCGAATTCCATGCCGACACAGAGG G-3' and 5'-CGAGGTCGACGGTATCG-3') and the template pBluescript<sub>4</sub> PKC (3) at the *Eco*RI site of pYTH9. pYTH9 $\lambda$ PKC<sup>REG</sup> was constructed from the regulatory domain of *X. laevis*  $\zeta P\zeta C$  (amino acids 1 to 250) and was made in the same way as pYTH9 $\lambda$ /<sub>*I*</sub>PKC but with the oligonucleotides 5'-GCGAATTC CATGCCGACACAGAGGG-3' and 5'-TTGGAATTCTCAGCTAGATGGGC<br>TCTTTCCAC-3'. pYTH9\/iPKC<sup>REG-C167S</sup> was obtained by replacing Cys-167 with a serine residue by PCR-directed mutagenesis. Deletions of the regulatory<br>domain were used to construct pYTH9)\/uPKC<sup>126</sup> (oligonucleotides 5'-GCGAA TTCCATGCCGACACAGAGGG-3' and 5'-GCCGAATTCTCATCCATTTG CACAATAC-3' at the *EcoRI* site of pYTH9) and pYTH9 $\lambda$ /<sub>*I*</sub>PKC<sup>ZF</sup> (oligonucleotides 5'-CTGCTCGAGGCTGTATTGTGCAA-3' and 5'-GCCGAAT TCTCATCCATTTGCACAATAC-39, subcloned into the *Sal*I-*Eco*RI sites of pYTH9). pYTH9 $\lambda$ /<sub>L</sub>PKC<sup>CAT</sup> contains the catalytic domain (oligonucleotides '-GCGAATTCCTGGGACTCCAAGACTT-3' and 5'-CGAGGTCGACGGT ATCG-3') at the *Eco*RI site of pYTH9. pYTH9¿PKC was constructed from full-length rat brain  $\zeta$ PKC derived by PCR (oligonucleotides 5'-GGAGAATTC CATGCCCAGCAGGACC-3' and 5'-ATTCCCGGGTCACACGGACTCCT CA-3') at the *EcoRI-SmaI* sites of pYTH9.pYTH9 $\zeta$ PKC<sup>REG</sup> was constructed from the regulatory domain (amino acids  $1$  to 250) made the same way as pYTH9zPKC but with oligonucleotides 5'-GGAGAATTCCATGCCCAGCA GGACC-3' and 5'-AGGAATTCTCACTGAGAGATTTTGATCCCATC-3' and with subcloning into the *Eco*RI site of the same vector. Deletions of the regu-<br>latory domain yielded pYTH9¿PKC<sup>126</sup> (oligonucleotides 5'-GGAGAATTC<br>CATGCCCAGCAGGACC-3' and 5'-TTGGAATTCTCAGCCGTTGGCTCG GTAT-3') and pYTH9<sup>z</sup>PKC<sup>ZF</sup> (oligonucleotides 5'-ATTGAATTCGCTATAC<br>CGAGCCAACGGC-3' and 5'-GCCGAATTCTCAATCTACTGGAGGCTC TTG-39) at the *Eco*RI site of pYTH9. pYTH9aPKCREG was constructed by

subcloning a *NcoI-BamHI* fragment, encompassing the regulatory domain of bovine αPKC, into the *NcoI-BglII* sites of pYTH9. pYTH9εPKC<sup>REG</sup> was obtained by subcloning a *Nco*I-*Pvu*II fragment, containing the regulatory domain of mouse εPKC, into the *Nco*I-*Sma*I-digested pYTH9. This vector is an influenza virus hemagglutinin (HA) epitope-tagged pYTH6 (Trp1 marker) derivative vector. pGBT9RafREG, containing the regulatory domain of c-Raf-1, was obtained by PCR with primers 5'-GCAGAATTCGAGCACATACAGGGA-3' and 5'-TCCGGATCCTACTCATGTAGCCAA-3' and with p627-Raf-1 as the tem-<br>plate, and inserted at *EcoRI-SalI* sites. pGBT9Raf, pGBT9Raf<sup>CAT</sup>, and pGBT9 Mos have been described previously (29). pGAD10-LIP contains the full-length cDNA LIP and was amplified by PCR with oligonucleotides 5'-GCGAATTCAT GCTGCATGAACTGGACGGT-3' and 5'-CGGAATTCCGAGAATCTGAAT GCAT-3' and subcloned into the *Eco*RI site of pGAD10.

Plasmids GST- $\lambda/\iota PKC^{REG}$ , GST- $\lambda/\iota PKC^{126}$ , and GST- $\lambda/\iota PKC^{ZF}$  were generated by PCR with pBluescript- $\zeta$ PKC as the template (3) and the primers 5'-AATACGACTCACTATAG-3′ and 5′-TTGGAATTCTCAGCTAGATGGGC<br>TCTTTCCAC-3′ for GST-λ/iPKC<sup>reg</sup>, 5′-ATTGGATCCACACAGAGGGA CAACAC-3' and 5'-GCCGAATTCTCATCCATTTGCACAATAC-3' for GST- $\lambda$ /lPKC<sup>126</sup>, and 5'-ATTGGATCCCTGTATTGTGCAAATGG-3' and 5'-GCC<br>GAATTCTCATCCATTTGCACAATAC-3' for GST- $\lambda$ /lPKC<sup>ZF</sup>. The PCR products were digested with *Bam*HI and *Eco*RI and cloned into *Bam*HI-*Eco*RIdigested pGEX-2TK (Pharmacia), except for  $\lambda/\mu P K C^{REG}$ , which was digested with *Xmn*I and *Eco*RI and subcloned into *Sma*I-*Eco*RI sites. Plasmids GST- $\zeta PKC^{REG}$ , GST- $\zeta P KC^{126}$ , and GST- $\zeta P KC^{ZF}$  were generated by PCR with MBP- $\zeta$ PKC as the template (8) and the primers 5'-ATTGGATCCAGCAGGACCG ACCCCAA-3′ and 5′-AGGAATTCTCACTGAGAGATTTTGATCCCATC-3′<br>for GST-ζPKC<sup>REG</sup>, 5′-ATTGGATCCAGCAGGACCGACCCCAA-3′ and 5′-TTGGAATTCTCAGCCGTTGGCTCGGTAT-3' for GST- $\zeta$ PKC<sup>126</sup>, and 5'-AT TGGATCCCTATACCGAGCCAACGGC-3' and 5'-GCCGAATTCTCAATC<br>TACTGGAGGCTCTTG-3' for GST-ζPKC<sup>ZF</sup>. The PCR products were digested with *Bam*HI and *Eco*RI and cloned into *Bam*HI-*Eco*RI-digested pGEX-2TK. pGEX-2TK constructs were transformed into *Escherichia coli* JM101, and expression of glutathione-*S*-transferase (GST) fusion proteins and their purification on glutathione-Sepharose were carried out as specified by the manufacturer. MBP-LIP(R4) contains the partial cDNA clone of LIP inserted in the *Eco*RI site of pMALc2 (New England Biolabs). The MBP-LIP(R4) fusion protein was expressed in *E. coli* and purified by binding to an amylose resin as specified by the manufacturer. Expression and purification of hnRNPA1 have been described previously (29).

To make the HA-tagged plasmids, pCDNA3-HA was constructed as follows. The following pair of complementary oligonucleotides was synthesized, annealed, and ligated into pCDNA3 (Invitrogen) digested with *Hin*dIII and *Eco*RI, to create pCDNA3-HA vector: 5'-AGCTTGCCGCCACCATGTATGATGTTCCTGAT TATGCTAGCCTCCCGGGG-3′ and 5′-AATTCCCCGGGAGGCTAGCAT<br>AATCAGGAACATCATACATGGTGGCGGCA-3′. To construct pCDNA3-<br>HA-ζPKC and pCDNA3-HA-ζPKC<sup>MUT</sup>, a fragment corresponding to the fulllength wild-type or kinase-inactive mutant of rat brain ¿PKC was obtained by<br>PCR with pBluescriptζPKC or pSelectζPKC<sup>MUT</sup>, respectively, as template and with the primers 5'-GGAGAATTCCATGCCCAGCAGGACC-3' and 5'-ATGT CTAGACACGGACTCCTCAGCAGA-3', digested with *Eco*RI and *XbaI*, and subcloned into the *EcoRI-XbaI* sites of pCDNA3-HA. pSelectζPKC<sup>MUT</sup> was derived by directed mutagenesis from pSelect $\zeta$ PKC and the mutagenic oligonucleotide 5'-GATTTACGCCATGTGGGTGGTGAAGAAGGAGC-3'. pSelect PKC was obtained by subcloning the *Eco*RI fragment containing full-length ζPKC from pBluescriptζPKC into pSelect (Promega). pCDNA3-HAλ/ι-PKC<br>and pCDNA3-HAλ/ι-PKC<sup>MUT</sup> were generated by PCR with pBluescriptλ/ιPKC<br>or pSelectλ/ιPKC<sup>MUT</sup> (3) as the template, respectively, and the primers 5'-GCG AATTCCATGCCGACACAGAGGG-3' and 5'-CGAGGTCGACGGTATCG-39. The PCR products were cut with *Eco*RI and ligated to pCDNA3HA previously cut with the same enzyme. To obtain the HA-tagged kinase-inactive mutants of λ/ιPKC and ζPKC, CMV-LIP(R4) was generated by PCR with primers<br>5′-TCGAAGCTTATGGGTCTTGAACATCCTAT-3′ and 5′-CGAGAATCTG AATGCAT-3' and with pGAD10-LIP(R4), the original clone obtained from the yeast two-hybrid screen, as the template and subcloned into *Hin*dIII and *Xba*I sites of pRcCMV (Invitrogen). All constructs were confirmed by nucleotide sequence analysis, and the expression of the fusion proteins was confirmed by immunoblotting.

**Northern (RNA) blots.** Samples (10  $\mu$ g) of total RNA from different human tissues (Clontech Laboratories, Inc.) were run on formaldehyde-agarose gels, blotted onto Hybond-N<sup>+</sup> filters, and hybridized overnight at 42°C in  $5 \times$  SSC (1 $\times$ SSC is 0.15 M NaCl plus 0.015 M sodium citrate)–5 $\times$  Denhardt's solution (1 $\times$ Denhardt's solution is 0.02% polyvinylpyrrolidone, 0.02% Ficoll 400, and 0.02% bovine serum albumin)–10 mM Tris-Cl (pH 7.5)–0.5% sodium dodecyl sulfate (SDS) to 50% formamide–200 µg of denaturated salmon sperm DNA per ml–50 µg of tRNA per ml with a <sup>32</sup>P-labelled cDNA probe of LIP (clone R4). The filters were washed for 15 min at room temperature in 2× SSC, three times ( each time) at  $56^{\circ}$ C with  $0.1 \times$  SSC–0.5% SDS, and 5 min at room temperature with  $2\times$  SSC.

In vitro binding studies. GST, GST- $\lambda$ <sup>LPKC</sup>, and GST- $\zeta$ PKC were incubated with the resin-bound MBP or MBP-LIP(R4) at the protein concentrations specified in the figure legends. The binding-reaction mixtures contained 85 mM NaCl,  $10\%$  glycerol, 0.6 mM guanine nucleotide, and 6 mM free magnesium.

After 60 min at  $4^{\circ}$ C, the resin was sedimented and washed with 0.5 ml (10 bed volumes) of 10 mM Tris-HCl (pH 7.6)-10% glycerol-5 mM  $MgCl<sub>2</sub>$ -1 mM dithiothreitol–0.1% Triton X-100–0.1 mM phenylmethylsulfonyl fluoride. The bound proteins were boiled in sample buffer, separated by SDS-polyacrylamide gel electrophoresis (PAGE), transferred, and immunoblotted with an anti-GST antibody (Santa Cruz Biotechnology).

**Antibody production and immunoblot analysis.** Antibodies against LIP were prepared by immunizing rabbits with the MBP-LIP(R4) fusion protein. For immunoblot analysis, 30  $\mu$ g of cellular protein was resolved in SDS–10% polyacrylamide gels. The protein was then electrophoretically transferred onto a nitrocellulose filter (Promega) and incubated with preimmune serum or anti-LIP antibody. Bands were visualized with the ProtoBlot AP System (Promega).

**Transfections.** Subconfluent cultures of Cos cells in 100-mm plates were transfected by the calcium phosphate method (Gibco, BRL) with 20  $\mu$ g of either pCDNA3-HA, pCDNA3-HA- $\lambda$ <sup>LPKC</sup>, or pCDNA3-HA-ZPKC. Plasmid DNA was removed 4 h later, and the cells were incubated for 16 h in Dulbecco's modified Eagle's medium containing 10% fetal calf serum. Then, medium was replaced with medium containing 0.5% fetal calf serum and the incubation was continued for 16 h, followed by an additional 8 h in serum-free medium. Cultures were then extracted with lysis buffer [50 mM Tris (pH 7.5), 150 mM NaCl, 1% Triton X-100, 2 mM EDTA, 1 mM ethylene glycol-bis( $\beta$ -aminoethyl ether)-*N*,*N*,*N'*,*N'*-tetraacetic acid (EGTA), protease inhibitors] and immunoprecipitated with 2 µg of anti-HA antibody (12CA5; Boehringer, Mannheim, Germany) per mg of protein extract. Immunoprecipitates were washed seven times with lysis buffer containing 0.5 M NaCl. For the in vitro kinase assay, immunocomplexes were incubated with  $1 \mu$ g of recombinant bacterially produced heterogeneous nuclear ribonucleoprotein A1 (29) in the presence or absence of 1  $\mu$ g of MBP, MBP-LIP(R4), or phosphatidylserine as sonicated vesicles (50  $\mu$ g/ml) and 5 to 10  $\mu$ Ci of [ $\gamma$ -<sup>32</sup>P]ATP (100  $\mu$ M) in kinase buffer (35 mM Tris-HCl [pH 7.5], 10 mM MgCl<sub>2</sub>, 0.5 mM EGTA, 0.1 mM CaCl<sub>2</sub>, 1 mM phenylphosphate) for 30 min at 30°C in a final volume of 20  $\mu$ l. Reactions were stopped by the addition of concentrated sample buffer. Samples were boiled for 3 min and separated by SDS-PAGE followed by autoradiography.

Subconfluent cultures of Cos cells in 100-mm-diameter plates were transfected with 5 μg of either pCDNA3-HA, pCDNA3-HA-λ/ιPKC, or pCDNA3-HA-ζPKC together with 20 μg of CMV or CMV-LIP(R4). Plasmid DNA was removed 4 h later, and cells were incubated for 16 h in Dulbecco's modified Eagle's medium containing 10% fetal calf serum. Then the medium was replaced with medium containing 0.5% fetal calf serum and the incubation was continued for 16 h, followed by an additional 8 h in serum-free medium. Cultures were then either untreated or stimulated with 10% fetal calf serum for 5 min. Immunoprecipitates and kinase assays were performed as above. In another set of experiments, subconfluent cultures of Cos cells were transfected with different amounts of plasmid CMV-LIP(R4) together with 500 ng of 3EConALuc reporter plasmid. In some experiments, these plasmids were cotransfected with  $5 \mu$ g of the different  $\lambda$ / $\mu$ KC expression vectors. After 4 h, the DNA-containing medium was removed and cells were made quiescent by serum starvation for 36 h. Then the cells were either untreated or stimulated with human TNF- $\alpha$  (500 U/ml) for 6 h as a control, extracts were prepared, and luciferase activity was determined as described previously (2). Data are expressed in terms of relative luciferase activity units, calculated as (light emission from experimental sample-light emission of lysis buffer alone) per microgram of cellular protein in the sample. In another set of experiments, Cos cells were transfected with the kB reporter plasmid with different concentrations of either empty vector or expression plasmids for wild-type and kinase-inactive mutants of  $\lambda$ / $\mu$ KC and  $\zeta$ PKC, and the experiments were processed as above.

**In vivo association.** Quiescent NIH 3T3 fibroblasts, either untreated or stimulated according to the experiments, or proliferating HeLa cells were extracted with lysis buffer (50 mM Tris [pH 7.5], 150 mM NaCl, 1% Triton X-100, 2 mM EDTA, 1 mM EGTA, 25  $\mu$ g of leupeptin per ml, 25  $\mu$ g of aprotinin per ml, 25 mg of pepstatin per ml, and 1 mM phenylmethylsulfonyl fluoride) and immunoprecipitated with an anti- $\lambda$ /<sub>*IPKC-* $\zeta$ PKC</sub> antibody (Gibco, BRL) either in the absence or in the presence of competing peptide as described previously (3). The immunoprecipitates were resolved by SDS-PAGE and immunoblotted with anti-LIP antibody.

**Nucleotide sequence accession number.** The GenBank accession number of the LIP sequence is U32581.

## **RESULTS**

**Functional role of**  $\lambda$ **/<b>iPKC** and *ZPKC*. Since transfection of a dominant negative mutant of  $\lambda / \mu$ PKC (identified as  $\zeta$ PKC in references 3, 4, 7, and 9) inhibited a number of cell functions including the activation of  $\kappa$ B-dependent promoters (4, 7), it was of interest to determine whether a dominant negative mutant of  $\zeta$ PKC similarly affected this parameter. Therefore, either Cos cells (Fig. 1) or NIH 3T3 cells (not shown) were transfected with different concentrations of expression vectors for HA-tagged  $\zeta$ PKC or  $\lambda/\iota$ PKC, which were either wild type or

dominant negative mutants along with a kB-driven reporter plasmid. Interestingly, cotransfection of the wild-type  $\lambda/\mu$ PKC significantly stimulated the  $\kappa$ B-dependent promoter activity, with a maximum around 15  $\mu$ g (Fig. 1A). Transfection of zPKC, although significantly less potent at lower concentrations, displayed a similar degree of activation of the reporter at high expression levels (Fig. 1A). Transfection of dominant negative  $\lambda/\mu$ PKC severely reduced the activation of this reporter activity, with complete inhibition at around 20  $\mu$ g (Fig. 1B), whereas a similar level of reduction was obtained with 30  $\mu$ g of the  $\zeta$ PKC expression vector. Figure 1C shows a representative immunoblot in which the expression levels of the four transfected constructs were very similar. Taken together, these results indicate that although the stimulation of the kB-dependent promoter activity appears to be more sensitive to the transfection of  $\lambda/\mu$ KC, no obvious differences were observed between the atypical isotypes at higher expression levels. This was as expected, because of the near identity of the catalytic domains of  $\lambda/\mu$ PKC and  $\zeta$ PKC. The different sensitivities of the kB-dependent promoter activity to low concentrations of  $\lambda$ / $\iota$ PKC and  $\zeta$ PKC could be due to the sequence divergences existing in their regulatory domain. The identification of proteins that selectively interact with the regulatory region of  $\lambda$ / $\iota$ PKC but not with  $\zeta$ PKC would help us to understand the potential functional and/or regulatory differences between the atypical PKCs.

**Yeast two-hybrid screen.** To identify potential specific activators of  $\lambda/\mu$ PKC, the regulatory domain of that kinase (amino acids 1 to 250) was fused with the DNA-binding domain of the yeast GAL4 protein  $(pYTH9\lambda/\mu PKC^{REG})$  to serve as the ''bait'' to screen a human placenta Matchmaker cDNA library. Colonies that grew on yeast dropout media lacking Leu, Trp, and His but containing 20 mM 3-amino-1,2,4-triazole and that were blue when assayed by X-Gal colony filter assay were selected. Twelve positive colonies that stained intensely blue within 20 min were obtained from  $2.5 \times 10^6$  screened. The expression of His-3 and LacZ in these colonies was shown to depend on the GAL4 fusion protein by retransforming the recovered plasmids into yeasts containing the bait construct (Fig. 2A, a and b; Table 1). The sequences of the 12 clones revealed that they were identical and partial (clone R4; 1,568 bp). To obtain the missing 5' region, a human placenta 5'-RACE Ready cDNA (Clontech Laboratories, Inc.) was used. This procedure yielded an additional 5' fragment of 453 bp. With that sequence, the appropriate oligonucleotide was used in a second 5'-RACE reaction, which produced another 1.3-kb fragment, including the initiation codon and some of the 5<sup>'</sup> untranslated region. The resulting full-length cDNA clone encodes for a novel protein of 713 amino acids, with a predicted molecular mass of 79.7 kDa, and with no exact matches in the cDNA and protein data banks searched (Fig. 3). From now on, this protein will be termed LIP (lambda-interacting protein). Northern blot analysis was done with RNAs derived from different human tissues. LIP appears to be expressed in the placenta, brain, lung, and spleen (Fig. 4).

Specificity of the interaction of LIP with the  $\lambda$ /*IPKC* regu**latory domain.** The specificity of the interaction between  $\lambda$ /<sub>L</sub>PKC<sup>REG</sup> and LIP was tested with an unrelated molecule, pYTH9-lamin, which fails to transactivate the reporter constructs (Fig. 2A, c; Table 1). Of note, the catalytic domain of  $\lambda$ / $\mu$ PKC did not interact with LIP whereas the full-length protein did show interaction, albeit less strongly than the regulatory region (Fig. 2A, d and e; Table 1). This indicates that the interaction of LIP with  $\lambda/\mu$ PKC takes place through the regulatory domain. To determine whether LIP could also bind to the regulatory domain of zPKC, this region (amino acids 1 to



FIG. 1. Role of  $\lambda$ /iPKC and  $\zeta$ PKC in the stimulation of  $\kappa$ B-dependent promoter activity. (A) Cos cells were transfected with different concentrations of either empty plasmid ( $\blacktriangle$ ) or expression vectors for HA-tagged wild-type  $\lambda$ <sub>i</sub>PKC ( $\blacktriangleright$ ) and  $\zeta$ PKC ( $\blacktriangleright$ ), along with 500 ng of the  $\kappa$ B enhancer-directed luciferase reporter plasmid (3EconALuc). After 4 h, the DNA-containing medium was removed and cells were made quiescent by serum starvation for 24 h. Then extracts were prepared, and the luciferase activity was determined as described in Materials and Methods. As a control, cells transfected with the maximal concentration of empty plasmid were stimulated with TNF- $\alpha$  (500 U/ml) for 4 h (empty bar). Results are the mean  $\pm$  standard deviation (SD) of three independent experiments with incubations in duplicate. (B) Cos cells were transfected with different concentrations of either empty plasmid ( $\bullet$ ) or expression vectors for HA-tagged kinase-inactive mutants of  $\lambda$ /iPKC ( $\blacksquare$ ) and  $\zeta PKC (\blacktriangle)$ , along with 500 ng of the  $\kappa B$  enhancer-directed luciferase reporter plasmid (3EconALuc). After 4 h, the DNA-containing medium was removed and cells were made quiescent by serum starvation for 24 h. Then cells were stimulated with TNF- $\alpha$  (500 U/ml) for 4 h. Extracts were prepared, and the luciferase activity was determined as described in Materials and Methods. Results are the mean  $\pm$  SD of three independent experiments with incubations in duplicate. (C) Representative immunoblot with anti-HA antibody in which the expression levels of the four transfected constructs were determined. Cells were transfected with 2.5 µg (lane 1), 10  $\mu$ g (lane 5), or 30  $\mu$ g (lane 9) of wild-type  $\zeta$ PKC, with 2.5  $\mu$ g (lane 2), 10  $\mu$ g (lane 6) or 30  $\mu$ g (lane 10) of kinase-inactive  $\zeta$ PKC; with 2.5  $\mu$ g (lane 3), 10  $\mu$ g (lane 7) or 30  $\mu$ g (lane 11) of wild-type  $\lambda$ /**iPKC**; or with 2.5  $\mu$ g (lane 4), 10  $\mu$ g (lane 8), or 30  $\mu$ g (lane 12) of kinase-inactive  $\lambda$ /**iPKC**.

250) from rat brain  $\zeta$ PKC was fused with the DNA-binding domain of the yeast GAL4 protein (pYTH9 $\zeta$ PKC<sup>REG</sup>) and its ability to interact with LIP in the two-hybrid system was determined. Interestingly, LIP does not interact with the regulatory domain of rat zPKC or with the regulatory domains of aPKC or εPKC (Fig. 2A, f; Table 1), indicating that its binding to  $\lambda$ / $\mu$ <sub>KC</sub> is highly specific for this atypical isotype. On the other hand, Raf-1 is a serine/threonine kinase with an overall structure similar to that of the atypical PKCs (33). Both type of kinases are critical components downstream of Ras in mito-



FIG. 2. Specificity of the interaction of LIP with  $\lambda/\mu$ KC<sup>REG</sup>. The *S. cerevisiae* SFY526 reporter host strain was transformed with pGAD10-LIP and the following plasmids: (A) pYTH9 (a), pYTH9 $\lambda/\mu$ KC<sup>REG</sup> (b), pGBT9Lam at 30°C for 3 days. Essentially identical results were obtained in another two experiments.

TABLE 1.  $\beta$ -Galactosidase activity induced by interaction between the regulatory domain of  $\lambda / \nu$ PKC and LIP

GAL4-BD fusion	β-Galactosidase activity for GAL4-AD fusion <sup>a</sup> :	
	pGAD10	pGAD10-LIP
pYTH9		
pYTH9 $\lambda$ /LPKCREG		
pYTH9 $\lambda$ /LPKC		
pYTH9 $\lambda$ /LPKC <sup>126</sup>		
pYTH9 $\lambda$ /LPKC <sup>ZF</sup>		
$\lambda$ / $\iota$ PKC <sup>REG-C167S</sup>		
pYTH9 $\lambda$ /LPKCCAT		
pYTH9ζPKCREG		
pYTH9ζPKC		
pYTH9ζPKC <sup>126</sup>		
pYTH9ζPKCZF		
pYTH9αPKCREG		
pYTH9εPKCREG		
pGBT9RafREG		
pGBT9Raf		
pGBT9Mos		
pGBT9Lamin		

 $a$   $\beta$ -Galactosidase activity was determined by a filter assay for the yeast strains containing the indicated plasmids as described in Materials and Methods. Plus signs represent a positive indication of  $\beta$ -galactosidase activity (blue color) in filter assays. Essentially identical results were obtained in three other independent experiments.

genic cascades (3, 6, 9, 10, 15–17, 19). Therefore, it was of great interest to determine whether Raf-1 would interact with LIP. The catalytic domain (Fig. 2A, g; Table 1), the full-length Raf-1 (Fig. 2A, h; Table 1), and the regulatory region (Fig. 2A, i; Table 1) of Raf-1 all failed to interact with LIP. The product of c-*mos* that is another serine/threonine kinase critically involved, like Raf-1 and the atypical PKCs, in mitogenic signal transduction in *X. laevis* oocytes and mammalian cells (36) did not interact with LIP (Fig. 2A, j; Table 1). Therefore, these data collectively indicate that LIP specifically binds to the regulatory domain of  $\lambda/\mu$ PKC but not to other structural and functional related kinases.

**LIP binds specifically to the zinc finger of**  $\lambda$ **/<b>iPKC**. To map the region in the regulatory domain of  $\lambda / \mu$ PKC where LIP binds, cDNA fragments corresponding to amino acids 1 to 126 and amino acids 127 to 194 (corresponding to the zinc finger region) of  $\lambda/\mu$ KC and  $\zeta$ PKC, respectively, were fused with the DNA-binding domain of the yeast GAL4 protein and their ability to interact with LIP in the two-hybrid system was determined. Interestingly, only the zinc finger and the whole regulatory domain of  $\lambda/\mu$ PKC displayed LIP-binding activity (Fig. 2B; Table 1). No binding was detected with the different zPKC fragments or with the region encompassing amino acids 1 to 126 of  $\lambda/\mu$ PKC (Fig. 2B; Table 1). As an important control, disruption of the cysteine finger by mutation of cysteine 167 to serine in the  $\lambda$ / $\mu$ PKC regulatory domain completely abolished the binding of LIP (Table 1). To our knowledge, this is the first report of a protein that interacts with a PKC through the putative zinc finger lipid-binding domain.

**LIP interacts with**  $\lambda/\iota PKC$  **in vitro and in vivo.** To further investigate the interaction between LIP and  $\lambda/\mu$ PKC, the cloned partial LIP cDNA (clone R4) was expressed as an MBP fusion protein and tested to see if it could interact in vitro with either the region encompassing amino acids 1 to 126, the zinc finger, or the whole regulatory domain of both  $\lambda/\mu$ KC and zPKC, which have been expressed as GST fusion proteins (Fig. 5A). Two different concentrations (200 or 400 nM) of MBP or MBP-LIP(R4) were incubated with 800 nM GST fusion proteins for 1 h at  $4^{\circ}$ C, after which MBP and MBP-LIP(R4) were immobilized on amylose resin. Following extensive washing with binding buffer plus 0.1% Triton X-100, bound MBP fusion proteins and any associated proteins were boiled in sample buffer, fractionated by SDS-PAGE, and immunoblotted with anti-GST antibody to detect binding of the different GST fusion proteins to LIP. Of note,  $\text{GST-}\lambda/\text{LPKC}^{\text{ZF}}$  and  $\text{GST-}\lambda/\text{LPKC}$  $i$ PKC<sup>REG</sup> but not GST, GST- $\lambda$ / $i$ PKC<sup>126</sup>, or any GST- $\zeta$ PKC fusion proteins bound to MBP-LIP(R4) (Fig. 5B; data not shown for  $\zeta$ PKC). Also, no binding of GST- $\lambda/\lambda$ PKC<sup>ZF</sup> or GST- $\lambda$ /**LPKC<sup>REG</sup>** to MBP alone was detected (Fig. 5B). Taken together, these data indicate that LIP specifically binds in vitro to the zinc finger domain of  $\lambda$ / $\mu$ PKC. Staining of a parallel gel confirmed that all the reactions contained equal molar amounts of GST (Fig. 5C) and MBP (not shown) fusion proteins.

To determine whether LIP and  $\lambda/\mu$ PKC can also interact in vivo, we next used the MBP-LIP(R4) fusion protein to immunize rabbits and generate an antibody against LIP. This antiserum specifically recognizes a band of 80 kDa in immunoblots of extracts from HeLa cells that is not seen with the preimmune serum. The molecular mass of that band is in good agreement with that predicted from the protein sequence (Fig. 3). Actively proliferating HeLa cells were immunoprecipitated, either in the absence or in the presence of the competing peptide, with an antibody that recognizes an epitope present in both  $\lambda$ / $\mu$ PKC and  $\zeta$ PKC. Immunoprecipitates were then resolved by SDS-PAGE and immunoblotted with anti-LIP antibody. Interestingly, results from Fig. 6A demonstrate that LIP is specifically detected in the immunoprecipitates performed in the absence of competing peptide, indicating the in vivo association of LIP with  $\lambda/\mu$ PKC and/or  $\zeta$ PKC in proliferating cells. Since the antibody used during the immunoprecipitation does not discriminate between  $\lambda/\mu$ PKC and  $\zeta$ PKC, the interaction between LIP and  $\zeta$ PKC in vivo cannot be completely ruled out, although the experiments described above and in the next section make this possibility highly unlikely. We next determined whether the association of LIP with  $\lambda/\mu$ PKC in vivo can be triggered by serum. Quiescent NIH 3T3 cells were stimulated with serum for different times, after which cell lysates were immunoprecipitated with the anti- $\lambda$ <sub>/</sub> $\lambda$ PKC- $\zeta$ PKC antibody and the immunoprecipitates were analyzed by immunoblotting with anti-LIP antibody, following their fractionation by SDS-PAGE. Of note, quiescent cells displayed little or no binding of LIP to  $\lambda/\mu$ PKC but their association was dramatically increased by stimulation with serum (Fig. 6B). This increased activation was maximal by 10 min (Fig. 6B). All the above data suggest that LIP may be an important regulator of  $\lambda$ / $\iota$ PKC activity in response to mitogenic activation.

LIP is a potent activator of  $\lambda$ /*i***PKC** but not of  $\zeta$ PKC in vitro **and in vivo.** Because LIP binds specifically to the zinc finger of  $\lambda/\mu$ PKC and that region in classical PKC isoforms has been shown to mediate the binding of stimulants (32, 34), we sought to determine if the interaction of LIP with  $\lambda / \nu P K C$  can regulate its enzymatic activity both in vitro and in vivo. Therefore, serum-starved Cos cells were transfected with HA protein epitope-tagged *X. laevis*  $\lambda/\mu$ PKC or rat brain  $\zeta$ PKC and the expressed proteins were immunopurified with the anti-HA monoclonal antibody 12CA5. The addition of phosphatidylserine (a classical activator of all PKCs) to the immunoprecipitates significantly activated both  $\lambda / \mu$  PKC and  $\zeta$  PKC (Fig. 7). Interestingly, the addition of 1  $\mu$ g of MBP-LIP(R4) but not of MBP alone produced a dramatic activation of  $HA-\lambda/\mu K\mathbb{C}$  but not of zPKC, comparable to that produced by phosphatidylserine (Fig. 7). Therefore, LIP not only binds specifically to

1	AATTCGTGATACACGTTAGAAAGTATGCTGCATGAACTGGACGGTCTTATTGAGCAGACCACCGATGGCGTT	72
1	L H E L D G L I E Q м т т D G V	16
73	CCCCTGCAGACTCTAGTGGAATCTCTTCAGGCCTACTTAAGAAACGCAGCTATGGGACTGGAAGAAGAAACA	144
17	L. $\bullet$ т L V E s. LQAY <b>LRNAAMG</b> E Ŧ L Е Е	40
145 41	CATGCTCATTACATCGATGTTGCCAGACTACTACATGCTCAGTACGGTGAATTAATCCAACCGAGAAATGGT н T а н Y D	216
217	VARLLHAQYGE L I Q - P R $\mathbf{N}$ G TCAGTTGATGAAACACCCAAAATGTCAGCTGGCCAGATGCTTTTGGTAGCATTCGATGGCATGTTTGCTCAA	64
65	K M A G Q M L L V A F D v n . Е. т s P G м F ٥	288 88
289	GTTGAAACTGCTTTCAGCTTATTAGTTGAAAAGTTGAACAAGATGGAAATTCCCATAGCTTGGCGAAAGATT	360
89	<b>VEKLNKMEIP</b> v E T A F - 5 L $\mathbf{L}$ r Α W R K Ι	112
361	GACATCATAAGGGAAGCCAGGAGTACTCAAGTTAATTTTTTTGATGATGATAATCACCGGCAGGTGCTAGAA	432
113	ARST Q V N F F D D D N H D I I R E $\mathbf{R}$ Q v L. E	136
433	GAGATTTTCTTTCTAAAAAGACTACAGACTATTAAGGAGTTCTTCAGGCTCTGTGGTACCTTTTCTAAAACA	504
137	I F F L K R L Q <b>TIKEF</b> F R L C G т F s K T	160
505	TTGTCAGGATCAAGTTCACTTGAAGATCAGAATACTGTGAATGGGCCTGCACAGATTGTCAATGTGAAAACC	576
161 577	s - 5 L E D Q N T $\mathbf{v}$ N G P A $\mathbf{Q}$ $\mathbf{I}$ v v K T G N	184
185	CTTTTTAGAAACTCTTGTTTCAGTGAAGACCAAATGGCCAAACCTATCAAGGCATTCACAGCTGACTTTGTG F R N S C F <b>S</b> <b>EDQMAKP</b> I K A F T v $\mathbf{A}$ D F	648 208
649	AGGCAGCTCTTGATAGGGCTACCCAACCAAGCCCTCGGACTCACACTGTGC +GTTTTATCAGTGCTCTGGGT	720
209	G L P N Q A L G L T L C S F I. $O$ L . L . I. S A L G	232
721	GTAGACATCATTGCTCAAGTAGAGGCAAAGGACTTTGGTGCCGAAAGCAAAGTTTCTGTTGATGATCTCTGT	792
233	I A Q V E A K D F G A E S K V D $\mathbf{I}$ s v n c D L	256
793	AAGAAAGCGGTGGAACATAACATCCAGATAGGGAAGTTCTCTCAGCTGGTTATGAACAGGGCAACTGTGTTA	864
257	<b>KKA VEHNT</b> Q I G K F S Q L V M N R А T V L	280
865	GCAAGTTCTTACGACACTGCCTGGAAGAAGCATGACTTGGTGCGAAGGCTAGAAACCAGTATTTCTTCTTGT т	936
281 937	A W K K H D L A s. s y n V R R L E T s I. s s с AAGACAAGCCTGCAGCGGGTTCAGCTGCATATTGCCATGTTTCAGTGGCAACATGAAGATCTACTTATCAAT	304
305	$\bullet$ Q R V LHIA ĸ т L $\mathbf{Q}$ м $\mathbf{F}$ $\mathbf{Q}$ <b>WQHED</b> L L Ι N	1008 328
1009	AGACCACAAGCCATGTCAGTCACACCTCCCCCACGGTCTGCTATCCTAACCAGCATGAAAAAGAAGCTGCAT	1080
329	R Þ Q A M <b>S</b> v. T. P P PRSA $\mathbf{I}$ T SMKK L. K L H	352
1081		1152
353	T V L s. ٥ I E T - 8 I A Q E K L A A L E s s I Е	376
1153	CAGCGACTCAAGTGGGCAGGTGCTGCCAACCCTGCATTGGCCCCCGTACTACAAGATTTTGAAGCAACGATA	1224
377	R. L к <b>W</b> $\mathbf{A}$ GGAN PALAPVL $Q$ D F E I ۰ A T	400
1225 401	GCTGAAAGAAGAAATCTTGTCCTTAAAGAGAGCCCAAAGAGCAAGTCAGGTCACATTTCTCTGCAGCAATATC <b>A E R R N L</b> K E T F L C S N <b>I</b>	1296
1297	V L SQRAS Q V ATTCATTTTGAAAGTTTACGAACAAGAACTGCAGAAGCCTTAAACCTGGATGCGGCGTTATTTGAACTAATC	424 1368
425	H F E S L T $R$ T AEALNLD I $\mathbf{R}$ AALF Е $\mathbf{L}$ I	448
1369	AAGCGATGTCAGCAGATGTGTTCGTTTGCATCACAGTTTAACAGTTCAGTGTCTGAGTTAGAGCTTCGTTTA	1440
449	K R c. QQM. $\mathbf{c} \cdot \mathbf{s}$ F A S Q F N S S V S E L E L R L	472
1441	TTACAGAGAGTGGACACTGGTCTTGAACATCCTATTGGCAGCTCTC{ATGGCTTTTGTCAGCACACAAACAG	1512
473	H P I G s s Ē o r v d т G L E <b>WLL</b> S A H K L o	496
1513		1584
497	т $Q$ D M S T Q R A I Q T E Κ Ε Ω Q I ε т v c E ACAATTCAGAATCTGGTTGATAATATAAAGACTGTGCTCACTGGTCATAACCGACAGCTTGGAGATGTCAAA	520
1585 521	т I. Q N L V D N I K T V L T G H N R Q L G D V K	1656 544
1657	CATCTCTTGAAAGCTATGGCTAAGGATGAAGAAGCTGCTCTGGCAGATGGTGAAGATGTTCCCTATGAGAAC	1728
545	A M A K D E E A A L A D G E D V P н L L K Y E N	568
1729	AGTGTTAGGCAGTTTTTGGGTGAATATAAATCATGGCAAGACAACATTCAAACAGTTCTATTTACATTAGTC	1800
569	VR. Q F L G E Y K S W Q D N I Q T V L F s T L <b>v</b>	592
1801	CAGGCTATGGGTCAGGTTCGAAGTCAAGAACACGTTGAAATGCTCCAGGAAATCACTCCCACCTTGAAAGAA	1872
593	O A M G O V R S Q E H V E M L Q E I T P т L K E	616
1873	CTGAAAACACAAAGTCAGAGTATCTATAATAATTTAGTGAGTTTTGCATCACCCTTAGTCACCGATGCAACA K T	1944
617 1945	$Q$ $S$ $Q$ S I Y N N L V S F A S P L V т. D A т. L AATGAATGTTCGAGTCCAACGTCATCTGCTACTTATCAGCCATCCTTCGCTGCAGCAGTCCGGAGTAACACT	640
641	S A T Y Q P S F A A A V R NEC <b>S</b> S P T S S N Ŧ	2016 664
2017	GGCCAGAAGACTCAGCCTGATGTCATGTCACAGAATGCTAGAAAGCTGATCCAGAAAAATCTTGCTACATCA	2088
665	$\mathbf{T}$ Q P D V <b>MSQNARKL</b> IQKNL A Ŧ. s o K	688
2089	GCTGATACTCCACCAAGCACCGTTCCAGGAACTGCAAGAGTGTTGCTTGTAGTCCTAAAAAGGCAGTCAGAG	2160
689	A D T P P S T V P G T A R V L L V V L K R Q S E	712
2161		2232
713	т	
2233	GTTAGAGGGCCGAGATGTTGATCCGAATAGGAGGATGTCAGTTGCTGAACAGGTTGACTATGTCATTAAGGA	2304
2305 2377	GGCAACTAATCTAGATAACTTGGCTCAGCTGTATGAAGGTTGGACAGCCTGGGTGTGAATGGCAAGACAGTA GATGAGTCTGGTTAAGCGAGGTCAGACATCCACCAGAATCAACTCAGCCTCAGGCATCCAAAGCCACACCAC	2376 2448
2449	AGTCGGTGGTGATGCAACTGGGGGCTTACTCTGAGGAAACCTAGGAAATCTCGGTGCACTAGGAAGTGAATC	2520
2521	CCGCAGGACAGCTGCACTCAGGGATACGCCACACACCATGGCCTGCAACCCCAGGGTCAAGGGTGAAGGAAA	2592
2593	GCAAGCTCACCGCCTGAACACGGAGATTGTCTTTCTGCCACAGAACAGCAGCAGACGTGTCGGGAGGTTAGC	2664
2665	TGCGGAAAGAAATCGGGATGCCGCGGAGCACAGAGTGATTTGGAACTCCATTCCACCTGACCCTGTGTTGAC	2736
2737	AATCCAGGAAAAAAAACAAACCCCACTCAGAAACAGAGAAAACTGGGGTCGCGAAGAAATCACAGCCGGAAG	2808
2809	ATTT _ATGCATT "A"* FCTCGTGTAACACTTGTTGCTTGGCAACAGTACTGGTTGGGCTGACCAGTAATGA	2880
2881	<b>GAAAAAGGT</b> \AGGCTATG GATATGAATTTCAGAAATGGACTGAAAATGGAGAGCTATGTAACAGATACA	2952
2953	CTACAGTAC. GACTTACTTCTGAAATGAAGGGA? '.AAAACCACCCCATCGTTCCCTACTCCTCC	3017

FIG. 3. DNA and deduced amino acid sequences of LIP. Nucleotides and amino acids are numbered on the left and right. Amino acid residue 1 is the putative initiator methionine. The single-letter amino acid code is used. Both strands of the cDNA were sequenced.

 $\lambda$ / $\mu$ PKC but also is a potent activator of this kinase in vitro. The addition of LIP plus phosphatidylserine together did not produce any additive or synergistic effect (not shown). To determine whether this is also true in vivo, quiescent Cos cells were transfected with either HA- $\lambda$ /<sub>L</sub>PKC or HA- $\zeta$ PKC and were simultaneously cotransfected with either an empty plasmid or an expression plasmid for LIP, after which they were stimulated with serum for 5 min, and both transfected PKCs were recovered with anti-HA antibody. Interestingly, expression of LIP dramatically activated  $\lambda/\mu$  KC but not  $\zeta$ PKC in vivo to an extent comparable to that produced by serum (Fig. 8). The

same stimulation was observed when  $\lambda$ /<sub>i</sub>PKC and LIP were transfected into NIH 3T3 cells (results not shown). Taken together, these results indicate that LIP is a novel protein capable of specifically and directly binding to the atypical  $\lambda$ <sub>I</sub>PKC isoform both in vitro and in vivo, which leads to its specific activation.

**Transactivation of a** k**B-dependent promoter by LIP.** Since the activation by overexpression of  $\lambda/\mu$ PKC leads to the transactivation of  $\kappa$ B-dependent promoters (7) (Fig. 1), transfection of a LIP expression vector should conceivably be able to activate that reporter plasmid. Results in Fig. 9 demonstrate that



FIG. 4. LIP tissue distribution. Total RNA  $(10 \mu g)$  from the indicated human tissues was run in formaldehyde-agarose gels, blotted onto a nylon filter, and hybridized to a cDNA probe for LIP, as described in Materials and Methods. Each RNA sample was normalized by ethidium bromide staining. The sizes (in kilobases) of RNAs are given to the right of the gel. Essentially identical results were obtained in another two experiments.

the transfection of a LIP expression vector promotes a dramatic activation of a kB-dependent promoter to an extent similar to that produced by TNF- $\alpha$  (7). Interestingly, cotransfection of a  $\lambda$ / $\mu$ PKC expression plasmid significantly synergizes with LIP to transactivate the **KB-reporter plasmid** (Fig. 10). Conversely, transfection of a kinase-inactive dominant negative mutant of  $\lambda/\mu$ PKC severely impairs the activation of the  $\kappa$ B promoter by LIP (Fig. 10). However, transfection of the kinase-inactive dominant negative mutant of zPKC does not produce any effect on the stimulation of that promoter by LIP (not shown). All the above data indicate that the activation by LIP of  $\lambda/\mu$ KC in vivo is physiologically relevant.

# **DISCUSSION**

PKCs form a large family of lipid-activable kinases that play pivotal roles in cell signalling. The so-called classical or conventional PKCs are critically involved in cell processes associated with the generation of increased cytosolic  $Ca^{2+}$  levels and diacylglycerol (32), such as those produced by the activation of the phospholipase C-mediated hydrolysis of phosphatidylinositol 4,5- $P_2$  (32). More recently, increased interest has been focused on the understanding of the functional role, as well as the mechanisms that regulate the novel and atypical PKC isoforms. Both kinds of PKC subtypes have been implicated in the control of key cellular events such as cell proliferation. Thus, overexpression of the novel εPKC leads to increased cell growth whereas overexpression of  $\delta PKC$  provokes the opposite effect (26, 32). Regarding the atypical PKC isotypes, it has been recently demonstrated that the microinjection of a peptide with the sequence of the pseudosubstrate of these isoforms dramatically inhibits oocyte maturation (10), cell proliferation (3), and NF-kB activation (11). The pseudosubstrate region of  $\zeta$ PKC is identical to that of  $\lambda$ / $\zeta$ PKC but is significantly different from that of conventional and novel PKCs (32), indicating that either or both atypical isoforms are important in cell signalling. The recent report of the sequence of  $\lambda$ / $\mu$ KC as a distinct atypical isotype (1, 38) has allowed the identification of the previously cloned *X. laevis*  $\zeta$ PKC isoform as actually  $\lambda$ / $\mu$ PKC. Inhibition of  $\lambda$ / $\mu$ PKC by antisense oligonucleotides (10) or by transfection or microinjection of a kinase-inactive dominant negative mutant (3, 7, 9) produced a severe reduction of important cell signalling parameters such as the stimulation of the  $\kappa$ B-dependent promoter activity (4, 7). We show here that transfection of kinase-inactive mutants of either  $\lambda$ /**LPKC** or  $\zeta$ PKC severely impaired the activation of a  $\kappa$ Bdependent promoter. Also, the overexpression of the wild-type



FIG. 5. Interaction of LIP and  $\lambda$ /<sub>v</sub>PKC in vitro. (A) Purified GST or GST fusion proteins encoding amino acids 1 to 126 (GST- $\lambda/\mu$ KC<sup>126</sup>), the zinc finger (GST- $\lambda/\mu$ RC<sup>REG</sup>) of  $\lambda/\mu$ RC at 800 nM were incubated with either 200 or 400 nM MBP or MBP-LIP(R4) for 1 h at 4°C, and the MBP fusion proteins were then immobilized on amylose resin. (B) After extensive washing, bound MBP fusion proteins and any associated proteins were boiled in sample buffer, fractionated by SDS-PAGE, and immunoblotted with anti-GST antibody to detect binding of the different GST fusion proteins. (C) Staining of a parallel gel confirming that all the reaction mixtures contained equal molar amounts of GST fusion proteins. Essentially identical results were obtained in another two experiments. PS, pseudosubstrate; ZF, zinc finger; MW, molecular weight (in thousands).

genes of either atypical isotypes activated this reporter construct. This is a reliable and sensitive biological readout of the mitogenic and inflammatory responses. Although both isotypes similarly regulate the  $\kappa$ B-promoter activity,  $\lambda/\nu$ PKC constructs were significantly more potent than  $\zeta PKC$  constructs were (Fig. 1). The fact that the two kinases displayed comparable behavior at high concentrations (Fig. 1) was to some extent predictable from the identity of their catalytic domains. Although the major differences between the atypical isoforms are located in their regulatory regions, both isotypes are activated by ceramide with similar kinetics and both bind Ras in vitro with identical affinity (23). Therefore, we reasoned that if functional differences underlay the sequence divergences existing in the regulatory domain of the two atypical isotypes, this could more probably be unveiled by the molecular characterization of hy-



FIG. 6. Interaction of LIP and  $\lambda/\mu$ PKC in vivo. (A) A 100- $\mu$ g portion of protein from actively proliferating HeLa cells was immunoprecipitated with an antibody that recognizes an epitope of  $\lambda$ /<sub>*i*</sub>PKC and  $\zeta$ PKC either in the absence (lane 1) or in the presence (lane 2) of competing peptide. Immunoprecipitates along with 20  $\mu$ g of protein of whole-cell extract (lane 3) were separated by SDS-PAGE and immunoblotted with an anti-LIP antibody. Essentially identical results were obtained in another three experiments. (B) Extracts from quiescent NIH 3T3 cells that were either untreated (lane 1) or stimulated with 10% serum (lanes 2 to 6) were immunoprecipitated with anti- $\lambda$ / $\iota$ PKC- $\zeta$ PKC antibody and immunoblotted with anti-LIP antibody as described for panel A. Essentially identical results were obtained in another three experiments.

pothetical novel regulatory proteins that could potentially interact with either  $\lambda$ / $\mu$ PKC or  $\zeta$ PKC and specifically regulate either activities. This could account for the different sensitivities of the kB-dependent promoter activity to low concentrations of  $\lambda/\mu$ KC versus  $\zeta$ PKC. We report here the molecular cloning and characterization of a novel protein, termed LIP, that specifically interacts with the zinc finger domain of  $\lambda/\mu$ PKC but not  $\zeta$ PKC. This interaction is detected by three different experimental approaches: (i) the yeast two-hybrid system used to clone it; (ii) in vitro assays with recombinant bacterially expressed LIP and different  $\lambda/\mu$ PKC- and  $\zeta$ PKC-expressed fragments; and (iii) coimmunoprecipitation experiments. What is really interesting about LIP is that it specifically activates  $\lambda$ / $\mu$ PKC but not  $\zeta$ PKC in vitro as well as in vivo and that its association with this PKC is dramatically activated following the mitogenic stimulation of quiescent cells. Therefore, although the two atypical PKC subspecies display similar functions, we demonstrate here the existence of at least one regu-



FIG. 7. Activation of  $\lambda/\mu$ PKC but not  $\zeta$ PKC by LIP in vitro. Cos cells were transfected with either control plasmid or expression vectors for HA-tagged  $\zeta$ PKC or  $\lambda$ / $\iota$ PKC, after which they were made quiescent by serum starvation, and the expressed proteins were immunoprecipitated with an anti-HA antibody, as described in Materials and Methods. The effect of 1  $\mu$ g of MBP, 1  $\mu$ g of MBP-LIP(R4), or phosphatidylserine (PS)  $(50 \mu g/ml)$  on regulation of the enzymatic activity of HA-¿PKC or HA $\lambda$ <sup>)</sup><sub>I</sub>PKC was determined. The two kinases were expressed at identical levels (not shown). Essentially identical results were obtained in another two experiments.



FIG. 8. Activation of  $\lambda/\mu$ PKC but not  $\zeta$ PKC by LIP in vivo. Cos cells were transfected with either control plasmid or expression vectors for HA- $\zeta$ PKC or HA- $\lambda$ / $\mu$ PKC along with either control plasmid (CMV) or a LIP(R4) expression vector, after which they were made quiescent by serum starvation and were either untreated or stimulated with 10% serum for 10 min. Then the HA-tagged PKCs were immunoprecipitated and their activity was determined as described in Materials and Methods. The two kinases were expressed at identical levels (not shown). Essentially identical results were obtained in another two experiments.

latory protein that is capable of specifically activating one of them but not the other in vitro and in vivo. The fact that expression of LIP leads to the activation of a kB-dependent promoter in a  $\lambda/\mu$ PKC-dependent manner underscores the likely physiological role of this novel PKC activator.

A number of PKC-interacting proteins have recently been identified and cloned. Thus, PICK1, a perinuclear protein that binds to the catalytic domain of  $PKC\alpha$  and is phosphorylated in vitro by this PKC isotype, has been described (40). Also, the characterization of another class of PKC-binding proteins, collectively termed RACKs, has been reported (27, 35). Interestingly, they appear to be important for the subcellular localization of activated classical PKC subspecies, a process that seems critical for their functionality in vivo (27, 35). One of the most remarkable aspects of LIP is that it activates  $\lambda / \mu$ PKC most probably by directly binding to the kinase zinc finger-like domain, a region thought to be stimulated only by lipids and their pharmacological analogs (32, 34). From the data presented here, the zinc finger domain of the PKCs should be considered a site for activation of these enzymes, not only by lipids but also



FIG. 9. Transfection of a LIP expression vector is sufficient to transactivate a kB-dependent promoter. Cos cells were transfected with different concentrations of plasmid CMV-LIP(R4) along with 500 ng of the  $\kappa$ B enhancer-directed luciferase reporter plasmid (3EconALuc). After 4 h, the DNA-containing medium was removed and cells were made quiescent by serum starvation for  $24$  h. Then extracts were prepared and the luciferase activity was determined as described in Materials and Methods. As a control, cells transfected with empty plasmid were stimulated with TNF- $\alpha$  (500 U/ml) for 4 h (open bar). Results are the mean  $\pm$ SD of three independent experiments with incubations in duplicate.



FIG. 10. Dependence on  $\lambda/\mu$ RC for the transactivation of a  $\kappa$ B promoter by LIP. Cos cells were transfected with different concentrations of plasmid CMV-LIP(R4) along with 500 ng of the  $\kappa$ B enhancer-directed luciferase reporter plasmid (3EconALuc) and either a control plasmid ( $\bullet$ ) or expression vectors for wild-type  $\lambda/\mu$ PKC ( $\blacksquare$ ) or a kinase-inactive mutant of  $\lambda/\mu$ PKC ( $\blacktriangle$ ). After 4 h, the DNA-containing medium was removed and cells were made quiescent by serum starvation. Then extracts were prepared and the luciferase activity was determined as described in Materials and Methods. Results are the mean  $\pm$  SD of three independent experiments with incubations in duplicate.

by functionally relevant regulatory proteins. Actually, a very recent report shows that the zinc finger domain of εPKC serves to localize this isoform to the Golgi apparatus (21). Whether this has a functional repercussion in the activity of εPKC deserves further investigation. Since LIP binds to  $\lambda/\mu$ KC but not zPKC, one can speculate on the existence of distinct LIP-like proteins specific for the different PKC isotypes. If further work confirms this model, it will mean that the specificity for the activation of the different PKC isoforms cannot be totally accounted for by lipid mediators but that specific PKC zinc finger-binding proteins are most probably also involved. This implies a change in the way we have so far envisioned the mechanism of PKC regulation.

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