

Complete cDNA encoding a putative phospholipase C from transformed human lymphocytes

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Phosphoinositide-specific phospholipase C (PLC) is a crucial enzyme in transmembrane signaling. A cDNA encoding the putative phospholipase C was cloned from human lymphocytes that were transformed by infection with Epstein-Barr virus. The deduced amino acid sequence of the cDNA accounted for 146.1 kDa of the molecular mass of the complete enzyme and showed 50.2% sequence similarity to bovine brain PLC. This cDNA contained regions, the sequences of which were similar to those of some tyrosine kinase-related oncogene products. Northern blotting demonstrated that the mRNA for this PLC is expressed in human promyelocytic leukemia cells (HL-60). Since the other cloned cDNAs for PLCs could not hybridize with the RNA from this cell, it is strongly suggested that the gene obtained here encodes an additional isozyme of PLC in blood cells.

Phospholipase C; Molecular cloning; Lymphocyte; (Human)

1. INTRODUCTION

Phosphoinositide-specific phospholipase C (PLC) is a crucial enzyme in transmembrane signaling that works by hydrolyzing phosphatidylinositol 4,5-bisphosphate to generate two messengers: the calcium mobilizer, inositol 1,4,5-triphosphate and protein kinase C activator, 1,2-diacylglycerol [1,2]. There have been many publications on the purification and characterization of PLCs from various tissues: rat liver (68 kDa) [3], sheep seminal vesicular gland (65 kDa) [4], bovine brain (88, 145 and 154 kDa) [5–7], rat brain (85 kDa) [8], guinea pig uterus (62 kDa) [9], calf thymocytes (68 kDa) [10], bovine platelets (143 kDa) [11] and human platelets (61 kDa) [12]. The observed differences in molecular mass may indicate the presence of multiple forms of PLCs.

To assess the multiplicity or diversity of PLC,

several laboratories have recently elucidated the primary structure of PLCs by cDNA cloning [13–18]. We report the molecular cloning and sequencing of a cDNA encoding the putative PLC in human lymphocytes transformed by Epstein-Barr virus.

2. MATERIALS AND METHODS

2.1. cDNA library from human lymphocytes

The lymphocytes were transformed by infection with Epstein-Barr virus [19] and cultured in RPMI medium supplemented with 10% fetal bovine serum. Purification of poly(A⁺) RNA and construction of the λ gt10 library were performed as described [20,21]. From 10 μ g of poly(A⁺) RNA, 10⁸ recombinants were obtained.

2.2. Oligonucleotides

Oligonucleotides for the cloning probes were synthesized in an automatic DNA synthesizer model 380B (Applied Biosystem, CA, USA). The oligonucleotides GTITGIC-CITGITAATACIGGCATCCITCIGGCCITCCCAGCAIT-C and TCITAITCIGCICIGCIAICITCIATITCIAIAIGG-ACAIACIATICC were selected by chance to encode some regions of the complementary sequences of bovine brain PLC [13] (the amino acid numbers from 367 to 383 and from 1106

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to 1122, respectively). The 5'-ends were labeled with [γ - 32 P]ATP and T₄ nucleotide kinase.

2.3. Cloning and sequencing

The cDNA library was screened with a mixture of the labeled

oligonucleotides. Hybridization was performed at 45°C in 3 $\times$ SSC, 0.1% SDS, 10 $\times$ Denhart's solution for 12 h, followed by washing with 2 $\times$ SSC and 0.1% SDS for 3 h at room temperature. The positive clones were purified by successive plaque hybridization. The isolated insert DNA fragments from

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GAATTCGGCGCTGAGTGACCCGAGTCGGGACGCGGGCTGCGCGCGCGGGACCCGGAGCCCAACCCGGGGCAGGCGGGCAGCTGTGCCGGGGCGGCAGGCCAGCTTCTGATTCTCC 120
CGATTCTCTCTCTCTCCCTGGAGCGGGCGACAAATGTCCACACGGTCAATGTAGATTCCCTTGGGAAATATGAGAAGAGCCAGATCAAGAGAGCCCTGGAGCTGGGGACGGTGATGACTG 240
MSTTVNVDSLAEYEKSKQIKRALLELGTVMTV 30
TGTTCAGCTTCGCAAGTCCACCCCGAGCGGAGAACCGTCCAGGTGATCATGGAGACCGCGCAGGTGGCCCTGGAGCAAGACCGCCGACAAGATCGAGGGCTCTTGGATATCATGGAAA 360
FSFRKSTPERRTTVQVIMETRQVAVWSKTDADKIEGFLDIMEI 70
TAAAGAAATCGCCCGAGGAAGAATCCAAAGATTTCGAGCGAGCAAAAGCAGTTCCGAGAAAGAAGACTGCTTCCACCATCTATATGGCACTCAGTTCGCTCCTCAGCAGCTCA 480
KEIRPGKNSKDFERAKAVRQKEDCCFTILYGTQFVLSLSTLS 110
GCTTGGCAGCTGACTTAAAGAGGATGCACTTAAGTCTCTGGCTTGAATACTTACACAGGAAGCGATGAATGCGTCCAGCCACCATTTATCGAGAGTTGGCTGAGAAAGCAGA 600
LAADSGKEDAVNWLSSLKILHQEAMNASTPTIIIESWLRKQI 150
TATATTCTGTGATCAACAGAGAAGACAGCATCAGTCTCGAGAGTTGAAGACCATCTGCCCTGATCAACTTTAAAGTGAGCAGTGCCCAAGTTCTTAAAGATAAGTTTGGGAAA 720
YSVDQTRRNSISLRELKTLPLINFKVSSSAKFKLKD KKFVEI 190
TAGGAGCACAAAGTAGCTCAGCTTGAACAGTTCCATCTCTTATAAAAACTATGTTTGAACAGCAAAATCGATTCTCGATGAATCAAAGAGGATTGCGCTGTTTATC 840
GHAHLKFYKLLMFEQKSLIDEFKKSILDEFFK 230
TGGGAACTGACAGGCGGATGCTCTGCTGTTTACCTGATGACTTCCAGAGGTTTCTCATACATGAACAGCAGGAGCATTGGGCTCAGGATCTGAACAAAGTCCGTGAGCGGATGA 960
GNTDRPDASAVLYPLHDFQRFLLIHEQQLHWAQDLN KVRERM 270
CAAAGTCTTATGATGACACCATGCGTGAAGTCTGAGCCTTCTGTTTGTGGATGAGTTCCACGTACCTGTTTTCAGGAGAAACAGCATCTGGGATGAGAAGTATGACGCGGTG 1080
KFIIDTMR ETAEFFLVDEFLLTYLFSRENSIWD EKV DAV 310
ACATGACGAGCATGAACAACTGCTTACTGATCTCTCTGACATACACAGTACCTTACAGTGCAGGAGCTGCTCCGAGAGCTTACATCGCTGAGCTG 1200
MQDMNPNPLSHYWISSSHNTYLTGDQLRSESSPEAYIRCLR 350
GCATGGCTGTGCTGCAATGAGTGTGCTGGGACGGGCGGATGGGAGCGGTCTACCATGGCTGGACGGGACTACCAAGATCAAGTTTGTAGCTGCTGAGGATCATCA 1320
MGCRCIELDCWDGPDGKPVIIYHGWTRRTTKIKFD D V V Q A I K 390
AAGACCAGCCTTGTACTCGAGCTTCCAGTGATCTGTCCATCGAGGAGCACTGACGGTGGAGCAACAGCGTCACATGGCCAAAGCCCTCAAGGAAGTATTGGGACCTGCTGT 1440
DHA F V T S S F P V I L S I E E H C S V E Q Q R H M A K A F K E V F G D L L L 430
TGACGAAGCCAGCGGAGGCTGCTGACGAGCTGCCCTCGCCAGCAGCTGCGGAGGAAGTATCATCAAGCATAAGAAGTGGGCCCCGAGGCGATGTTGGATGTCAACATGGAGG 1560
TKPTDEASPNPSPSQRLREKIKHKKKLGP R G D V D V R E R M T 470
ACAAGAAGGACGAACACAGCAACAGGGGAGCTGTACATGTTGGGATTCATTGACGAGAAATGGACTCGGCACTACTGCGCCATTGCTGATGCCAAGCTGTCTTCACTGATGACATTG 1680
KKDEHKKQGLELYMWDSDIQKWTRHYCAIADAKLSFSDIE 510
AACAGACTATGGAGGAGGAGTGGCCAGGATATACCCCTACAGAACTACATTTGGGAGAAATGGTTCCAGCAAGGTTGGAGAAGAGGAGGAGTCCGAGAGAGTTGCTGAGGAAAT 1800
QTMEEEVPPQDIPTTELEHFGKEKWFHKKKVEKRTSAEKLLOEY 550
ACTGCTGGAAGCGGGGCAAGGATGGCTTCTGTTGGGAGCGGAGCTTCCCAATGCTGACGAGTGGGCTGCTTCTGGCGGTGAGGCGGCTGAGGCGGATGAGTGGGATCGCT 1920
CME T G G K D G T F L V R E S E T F P N D Y T L S F W R S G R V Q H C R I R S 590
CCACCATGGAGGGCGGACCTGAAATACTACTGACTGACAACCTGAGGTTCCAGGAGGATGATGCCCCATCAGCACTACCGGAGAGCGACCTGCGCTGGCGGAGTTTCGAGCTGC 2040
TMEGDTLHNVSKEPGLTDNLFRFRMRYALIQHYRETHLPCEAEFV 630
GGCTCAGGACCTTGCCTCAACCCCAACCCACGAGTCCAAGCGGTGGTACTAGCAGGCTGAGCGCGGAGGAGGAGGAGGACATGCTGATGAGGATTCCTCCGGGACGGGCGTTCC 2160
LTDPTVPNPNPHESKPNWYYSDEAEEDMLMRIRP D M L M R I 670
TGATCGGAGGAGGAGGAGGAGGAGTCTATGCCATACCTTCAGGGTAGGGGCAAGTAAAGCATGTGCGATCAACCGGAGCGGCGGCACTTTGTGCTGGGACCTCCGCTATT 2280
IRKREGSDSYAITFRARAGKVKHCRINRDGRHFLVLTGSTAYF 710
TTGAGACTTGGTGGAGCTCGTAGTACTACGAGAAGCATCTACCTACGAAAGATGAGACTGCGCTACCCGAGCTGCTGGAGGCTACAAATAGGAAAGAGATATAA 2400
ESLVELVSTSYEYKHSLYRKMRLRYPVTPPELLLERYNTERDIN 750
ACTCCCTTACGAGCTCAGCAAGATGTGTGGATCCAGTGAATCAATCGTCCATGCTCAGAGAACGCTGAAAGCTCTGTATGACTAGAAAGCCAGCGAAGCATGAGTGAAGCT 2520
SLYDVSRMYVDPSSEINPSPMPQRTVVKALYDYKAKRSDEL S F 790
TCTGCCGTGGTCCCTCATCCAAATGTCTCAAGGAGCCGCGGGGCTGGTGGAAAGGAGACTGGAACAGGATCCAGCAGTACTCCCATCAACTCGTGAGGACATCTCAACTG 2640
CRGALILHNVSKEPGLTDNLFRFRMRYALIQHYRETHLPCEAEFV 830
CAGACTTCCAGGAGCTAGAAAGAGATATTGAAGACAATCCCTTAGGGTCTCTTTCGAGGAGAAATTTGAGCTCAATACCTATAACGTCGTGAAAGCCCTCAGGGAAGAAACCGA 2760
DFEELKQIILEDNPLGSLRCGLILDNLNTYNNVVKAPQKGNQ 870
AGTCTTTGTCTTATCTGAGGAGCCAGGAGCAGGCGATCTCCGGTGGAGTTGCCACAGACAGGTTGAGGAGCTCTTTGAGTGGTTTCAGAGCATCCGAGAGATCAGTGGGAAGA 2880
SFVFI LEPKEQGDPPEVF EATDTRVEELFEWFQSI REITWKI 910
TTGACAGCAAGGAGAAACATGAAGTCTGGGAGAGAACCATCGCATCGAGCTCTGACCTGGTTGTCTACTGCAAAACCAACAGCAAAACCAAGGACAACCTTAGAAAATC 3000
DSK ENNMKYWEKNQSI AIELSDLVVYCKPTSKTKDNL ENP 950
CTGACTCCGAGAAATCGCTCTTTTGGAGACGAAGGCTGACAGCATCATCAGACAGAAGCCGCTGACCTCTGAAATACAATCAAAGGGCTGACCCGCTACCCAAAGGGAC 3120
DFREIRSFVETKADSIIIRQKPVVDLLKYNNQKGLTRVYYPKGQ 990
AAAGAGTGACTTCAAACTACGACCCCTCCGCTCTGGCTGTGGCTTCTCAGATGGTGGCACTCAATTTCCAGACGGCAGATAAGTACATGCAGATGAATCAGCATTGTTTCTC 3240
RVDS SNYDPFRRLWL LCGS QMV ALN F Q T A D K Y M Q M N H A L F S L 1030
TCAAGCGGCGCAGGGCTAGVLTGCAAGCTGAGAGCATGAGGACAGAGAAATGACCGAGTGCCACNCFAGTCCAGAGGAAGATCTGTATGACGCTGACAGTCAAGTTCTCGGTG 3360
NGRTGTGQYCSMRTEK Y D P M P P E S Q R K I L M T V L G A 1070
CTGCCATCTCCCAAACTTGAAGCAAGTATTGCTGTCTCTTTGTAGAAGTGAAGATCTGTGGAGCGGAGTATGGCAACAACAGTTCAAGACGACGTTGTGAATGTATAATGGCTCA 3480
RHLPLKLGRLSIA C P F V E V E I C G A E Y G N N K F K T T V N D N G L S 1110
GCCCTTCTGGGCTCAAACACAGAGAGGTGACATTTGAAATTTATGACCCAACCTGGATTTCTGGCTTTGTGGTTTATGAAGAAGATATGTTAGCGATTCCTCACTTCTTGTCT 3600
PIWAPTQEKVTFEIIYD PNLALF L R F V V Y E E D M F S D P N F L A H 1150
ATGCCATTCACCCATTAAGCAGTCAAGATCAGGTCGTTCTCTGAAAGATGGGTACAGCGAGGACATAGAGTGGCTTCTCTGTTTCTGTTGAGATCGGCGGAGTCC 3720
ATYPIKAVKSGFRSVP L K N G Y S E D I E L A S L L V F C E M R P V L 1190
TGGAGAGCAAGGAAGCACTTACTCTCTGTGCGCAGCTGAGGAGGCGGCAAGAAGAACTGAACAACAGCTCTTCTGTATGACACACAGCAACTTGCAGTATGCAACCGGGATG 3840
ESEELLYS S C R Q L R R Q E A L L N N Q L R L Y D T H N R N A N R D A 1230
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LVEKFVS V N E N H S C T R N A T R G *
TGTGTGTAAGGATATGTGTGTGTCGCATGTGTGTTGTCATGTAGGAGAACGTGCCCTATTACACTCTGGGAAGACGCTAATCTGTGACATCTTTCTTCAAGCTGCCATCAAGGAC 4080
ATTTCTTAAGACCACTGGCATGAGTTGGGTAATTTCTATTATTTTCATCTTGGACAACCTTCACTTATATCTTTATAGAGGATCCCCAAAATGTCTCTCATTTTGGCTCT 4200
CATGTCCAAACCTCATTGAATAAAAAGCAATGAAAACCTTGAAAAAAGAAAAA

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Fig.1. Nucleotide sequence of the putative phospholipase C and the deduced amino acid sequence. The first methionine in the open reading frame is proposed to the initiation codon and the numbers start at the methionine for the deduced sequence.

Human PLC	312	QDMNNPLSHYWLSSSHNTYLTGDLRSESSPEAYIRCLRM
Rat PLC I	316	EDMSQPLSHYFINSSSHNTYLTAGDLAGNSSVEMYROVLLS
Rat PLC II	320	ETMNNPLSHYWLSSSHNTYLTGDOFSSESSLEAYARCLRM
Rat PLC III	296	QDMQPLSHYLVSSSHNTYLLFDQLTGPSSTEAYIRALCK
Human PLC		GRCIELDCWDG--PDGKPVIIYHGWIETTKIKFDVVQAI
Rat I PLC		GRCVELDCWIKGRTAEEPPVITHGFTMTTEISFKEVIEAI
Rat II PLC		GRCIELDCWDG--PDGMPVIIYHGHIETTKIKESDVLHTI
Rat III PLC		GRCLELDCWDG--ENQEPVIIYHGYETTSKILECDVLRAT
Human PLC		KDAFVITSSFPVILSIEEHC-SVEQQRHMAKAFKEVFGDL
Rat I PLC		AECAFKTSFPFILLSEFNHVDSPKQQAQMAEYORLIFGDA
Rat II PLC		KEHAFVASEYPVILSIEDHC-STAQQRMAQHERKVLGDT
Rat III PLC		RDYAFKASFPYPVILSLENHC-SLEQQRVMARHILAILGFI
Human PLC		LLTKPTEAS-ADQL-ESPS--QLREKIIKHKK
Rat I PLC		LLMEPLEKYPLESGVPLPSPMDLKYKILVKNKK
Rat II PLC		LLTKPVDT-AAD-G-LPSENLKRRKILIKHKK
Rat III PLC		LLDQPLDG-VTTS---LPSFEOLKGKILLKCKK
Human PLC	929	ELSDLVVYCKPITS--KIKDNLNPDFR-EIRSFVETKADS
Rat I PLC	539	ELSNLVNYLCPVKFESFE-TSKKRNKSEMSFVETKGLE
Rat II PLC	952	ELSELVVYCRPVPTD-EKIGTERACYROMSSFETKAEK
Rat III PLC	491	ELSDMIYCKSMVHGGEFSSPGTSGQAFYEMASFESRALR
Human PLC		ITROKPVDLLKYNQKG-LTRVYPKGQORVDSSNYDFRLWL
Rat I PLC		QITKSPVE-FVEYNKMOLSRIYPKGIRVDSSNYDFOLFWN
Rat II PLC		YVNAKAGKKFLOYNRIOLSRIYPKGORLDSSNYDPLPMWI
Rat III PLC		LIQESGNG-FVRHNVLSLSRIYFAGWNTDSSNYSEVEMVN
Human PLC		CGSQMVVALNFQTADRYMOMNHAFSLNGRIGYVLOPESMR
Rat I PLC		AGSQMVVALNFQTVDLAMCINMGMYEYNGKSGYRLKPEFMR
Rat II PLC		CGSQMVVALNFQTEPRMOMNCALEFMAGGHCYVLOPSTMR
Rat III PLC		GGQMVVALNFQTPGPEMDVYLGCFODNGGCGYVILKEAELR
Human PLC	777	ALYDYKAKRSELSFQRGALIHNVSKPEGGWVKGDGTT-RIQCYEFPNIV
v-crk	375	ALDFDKGNDGDLIFKKGDILKIRDKPEECWNAEDMDCKR-CHIVPYV
v-src	88	ALYDYESRIETDLSFKKGERLQIVMNTGEGWVAHSLTITGOTGYIPSMYV
Human PLC	532	WFHKVKEKRTSAEKLLOEYCMETGGKDGTFVRESETFENDYILS
Human PLC	646	WYYDSI-SRGEAEDMIMRI----PRDCAFLIRKEGSDSYAITF
v-crk	248	WTWGRI-SRGDAVSLI-QGQ----RHGTFLVRDSGSI PGDFVLS
v-src	140	WTFGKI-TRRESERLLLNPEM--PR-GTFLVRESETTKAYCLS
Human PLC	710	FESIVELVSYYEKH
v-crk	330	FDSLPSLLEFY-KT
v-src	212	FSSLOQLVAYYSKM

Fig.2. Comparison of part of the amino acid sequence with the sequences of other PLCs and tyrosine kinase-related oncogene products. The identical or conservatively changed amino acids are enclosed in boxes. See [13,14,16] for the published sequences.

the purified phage DNA (*EcoRI* and *HindIII* fragments) were directly analyzed by sequencing as described [22] (one of the *HindIII* sites is located in the λ gt10 DNA and one of the *EcoRI* sites is located in the cloning site).

3.3. Northern blotting

Northern blotting was performed as described [23]. The *EcoRI* fragment of the cDNA was used as the hybridization probe.

3. RESULTS AND DISCUSSION

A human cDNA library of transformed lymphocytes was screened with oligonucleotide probes as described in section 2. Out of 1.2×10^6 recombinants, three positive clones were isolated and purified. Since the nucleotide sequence of the insert suggested that it did not contain the full length of the cDNA, the library was screened again with the cloned insert as the probe. The nucleotide sequence and the deduced amino acid sequence of the longest insert are shown in fig.1. The parts of the deduced amino acid sequence were compared with those of the published PLCs [14,16] as illustrated in fig.2. The similarity of the deduced amino acid sequence to the published sequences strongly suggest that the cDNA encodes a kind of PLC. Although 97% of the amino acids of the bovine brain 148-PLC [13] were identical with those of the rat brain (PLC II) [13], only 50.2% of the total amino acids were identical with PLC II (rat brain) or 148-PLC (bovine brain) by a maximum matching method. In addition, this cDNA contained regions, the sequences of which were similar to those of some tyrosine kinases-related oncogene products (fig.2).

In Northern blot experiments, three bands of poly(A⁺) RNA prepared from human promyelocytic leukemia cells (HL-60) were hybridized with the cloned cDNA under weakly stringent conditions (indicated by arrows in fig.3). Only one band was hybridized under strongly stringent conditions (fig.3). Since the published clones [13,15] could be hybridized with human fibroblast RNA but not with HL-60 RNA, this putative PLC cDNA should be a different species of isozyme. In addition, the Northern blot experiment suggests that HL-60 cells may contain two additional isozymes of PLC. One of them may be a PLC of 61 kDa that was purified from human platelet membrane [12]. The interaction between PLC and GTP-binding proteins have been investigated in

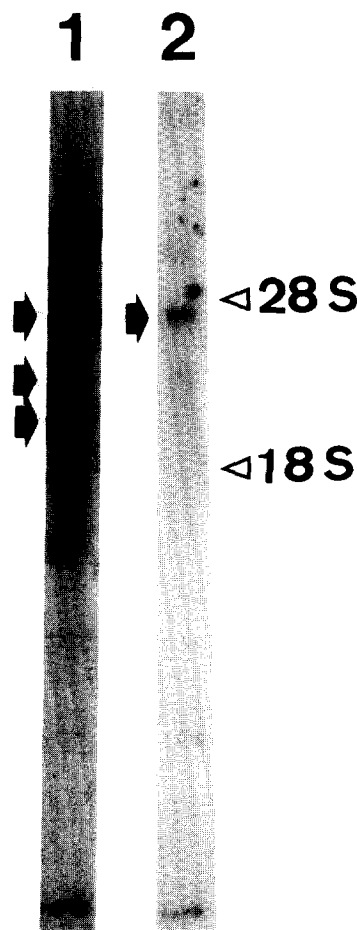


Fig.3. Northern blotting of mRNA from HL-60. Hybridization was performed using the 'Rapid hybridization system' (Amersham) at 55°C, and the membrane was washed with $2 \times$ SSC and 0.1% SDS for 2 h at room temperature, then for 1 h at 55°C (lane 1) and for an additional 1.5 h at 65°C with 0.1% SDS and $0.1 \times$ SSC (lane 2).

HL-60 [24]. Therefore, this clone will be potentially useful for various investigations on transmembrane signaling at the cellular level.

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