






ORIGINAL ARTICLE

Extracellular PKC δ signals to epidermal growth factor receptor for tumor proliferation in liver cancer cells

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Funding information

Japan Society for the Promotion of Science (KAKENHI), Grant/Award Number: 20K07621, 19H03519, 16K18434, 18K19484, 21K06192, 17H03584, 18K15253, 20H03519; AMED, Grant/Award Number B326TS; The Jikei University Graduate Research Fund; Science Research Promotion Fund

Abstract

Protein kinase C delta (PKC δ) is a multifunctional PKC family member and has been implicated in many types of cancers, including liver cancer. Recently, we have reported that PKC δ is secreted from liver cancer cells, and involved in cell proliferation and tumor growth. However, it remains unclear whether the extracellular PKC δ directly regulates cell surface growth factor receptors. Here, we identify epidermal growth factor receptor (EGFR) as a novel interacting protein of the cell surface PKC δ in liver cancer cells. Imaging studies showed that secreted PKC δ interacted with EGFR-expressing cells in both autocrine and paracrine manners. Biochemical analysis revealed that PKC δ bound to the extracellular domain of EGFR. We further found that a part of the amino acid sequence on the C-terminal region of PKC δ was similar to the putative EGFR binding site of EGF. In this regard, the point mutant of PKC δ in the binding site lacked the ability to bind to the extracellular domain of EGFR. Upon an extracellular PKC δ -EGFR association, ERK1/2 activation, downstream of EGFR signaling, was apparently induced in liver cancer cells. This study indicates that extracellular PKC δ behaves as a growth factor and provides a molecular basis for extracellular PKC δ -targeting therapy for liver cancer.

KEYWORDS

epidermal growth factor receptor, extracellular secretion, liver cancer, PKC δ

1 | INTRODUCTION

Human liver cancer is one of the most common and deadly tumors in the world.¹ Accumulating studies have shown that the major risk factors for liver cancer are well identified, such as nonalcoholic fatty liver disease as well as viral infections.² However, the molecular

mechanisms of carcinogenesis and tumor progression in liver cancer remain poorly understood.³

The PKC family comprise serine/threonine protein kinases, which are generally categorized as conventional (α , β I, β II, and γ), novel (δ , ϵ , η , and θ), and atypical (ζ , λ /I) PKC subfamilies.^{4,5} These PKC isoforms are commonly comprised of an N-terminal regulatory domain and

Abbreviations: EGF, epidermal growth factor; EGFR, epidermal growth factor receptor; GPC3, glypican3; IGF1R, insulin-like growth factor 1 receptor; PKC δ , protein kinase C delta; PMSF, phenylmethylsulphonyl fluoride; rPKC δ , recombinant protein kinase C delta; RTK, receptor tyrosine kinase.

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a C-terminal kinase core domain.⁵ Although the C-terminal kinase core domain is conserved between PKC isoforms and includes an ATP-binding site, a kinase core along with a substrate-binding site, the N-terminal regulatory domain is much less conserved and contains specific motifs for each isoform that are activated by unique signals.^{6,7} Indeed, each isoform differs in structure, function, and biological properties. Especially, PKC δ , one of a novel PKC subfamily, is known to be structurally and functionally affected by a variety of cellular stimuli, including growth factors and DNA damage.⁸

Human PKC δ is ubiquitously expressed in many types of tissues, and has been implicated in the regulation of various cellular processes, including proliferation, migration, and apoptosis as well as tumor promotion and tumor suppression.^{9,10} It is well known to be functionally translocated to diverse locations, including the cytosol and nucleus, in response to different stimuli and cell types.¹¹ After PKC δ is translated by the ribosome at the cytosol, it is generated as an inactive cytosolic form. Similar to other conventional and novel PKC subfamilies, in response to diacylglycerol, PKC δ migrates just below the plasma membrane, which triggers subsequent phosphorylation cascades. For example, PKC δ activation is known to be required for Akt activation by Ras.¹² Protein kinase C δ is also known to induce ERK1/2 activation.^{13,14} These PKC δ pathways are implicated in anchorage-independent growth and resistance of pancreatic ductal cancer cells to apoptotic stimuli.¹⁵ Conversely, cytosolic PKC δ has been reported to induce apoptosis by activating p38 MAPK to inhibit Akt.¹¹ These findings indicate that PKC δ might also act as a pro-survival or pro-apoptotic factor, depending on its subcellular localization. Furthermore, PKC δ contains a nuclear localization signal in its C-terminal kinase core domain, which is necessary for nuclear proteins to transit across the nuclear pore.^{16,17} Nuclear localization of PKC δ is associated with pro-apoptotic functions.¹⁶ However, it has been recently reported that nuclear PKC δ is involved in EGFR-kinase inhibitor resistance in EGFR-activating mutant lung cancer.¹⁸ These results suggest that PKC δ has a diversity in subcellular localization and functions according to tissues and stimuli. Recently, we have revealed that PKC δ is observed at the cell surface and in the extracellular space in liver cancer.¹⁹ Extracellular PKC δ was associated with GPC3, a heparan sulfate proteoglycan highly expressed on the cell surface of liver cancer cells, to activate IGF1R, which consequently contributes to cell proliferation and tumorigenesis.¹⁹ On the contrary, other types of cells, such as normal hepatocytes, did not show extracellular localization of PKC δ , although they express PKC δ in the intracellular area. In addition, treatment with the mAb against PKC δ has shown antitumor effects in liver cancer cells, suggesting that extracellular PKC δ acts in tumor promotion and could be a suitable therapeutic target for liver cancer. However, the impact of extracellular PKC δ on the cell surface is still not well characterized.

In this study, we explored additional receptors activated following extracellular PKC δ treatment in a liver cancer cell line, and found EGFR to be one of the targeting receptors. Extracellular PKC δ was found to bind to the extracellular domain of EGFR, leading to the activation of EGFR signaling. Furthermore, cellular imaging analysis

revealed that secreted PKC δ interacted with the surrounding EGFR-expressing cells.

2 | MATERIALS AND METHODS

2.1 | Cell culture

Human liver cancer line HepG2, human embryonic kidney cell line HEK293, human gastric cancer line AGS, and mouse fibroblast NIH3T3 were obtained from the Japanese Collection of Research Bioresources. Tetracycline-inducible HepG2 cells were purchased from Takara in 2018. HepG2, HEK293, and NIH3T3 cells were maintained in DMEM (Sigma) supplemented with 10% FBS (Sigma). AGS cells were maintained in RPMI-1640 (Sigma) supplemented with 10% FBS (Sigma). Tetracycline-inducible HepG2 cells were maintained in α -MEM (Nacalai Tesque) supplemented with 0.1 mM nonessential amino acids, 500 μ g/ml G418, and 10% Tet system-approved FBS (Takara).¹⁹ Cell lines were routinely monitored for *Mycoplasma* (4A Biotech Co.). Authentication of the cell lines was confirmed by short tandem repeating profiling every 6 months. The cells used for experiments were passaged within 10 times after thawing.

2.1.1 | Clinical samples

Tumor specimens from liver cancer patients were obtained from Jikei University Hospital. The protocol used in the study conformed to the ethical guidelines of the 1975 Declaration of Helsinki and were approved by the Jikei University School of Medicine Ethics Review Committee (ethics approval license: 29-038 [8654] and 29-006 [8622]), and written informed consent was obtained from all patients.

2.1.2 | Plasmid constructs and transfection

Protein kinase C δ , EGFR, GFP, and mCherry cDNA were cloned into the pcDNA3 vector by a HiFi DNA Assembly kit (New England Biolabs). Various deletion and point mutations were introduced by site-directed mutagenesis (Toyobo). Each plasmid construct was transfected using Lipofectamine 3000 (Thermo Fisher Scientific).

2.1.3 | Secreted protein preparation

Cells were maintained in a 0.1% FBS-containing medium for 24 h. After incubation, conditioned media (containing secreted proteins) were collected and subjected to sequential centrifugation: first at 300 g for 5 min to remove contaminated cells, then at 1000 g for 10 min to remove cell debris. Finally, the media were passed through a Millex 0.22 μ m GV filter (Merck Millipore).

2.1.4 | Immunoprecipitation and immunoblotting

Cells were harvested and resuspended in lysis buffer (50 mM Tris-HCl [pH 7.6], 150 mM NaCl, 1 mM PMSF, 1 mM DTT, 10 μ g/ml aprotinin, 1 μ g/ml leupeptin, 1 μ g/ml pepstatin A, and 1% NP-40) with or without phosphatase inhibitor (10 mM NaF and 1 mM Na_3VO_4). The supernatants were isolated by centrifugation and used as cell lysates. For immunoprecipitation, lysates were resuspended in a washing buffer (50 mM Tris-HCl [pH 7.6], 150 mM NaCl, 1 mM PMSF, 1 mM DTT, 10 μ g/ml aprotinin, 1 μ g/ml leupeptin, 1 μ g/ml pepstatin A, and 0.1% NP-40) with or without phosphatase inhibitor (10 mM NaF and 1 mM Na_3VO_4), and incubated with each Ab or GFP beads for 1 h. The solutions were then incubated with protein A-Sepharose for 2 h. The beads were washed five times in the washing buffer. The lysates and immunoprecipitates were boiled for 10 min, subjected to SDS-PAGE, and transferred to a nitrocellulose membrane. The membranes were probed with the following Abs: anti-PKC δ rabbit mAb (1:2000 dilution; Abcam), anti-phospho-EGFR rabbit mAb (1:1000 dilution; Cell Signaling Technology), anti-EGFR rabbit mAb (1:1000 dilution; Cell Signaling Technology), anti-phospho-ERK1/2 rabbit mAb (1:1000 dilution; Cell Signaling Technology), anti-ERK1/2 rabbit mAb (1:1000 dilution; Cell Signaling Technology), anti-actin mouse mAb (1:1000 dilution; Abcam), anti-GFP mouse mAb (1:1000 dilution; Nacalai Tesque), and anti-HA rat mAb (1:1000 dilution; Roche). The signals were detected by enhanced chemiluminescence (Thermo Fisher Scientific).

2.1.5 | Characterization of RTK activity

For analysis of RTK activity in HepG2 cells, the Human Phospho-RTK array kit (ARY001B; R&D Systems) was utilized to profile the RTK activity of the HepG2 cells treated with rPKC δ . Concisely, lysates were extracted using the lysis buffer, incubated overnight over the array, then incubated with HRP detection Ab, and visualized with the chemiluminescent reagent.

2.1.6 | Cell-to-cell PKC δ transmission analysis

Two distinct cells were cocultured and observed using ImageXpress Pico system (Molecular Devices). Images were processed using ImageXpress software to generate analysis mask.

3 | RESULTS

3.1 | Extracellular PKC δ activates EGFR in liver cancer cells

To examine the biological impact of the extracellular PKC δ on liver cancer cells, we performed an antibody array for phosphorylated RTKs using liver cancer cell line HepG2, which secretes PKC δ to the extracellular space (Figure 1A). Lysates of HepG2 cells were

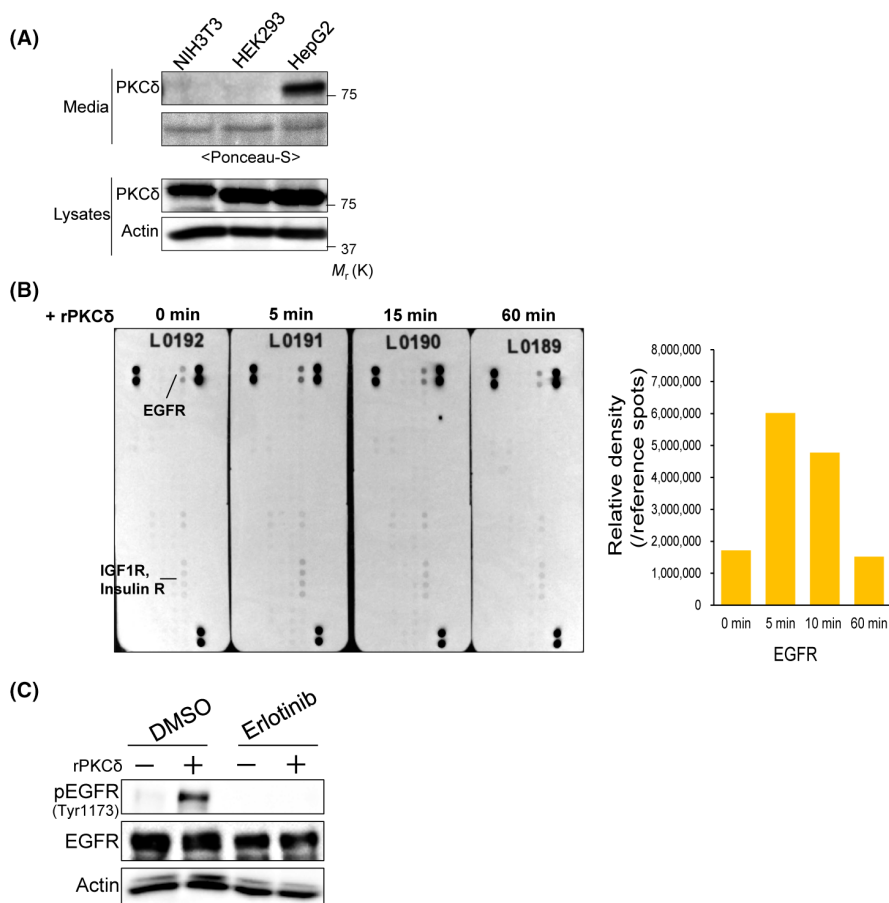


FIGURE 1 Extracellular protein kinase C delta (PKC δ) activates epidermal growth factor receptor (EGFR) in liver cancer cells. (A) Immunoblot analysis of PKC δ in media and lysates of NIH3T3, HEK293, or HepG2 cells. The Abs against PKC δ and actin (positive marker) were used. Ponceau S staining was used as loading control. (B) Human phospho-receptor tyrosine kinase Ab array analysis of starved HepG2 cells, followed by recombinant PKC δ (rPKC δ ; 100 ng/ml) treatment for 0, 5, 15, and 60 min. (C) HepG2 cells were pretreated with DMSO or erlotinib (1 μ M), followed by rPKC δ treatment for 5 min, and were subjected to immunoblot analysis with phospho-EGFR (pEGFR; Tyr1173), total EGFR, and actin (loading control). IGF1R, insulin-like growth factor 1 receptor

collected after treatment with sufficient rPKC δ (100 ng/ml) for 0, 5, 15, or 60 min, and reacted with each membrane of the Ab array (Figure S1). As shown in our previous results with HEK293 cells,¹⁹ rPKC δ treatment was shown to induce phosphorylation of IGF1R (Figure 1B and Figure S2). Interestingly, we found that EGFR1 (EGFR) was also activated by rPKC δ treatment in HepG2 cells, peaking at 5 min and then decreasing by 1 h to close to the original level (Figure 1B). It has been well known that EGFR is expressed in various tumor tissues, including liver cancer.^{18,20} The expression and the rPKC δ -induced activation of EGFR in HepG2 cells was confirmed by western blot analysis (Figure 1C). The activity of other EGFR families was not affected in this phosphorylation array, suggesting that PKC δ might be EGFR-specific (Figure 1B). We further confirmed the rPKC δ -mediated EGFR activation by pretreatment of HepG2 cells with erlotinib, an EGFR inhibitor (Figure 1C), indicating that extracellular PKC δ activates EGFR in liver cancer cells.

3.2 | Protein kinase C δ binds to the extracellular domain of EGFR

Given that IGF1R activation by rPKC δ treatment has been mediated by the PKC δ -GPC3 interaction,¹⁹ we investigated the involvement of GPC3 expression in activation of EGFR following PKC δ treatment. Knockout of GPC3 had no effect on EGFR activation in response to PKC δ treatment (Figure S3), indicating that GPC3 is not engaged in the activation of EGFR following PKC δ treatment. Next, we further examined the relationship between extracellular PKC δ and EGFR. When we carried out co-immunoprecipitation experiments using HEK293 cells, PKC δ was associated not only with full length of EGFR, but also a mutant lacking the intracellular domain of EGFR (Figure 2A), indicating that PKC δ interacts with the extracellular domain of EGFR. Similar results were obtained by co-immunoprecipitation analysis using HEK293 cells transfected with other Tag-fused constructs (Figure 2B). These data suggested that secreted PKC δ was likely to directly bind to EGFR in the extracellular space.

3.3 | Protein kinase C δ contains putative EGFR binding sites similar to EGF

To test this hypothesis, we explored the binding region of PKC δ to extracellular EGFR. First, we generated plasmid constructs of several PKC δ deletion mutants, and introduced them into HEK293 cells (Figure 3A). Co-immunoprecipitation analysis showed that the C-terminal kinase core domain of PKC δ (amino acids 330-676; Δ N) interacted with the extracellular domain of EGFR, whereas the association with that of EGFR was abolished when the N-terminal regulatory domain of PKC δ (amino acids 1-329; Δ C) was expressed (Figure 3B), indicating that the C-terminal region of PKC δ was required for the extracellular interaction with EGFR. Next, to determine the amino acid sites in the C-terminal kinase core domain of PKC δ that can

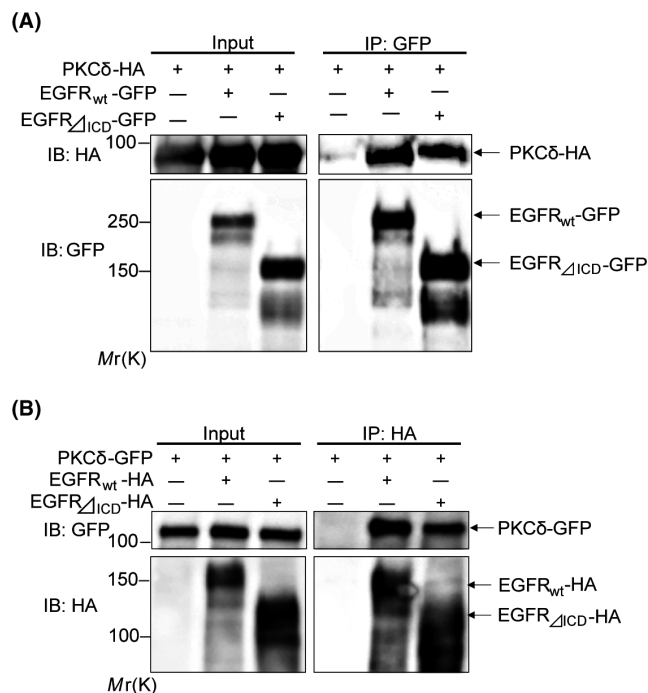


FIGURE 2 Protein kinase C delta (PKC δ) associates with the extracellular domain of epidermal growth factor receptor (EGFR). (A) HEK293 cells were cotransfected with HA-tagged PKC δ and GFP-tagged EGFR containing full-length (wt) or deleted intracellular domain (Δ ICD) expression plasmids. GFP beads were used for immunoprecipitation. (B) HepG2 cells were cotransfected with GFP-tagged PKC δ and HA-tagged EGFR containing wt or Δ ICD expression plasmids. Anti-HA Ab was used for immunoprecipitation. IB, immunoblot

bind to EGFR, we compared the sequence similarity between PKC δ and EGF, one of the major ligands of EGFR. Among the sequences of EGF, we noticed that PKC δ contained the identical sequences to the putative EGFR binding sites (amino acids 44-48; YRDLK) of EGF, which are common recognition sites for cetuximab, an EGFR-specific inhibitor (Figure 3C).²¹ To verify whether this sequence is crucial for the association of PKC δ with EGFR, we generated a plasmid construct of the point mutant of PKC δ , in which three representative amino acids were replaced with alanine (Y471A/L473A/K475A). Co-immunoprecipitation analysis showed that this mutant apparently lacked the ability to bind to EGFR (Figure 3D). These results suggested that PKC δ directly bound to EGFR as a humoral factor.

3.4 | Extracellular PKC δ -dependent EGFR signaling is transmitted to surrounding cells

To investigate whether PKC δ acts as a growth factor after its secretion, we undertook cell-to-cell transport analysis on the secreted PKC δ . We cocultured HepG2 cells expressing GFP-fused PKC δ with HepG2 or NIH3T3 cells expressing mCherry-fused EGFR (1:1), and then detected mCherry-positive and GFP-positive cells (Figure 4A). The results indicated that GFP(+)-mCherry(+) double-positive cells

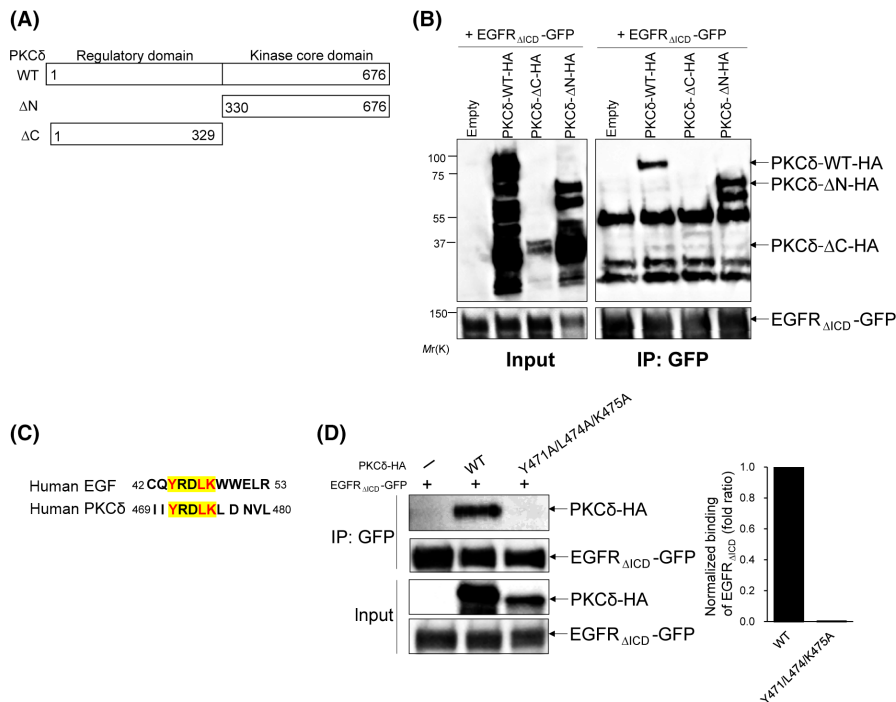


FIGURE 3 Part of the amino acid sequences of protein kinase C delta (PKC δ) is necessary for the association with epidermal growth factor receptor (EGFR). (A) Schematic diagram of the WT, C-terminal cartilistic domain (amino acids 330–676; Δ N), and N-terminal regulatory domain (amino acids 1–329; Δ C) constructs of PKC δ -HA. (B) HEK293 cells were cotransfected with HA-tagged PKC δ and GFP-tagged intracellular domain-deleted EGFR expression plasmids. GFP beads were used for immunoprecipitation. (C) Sequence alignment of human epidermal growth factor (EGF) and human PKC δ . Filled areas indicate 100% identity, and red characters show EGF-EGFR binding sites. (D) HEK293 cells were cotransfected with WT or point mutant (Y471A/L474A/K475A) of HA-tagged PKC δ , and GFP-tagged intracellular domain-deleted EGFR expression plasmids. GFP beads were used for immunoprecipitation (IP). Δ ICD, deleted intracellular domain

were observed in both HepG2 (7.5%) and NIH3T3 cells (0.2%) (Figure 4B and Figure S4), suggesting that the secreted PKC δ not only interacted with liver cancer cells in an autocrine manner, but also with surrounding EGFR-positive heterogeneous cells in a paracrine manner. This higher percentage of GFP(+)-mCherry(+) double-positive cells in HepG2 cells might be due to the fact that HepG2 cells highly express additional cell surface receptors, such as GPC3, which can interact with the extracellular PKC δ .¹⁹ We also observed that the GFP(+)-mCherry(+) double-positive cells were located in the vicinity of GFP(+)-only positive HepG2 cells (Figure 4B,C), indicating that PKC δ secretion was likely to affect the perisecretory environment. Furthermore, we confirmed EGFR-positive fibroblasts in tumors of patients with liver cancer (Figure S5).

To further understand the biological significance of PKC δ in communication between cells, we evaluated the activation of downstream signals of EGFR by western blot analysis. According to previous results of intracellular kinase phosphorylation array using HepG2 cells, we found that rPKC δ treatment strongly induced activation of ERK1/2, one of the downstream signaling molecules of EGFR.¹⁹ Therefore, we investigated whether ERK1/2 is activated by rPKC δ treatment in EGFR-expressing cells. Exogenous rPKC δ treatment increased ERK1/2 activation not only in the HepG2 liver cancer cell line, which secretes PKC δ endogenously, but also in other EGFR-expressing cells (AGS and EGFR-transfected NIH3T3 cells),

which do not secrete PKC δ (Figures 1A and 4D–F).¹⁹ Taken together, these results indicate that PKC δ acts as a direct agonistic ligand for EGFR after its secretion.

4 | DISCUSSION

On the basis of our current findings, we provide a model demonstrating that PKC δ secretion in the liver cancer microenvironment induces activation of EGFR signaling in an autocrine or paracrine manner. In addition to enhancement of liver cancer cell proliferation and tumorigenesis by extracellular PKC δ ,¹⁹ it has been known that EGFR expression is involved in tumorigenesis and tumor progression in various types of cancers, including lung, pancreatic, and liver cancers.^{22,23} Taken together, these facts suggest that the PKC δ -EGFR axis could play a critical role in the pathogenesis of liver cancer. Furthermore, our current study observed that secreted PKC δ could interact with a type of stroma cell (fibroblasts), which were increased in EGFR signaling (Figure 4B). Given that tumor-associated endothelial cells also express high levels of EGFR, and the EGFR signaling is required for their proliferation and angiogenesis,²⁴ we propose a mechanistic insight into the interplay between PKC δ and EGFR in the modulation of the liver cancer microenvironment (Figure 5).

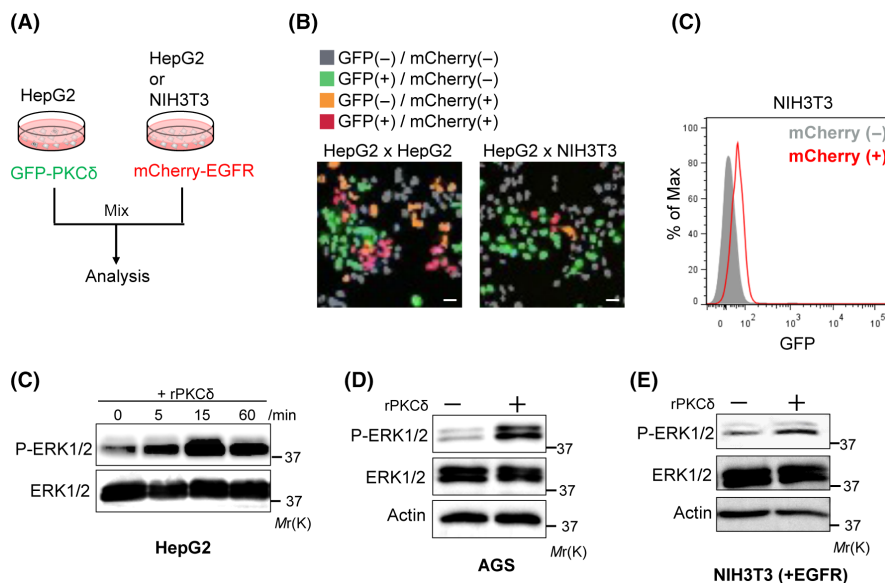


FIGURE 4 Extracellular protein kinase C delta (PKC δ) functions as a growth factor to activate epidermal growth factor receptor (EGFR) signaling. (A) Schematic outline of a mixture experiment of two distinct cell lines. (B) Cell-to-cell PKC δ transmission analysis using the ImageXpress Pico system in co-culture with doxycycline-inducible HepG2 cells expressing PKC δ -GFP and HepG2 (left panel) or NIH3T3 (right panel) cells expressing EGFR-mCherry. Image analysis masks showing GFP(-)-mCherry(-) cells (gray), GFP(+)-mCherry(-) cells (green), GFP(-)-mCherry(+) cells (orange), or GFP(+)-mCherry(+) cells (red). Each cell was analyzed for more than 10,000 cells. Scale bars, 20 μ m. (C) Flow cytometric analysis of mCherry-EGFR or mCherry-control-expressing NIH3T3 cells. These cells were treated with conditioned medium of PKC δ -GFP-expressing HepG2 cells for 24 h. (D) Immunoblot analysis of phospho-ERK1/2 (P-ERK1/2) and total ERK1/2 (loading control) in HepG2 cells treated with recombinant PKC δ (rPKC δ) for 0, 5, 15, and 60 min. (E) Immunoblot analysis of P-ERK1/2, total ERK1/2, and actin (loading control) in AGS cells treated with rPKC δ for 15 min. (F) Immunoblot analysis of P-ERK1/2, total ERK1/2, and actin (loading control) in EGFR-overexpressing NIH3T3 cells treated with rPKC δ for 15 min

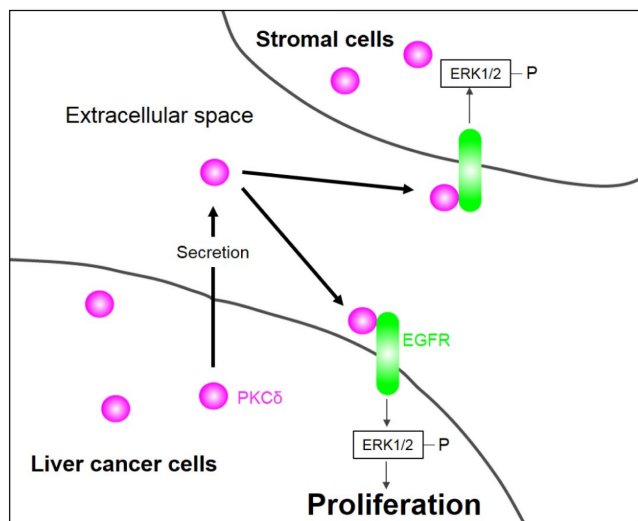


FIGURE 5 Protein kinase C delta (PKC δ)-epidermal growth factor receptor (EGFR) interaction at the cell surface. A model for PKC δ secreted from liver cancer cells to act on surrounding EGFR-positive cells in a paracrine and autocrine manner

We have previously found extracellular distribution of PKC δ .¹⁹ Generally, PKC δ is usually thought of as an intracellular protein because it does not have a signal peptide. Similarly, we and other groups have reported the extracellular presence of importin α 1 and nucleolin in several cancer cells.^{25,26} An important point is that these

extracellular localizations are observed under normal cell culture conditions, which are apparently independent of cell death. In the current study, we also observed that PKC δ , which is expressed in a doxycycline-inducible manner, was delivered to EGFR-positive cells through the extracellular space. Given the fact that these secreted nonsignal peptide molecules are involved in tumor enhancement, such as cell proliferation and angiogenesis,²⁷ this unconventional secretion system appears to be crucial for tumorigenesis. Indeed, the development of aptamer targeting cell surface nucleolin has been implemented in various diseases such as gastric and renal cancers.^{28,29} Together with the evidence that the Ab to PKC δ has anti-tumor activity in liver cancer,¹⁹ it can be assumed that many drugs targeting unconventional secretory proteins will be developed in the future.

In this study, we found that PKC δ directly bound and activated to one of the RTKs. Our previous work has also found that extracellular PKC δ activates IGF1R, mediated by GPC3.¹⁹ Thus, it is conceivable that extracellular PKC δ is an auxiliary ligand for growth factors that enhances proliferative signaling and contributes to tumorigenesis. Indeed, the extracellular PKC δ enhances proliferative signals such as ERK1/2 and STAT3.¹⁹ Given that PKC δ secretion is specific to liver cancer and is missing in normal hepatocytes and precancerous patients,¹⁹ we speculated that the PKC δ -EGFR-ERK1/2 pathway might play an indispensable role in tumor initiation or progression.

In this current study, we found that PKC δ has a sequence similar to that of EGF, which is important for binding to EGFR (Figure 3).

Although the relationship between EGF and PKC δ , such as the difference in its affinity to associate with EGFR, is not uncovered in the current study, the functional similarity suggests that they mutually complement each other in increasing the proliferation of liver cancer cells. Likewise, there is a possibility that PKC δ binds to EGFR sequences that are quite distinct from EGF, requiring further work to clarify.

Epidermal growth factor receptor is correlated with the promotion of various cancerous tissues, and has been reported to regulate cell proliferation through a variety of biological mechanisms.^{30,31} For example, although EGFR typically localizes to the cell surface, it has also been shown that EGFR can be translocated to the nucleus. Nuclear EGFR cooperates with E2F1 to transactivate the *B-MYB* gene in a cell cycle-dependent manner.³² It has also been found that in pancreatic ductal adenocarcinoma, extracellular human RNase 5 (angiogenin) binds to EGFR, which contributes to tumorigenesis.³³ In view of such functional redundancies, our present study indicated that PKC δ was a novel active ligand for EGFR in liver cancer cells. Taken together with EGFR-activating mutations in other cancer types, such as lung cancer,³⁴ these findings strongly support that EGFR redundantly regulates cell proliferation. In fact, EGFR tyrosine kinase inhibitors are now considered promising drugs to treat various cancers, such as lung and pancreatic cancers.^{35,36} Therefore, in the future, the utilization of EGFR inhibitors could be evaluated for their efficacy in the treatment of liver cancer in accordance with the expression and secretion of PKC δ .

This study showed that EGFR activation is independent of GPC3 expression (Figure S3). The secretion of EGF, a normally secreted protein, appears to be diminished upon nutritional starvation, whereas PKC δ secretion occurs consistently¹⁹ (Figure 1A and Figure S1). Thus, it is likely that EGF is responsible for EGFR activation under a normal nutritional condition, whereas PKC δ activates EGFR during nutrient starvation.

In conclusion, we identified EGFR as a new receptor for extracellular PKC δ , and showed that extracellular PKC δ behaves as its ligand. The fact that PKC δ acts on liver cancer cell membranes to enhance proliferative signaling provides a rationale for the development of drugs targeting extracellular PKC δ for the treatment of liver cancer.

AUTHOR CONTRIBUTIONS

K. Yamada, R. Kizawa, and K. Yoshida contributed to the experimental concept and design and wrote the manuscript. K. Yamada and R. Kizawa contributed to data analysis and interpretation. K. Yamada, R. Kizawa, and K. Yoshida developed the methodology. K. Yamada, R. Kizawa, A.Y., S.M., R. Koizumi, S.Y., Y.S., and Y.H. performed in vitro experiments. T.O. and M.S. obtained and analyzed clinical samples, and K. Yoshida supervised the project.

ACKNOWLEDGMENTS

We thank Ms. N. Tago for secretarial and technical assistance. We also thank Dr. Yamamoto and Dr. Shima for technical assistance in the ImageXpress Pico system. This work was supported by grants

from the Japan Society for the Promotion of Science (KAKENHI Grant Numbers 20K07621, 19H03519, 16K18434, and 18K19484 to K. Yamada, 21K06192 to S. Yoshida, 17H03584, 18K15253, and 20H03519 to K. Yoshida), AMED under Grant Number B326TS to K. Yamada., The Jikei University Graduate Research Fund to K. Yamada., and the Science Research Promotion Fund to K. Yoshida.

DISCLOSURE

No potential conflicts of interest were disclosed.

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SUPPORTING INFORMATION

Additional supporting information may be found in the online version of the article at the publisher's website.

How to cite this article: Yamada K, Kizawa R, Yoshida A, et al. Extracellular PKC δ signals to epidermal growth factor receptor for tumor proliferation in liver cancer cells. *Cancer Sci*. 2022;113:2378-2385. doi:[10.1111/cas.15386](https://doi.org/10.1111/cas.15386)