

# Expression of Protein Kinase C Family in Human Hepatocellular Carcinoma

Hsiu-Chin Lu · Fen-Pi Chou · Kun-Tu Yeh ·  
Ya-Sian Chang · Nicholas C. Hsu · Jan-Gowth Chang

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**Abstract** Protein kinase Cs (PKCs) play important roles in signal transduction, cell regulation, and tumor formation. In the present study, we analyzed the expression of PKCs in human hepatocellular carcinoma (HCC) tissues and explored their roles in the development of HCC. Real-time quantitative PCR and immunohistochemistry showed that PKC $\beta$  and PKC $\theta$  were down-regulated in HCC tissues. Reduced expression of PKC $\theta$  is well correlated with the grade of cancer cells ( $p=0.009$ ), and the down-regulated expression of

PKC $\beta$ II is associated with HBV infection ( $p=0.035$ ). Our findings suggest particular roles of the two PKC isoenzymes in the hepatocarcinogenesis of human HCC.

**Keywords** Protein kinase C · Human hepatocellular carcinoma

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H.-C. Lu · Y.-S. Chang · N. C. Hsu · J.-G. Chang  
Department of Laboratory Medicine,  
Kaohsiung Medical University Hospital,  
Institute of Clinical Research, College of Medicine,  
Kaohsiung Medical University,  
Kaohsiung, Taiwan

H.-C. Lu · F.-P. Chou  
Institute of Biochemistry and Biotechnology,  
Chung-Shan Medical University,  
Taichung, Taiwan

K.-T. Yeh  
Department of Pathology, Changhua Christian Hospital,  
Changhua, Taiwan

J.-G. Chang  
Center for Excellence in Environmental Medicine,  
Kaohsiung Medical University,  
Kaohsiung, Taiwan

J.-G. Chang (✉)  
Department of Laboratory Medicine,  
Kaohsiung Medical University Hospital,  
Kaohsiung, Taiwan  
e-mail: jgchang@ms.kmuh.org.tw

## Introduction

Hepatocellular carcinoma (HCC) is commonly associated with chronic hepatitis B virus (HBV) or hepatitis C virus (HCV) infection, with chronic exposure to aflatoxin B, or with complications as a consequence of alcoholic cirrhosis [1–5]. The oncogenesis of HCC is thought to be a multiple-step process which includes inactivation of tumor suppressor genes, activation of oncogenes, or disturbance of other genes that ultimately lead to the formation of tumor [1, 6–9].

Protein Kinase C (PKC) family consists of at least 12 serine-threonine kinases which are classified into three groups: classical ( $\alpha$ ,  $\beta$ , and  $\gamma$ ), novel ( $\delta$ ,  $\epsilon$ ,  $\eta$ , and  $\theta$ ) and atypical ( $\mu$ ,  $\xi$ , and  $\iota$ ). Activation of classical enzymes is dependent on calcium and diacylglycerol (DAG), novel enzymes are activated by diacylglycerol. Atypical enzymes are not activated by calcium or DAG, but they may be activated by other PKCs [10–13]. Sustained activation of PKCs induces long-term effects including proliferation, differentiation, apoptosis, migration and tumorigenesis [14–21]. PKC isoenzymes are ubiquitously expressed in tissues. PKC  $\alpha$ ,  $\beta$ , and  $\delta$  are the most abundant isoenzymes in various tissues [22]. Activation of different PKC isoenzymes has been shown to result in different cellular response, and there is an extensive cross-talk with different isoenzymes, and the overall response is dependent on presence or activity of the other isoenzymes in particular cell type [18, 21].

PKC plays a major role in intracellular signal transduction and is thought to be involved in cancer biology. Moreover, the biological effects of PKC seem to be tumor-specific rather than unique. PKC $\alpha$  is overexpressed in high grade urinary bladder, prostate, and endometrial cancers, but low grade tumors and normal epithelia of the respective organs show significantly reduced expression [23–28]. In contrast, breast, colon, hepatocellular and basal cell cancers show down-regulated PKC $\alpha$  expression [29–33]. PKC $\beta$  expression has been shown to be up-regulated in colon and prostate cancers [24, 30], but down-regulated in bladder cancer [25, 26, 28]. In this study, we analyzed the expression of 10 PKCs in HCC and explore their clinical significance.

## Materials and Methods

### Samples

Fifty-five histologically confirmed resected HCCs and paired non-cancerous tissue samples were obtained on protocols approved by the Institutional Review Board of Changhua Christian Hospital. The age of the patients ranged from 24 to 77 years with a mean of 56.8 years. All patients were staged according to the 2002 American Joint Committee on Cancer staging system. The Edmondson-Steiner grading system was used [34]. Pathologically, all tumors were HCC with 12 cases at grade I, 28 cases at grade II and 15 cases at grade III. Slides from tumors were reviewed by two pathologists to define the histological grading. Tissues were frozen immediately after surgical resection and stored in liquid nitrogen until extraction of DNA or RNA. DNA extraction was performed as previously described [35]. Total RNA was extracted using a commercial kit (RNA-Bee™, Tel-Test, Inc., Texas, USA), and stored in  $-70^{\circ}\text{C}$  deep freezer either as a pellet in ethanol or solubilized in RNase-free water.

### Real-Time Quantitative RT-PCR (qRT-PCR) Analysis

The mRNA sequences of the 10 PKC genes were evaluated for the purpose of designing specific forward and reverse primers and specific probes with the aid of the Primer Express Software (Roche, USA). The probes were synthesized and labeled with appropriate fluorescent dyes (Roche). Sequences of the forward and reverse primers for 10 PKC genes are listed in the Supplement 1. We used *HPRT* gene as internal RNA control for RT-PCR. The expression levels of the PKC genes were normalized to the endogenous *HPRT* reference to obtain the relative threshold cycle ( $\Delta\text{Ct}$ ) which was in turn related to the  $\Delta\text{Ct}$  of the paired non-cancerous tissue to obtain the relative expression level ( $2^{-\Delta\Delta\text{Ct}}$ ) of the PKC gene.

Reverse transcription was performed in a final volume of 25  $\mu\text{L}$  containing 2  $\mu\text{g}$  RNA, 0.5  $\mu\text{g}$  random primers

(10 mers), 2 mM dNTPs, 25 U RNasin (Promega, Madison, WI, USA), 50 mM Tris-HCl (pH 8.3), 75 mM KCl, 3 mM  $\text{MgCl}_2$ , and 200 U Moloney Murine Leukemia Virus reverse transcriptase (Promega). The reaction was first denatured for 5 min at  $70^{\circ}\text{C}$  and incubated at  $37^{\circ}\text{C}$  for 60 min, then stopped by heat inactivation at  $95^{\circ}\text{C}$  for 5 min. Real-time quantitative PCR was performed as described [35].  $2^{-\Delta\Delta\text{Ct}}$  indicates the ratio of concentration of PKC mRNA of tumor/normal.

### Analysis of Alternative Splicing of Pre-mRNA of PKC $\beta$ in HCC

The RT-PCR analysis were performed as described [36]. The sets of primers used for screening alternative splicing of PKC $\beta$  were shown in Supplement 2. The PCR was performed with a denaturing step at  $94^{\circ}\text{C}$  for 5 min, then 30 s at  $94^{\circ}\text{C}$ , 30 s at  $T_m$  of primers, and 1 min at  $72^{\circ}\text{C}$  for 35 cycles, followed by a final 5 min at  $72^{\circ}\text{C}$ . The PCR products were separated on 2.5% agarose gel and the intensity of the PCR products were analyzed by LabWorks Image Acquisition and Analysis Software (UVP BioImaging Systems).

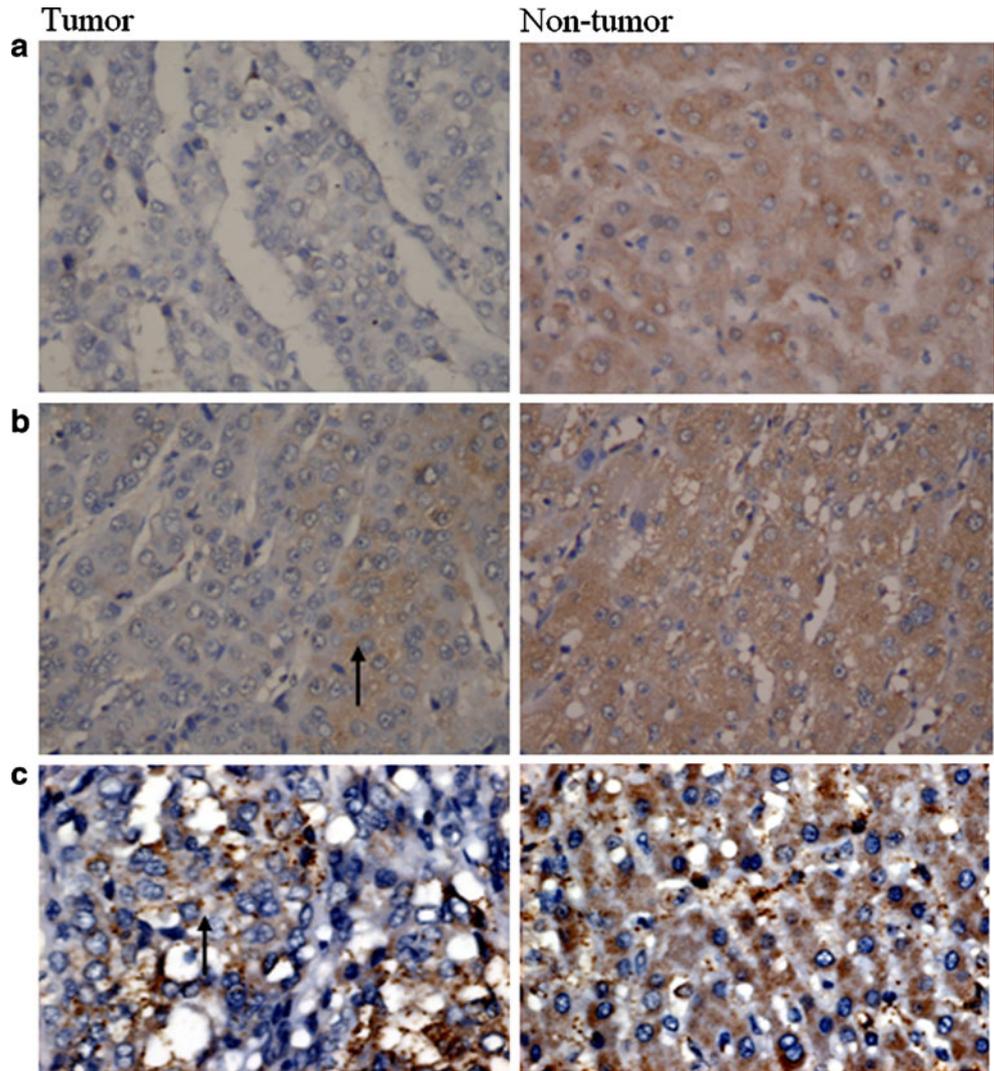
### Analyses of PKC Isoenzymes Expression by Immunohistochemistry

The percentage of immunoreactivity was scored as 0 to +2. Immunoreactivity in <10% of cells was considered as negative expression (0), 10–50% (+1), and >50% (+2). Five-to-ten fields were examined for each section, and at least 1000 cells were scored. Investigator-bias was avoided by two investigators independently scoring coded sections. The staining intensity of non-tumorous hepatocyte was considered as an internal positive control and 1+ staining. Briefly, paraffin-embedded HCC and paired non-cancerous tissue sections (4  $\mu\text{m}$ ) on poly-L-lysine coated slides were deparaffinized. After treatment of 3 %  $\text{H}_2\text{O}_2$  in methanol, the sections were hydrated with gradient alcohol and PBS, incubated in 10 mM citrate buffer and, finally, heated at  $100^{\circ}\text{C}$  for 20 min in PBS. After incubation with the anti-PKC $\beta$ I, PKC $\beta$ II, or PKC $\theta$  antibody (all purchased from Santa Cruz Biotechnology, Santa Cruz, CA) for 20 min at room temperature, slides were incubated with a horseradish peroxidase (HRP)/Fab polymer conjugate for another 30 min after being thoroughly washed three times with PBS. The sites of peroxidase activity were visualized using 3, 3'-diamino-benzidine tetrahydrochloride as a substrate and hematoxylin as the counter stain. The paired non-cancerous liver tissues were used as positive controls for the PKC protein. Negative controls were defined as tissues of negative immunoreactivity with PBS substituting the anti-PKC antibody in IHC.

**Table 1** Expression of 10 PKC genes in 55 pairs of HCC and their paired nearby normal tissues by qRT-PCR

Gene name	Tumor $\Delta$ Ct (PKC-HPRT1)	Normal $\Delta$ Ct (PKC-HPRT1)	$-\Delta\Delta$ Ct $-(\text{tumor } \Delta\text{Ct} - \text{normal } \Delta\text{Ct})$	$2^{-\Delta\Delta\text{Ct}}$	<i>P</i> value
PKC $\alpha$	-2.157	-2.049	0.108	1.078	0.812
PKC $\beta$	2.875	0.981	-1.894	0.269	1.29E-05
PKC $\delta$	-0.163	-0.049	0.114	1.082	0.729
PKC $\epsilon$	0.449	-0.003	-0.451	0.731	0.229
PKC $\theta$	3.288	1.972	-1.315	0.402	0.014
PKC $\zeta$	-0.099	-0.900	-0.801	0.574	0.090
PKC $\mu$	1.940	1.348	-0.591	0.664	0.138
PKC $\nu$	1.074	0.978	-0.100	0.936	0.812
PKC $\iota$	6.78	6.16	-0.62	0.65	0.06
PKC $\gamma$	11.32	10.58	-0.74	0.6	0.3

**Fig. 1** Immunohistochemical analysis of **a** PKC $\beta$ I, **b** PKC $\beta$ II, and **c** PKC $\theta$  in HCC. Representative figures of heterogeneous expression (*arrow*) in the tumor part and homogeneous expression in the paired non-tumor part are shown



**Table 2** Correlation between clinicopathological features and the expression of PKC $\beta$ II and PKC $\theta$  in HCC

		PKC $\beta$ II				PKC $\theta$			
		T < N	T $\geq$ N	Total	P-value	T < N	T $\geq$ N	Total	P-value
Gender	Female	7	5	12	0.751	12	0	12	0.319
	Male	22	21	43		36	6	42	
Tumor size	$\leq$ 2 cm	3	4	7	0.696	5	2	7	0.169
	$>$ 2 cm	26	22	48		43	4	47	
Grade	Well	4	1	5	0.351	2	3	5	0.009
	M + P	22	23	45		42	3	45	
Stage	I, II	18	10	28	0.173	25	2	27	0.662
	III, IV	11	14	25		22	3	25	
Survival	$\leq$ 2 years	10	9	19	1.000	18	1	19	0.408
	$>$ 2 years	19	17	36		30	5	35	
HBV infection	-	3	8	11	0.035	10	1	11	1.000
	+	24	12	36		32	3	35	
HCV infection	-	16	13	29	1.000	27	2	29	0.162
	+	7	7	14		10	3	13	
Cirrhosis	-	9	8	17	1.000	17	0	17	0.286
	+	15	14	29		26	3	29	
Smoker	-	19	16	35	0.734	32	2	34	1.000
	+	5	6	11		11	0	11	
Drink	-	20	15	35	0.217	32	2	34	1.000
	+	5	9	14		13	1	14	
$\alpha$ -fetoprotein	$<$ 20	15	13	28	1.000	22	5	27	0.193
	$>$ 20	13	12	25		24	1	25	

P-value by Chi-square test or fisher's exact test when appropriated

## Statistics

Comparisons between the RNA expression levels of the ten PKC genes in HCC and non-tumor tissues were analyzed by *t*-test run on SPSS for Windows Release 9.0 (SPSS, Chicago, IL).

## Results

### Expression of 10 PKC Genes in HCC

We used qRT-PCR to analyze the expression of 10 PKC genes in 55 pairs of HCC and their paired nearby non-cancerous tissues. The results are shown in the Table 1. We found that PKC $\beta$  and PKC $\theta$  are down-regulated in HCC in comparison with their paired nearby non-HCC tissues. There are no statistical difference for the expression of PKC $\alpha$ , PKC $\delta$ , PKC $\epsilon$ , PKC $\zeta$ , PKC $\mu$ , PKC $\iota$ , PKC $\nu$ , and PKC $\gamma$  between HCC and their paired non-cancerous tissues.

### RT-PCR Analysis of Splicing Variants of PKC $\beta$

We analyzed the expression of the splicing variants of PKC $\beta$  in HCCs and paired non-HCC tissues. The results showed that PKC $\beta$ II variant form was found in 21/55 of non-HCC and 11/55 cancerous tissues.

### Immunohistochemical Analysis of 2 PKC Isoforms in HCC

In order to confirm the results of qRT-PCR, we used the immunohistochemical staining to analyze the expression of PKC $\beta$  and PKC $\theta$ . The results show significant reduction of PKC $\beta$  and PKC $\theta$  in HCC cancerous cells in comparison with nearby non-cancerous cells, compatible with the results of qRT-PCR (Fig. 1). The normal tissues show homogenous expression pattern in liver cells in comparison with the heterogeneous expression feature of HCC cells which includes expressed and decreased or unexpressed PKC $\theta$  or PKC $\beta$  proteins in different cancerous cells in the tumor tissue (Fig. 1). We compare the clinicopathological data with the expression of PKC $\beta$ I, PKC $\beta$ II, and PKC $\theta$ ,

and find that the down-regulated expression of PKC $\theta$  is well correlated with the grade of cancerous cells ( $P=0.009$ ), and the reduced expression of PKC $\beta$ II is associated with HBV infection ( $P=0.035$ ) (Table 2).

## Discussion

Within the cell, each PKC isoform mediates distinct functions including regulation of mitogenesis cell cycle, apoptosis and gene expression [13–21]. PKC isoforms also play an important role in neoplastic transformation, the growth and metastasis of tumor in a variety of tissues [15–18, 21, 22, 26, 37–40]. In HCC cells, aberrant levels of PKCs are suggested to contribute to liver neoplasia and transformation [41–43]. PKC $\alpha$  has been associated with tumor cell proliferation and various stimuli can lead to increased PKC $\alpha$  activation in the liver [27, 41–43]. PKC $\theta$  has been demonstrated with proliferation of aortic smooth muscle cells and colonic cells [44, 45], and it plays an essential and important function for T-cell and immunological synapse [46, 47]. PKC $\theta$  regulates AKT signaling pathway and KIT expression [48]. Over-expression of PKC $\theta$  may result in cancer development [48–52]. Inactivation of PKC $\theta$  leads to increased susceptibility to obesity and dietary insulin resistance in mice [53, 54], and impaired anti-leukemic immune response [55]. We find that unlike other types of cancer, PKC $\theta$  in HCC is downregulated [48–52]. These discrepancy maybe due to increase susceptibility of insulin resistance which favors the survival of HCC cells. The down-expression of PKC $\theta$  is well correlated with poorer grade of HCC cells.

Over-expression of PKC $\beta$ II results in poor prognosis in nodal diffuse large B-cell lymphoma [56]. In our study, we are unable to establish an association between prognosis and the expression of PKC $\beta$ II, but we found a correlation between HBV infection and the downregulation of PKC $\beta$ II. Bazarsky et al demonstrated that persistent measles infection affects the expression of PKC $\alpha$ ,  $\epsilon$  and  $\zeta$  in neuroblastoma cell lines [57]. We suggest that HBV infection may influence the expression of PKC $\beta$ II which play a role in the early phase of oncogenesis but not at late stage. Similar results have been found in transitional cell carcinoma of bladder [58].

Despite of considerable heterogeneity in the expression of PKCs, correlations could be established between certain PKC expression patterns and pathological or virological features of HCC. Individual genetic variations cannot account for the heterogeneity of PKC expression pattern, because cancer and non-cancerous tissues from the same patients were examined in this study. We reasoned that the heterogeneity of PKCs is a direct result of the complexity of hepatocarcinogenesis in human HCC.

There is accumulating evidence against the specificity of alpha-fetoprotein (AFP) in making a diagnosis of HCC

because AFP can also be produced by other malignancies, such as gastric, pancreatic, colon, bladder, and lung cancers [59–61]. Moreover, given the high heterogeneity of HCC, AFP is normal in many HCC patients [62]. Because of its limited sensitivity and specificity, AFP alone is not considered useful for the surveillance of HCC [63]. More than 50% of our patients in this study have normal AFP which makes AFP a poor indicator of HCC (Table 2).

In conclusion, our results indicate that aberrant signal transduction via PKC may occur during the formation of liver cancer. The fact that down-regulated expression of PKC $\beta$ II and PKC $\theta$  were correlated with HBV infection and the grade of cancer cells, respectively, suggest particular roles of the two PKC isoenzymes in the development of human HCC.

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