

ORIGINAL ARTICLE

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Selective inhibition of cyclooxygenase-2 enhances mitomycin-C-induced apoptosis

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Abstract Purpose: Cyclooxygenase-2 (COX-2) is involved in antiapoptosis signaling, and its induction may require activation of protein kinase C (PKC). Safingol (SAF), a PKC inhibitor, has been shown to enhance apoptosis induced by mitomycin-C (MMC) in human gastric cancer MKN-74 cells. The aim of this study was to identify the role of COX-2 in MMC-induced apoptosis in MKN-74 cells. **Methods:** Protein expression of COX-2 and Bcl-2 and activation of PKC α were examined by Western blot analysis. Apoptosis induction was examined by staining with bisbenzimidazole trihydrochloride (Hoechst-33258) of condensed chromatin, which characterizes the cells undergoing apoptosis. COX-2 mRNA levels were examined by Northern blot analysis. **Results:** After exposure for 1–2 h to 1 μ g/ml MMC, upregulation of COX-2 and Bcl-2 protein expression was noted. The activation of PKC α occurred within 1 h of MMC exposure, and temporally preceded the induction of COX-2. Similar results were observed in cells exposed to the PKC activator, 3-phorbol 12-myristate 13-acetate. Cotreatment with SAF and MMC abolished the induction of COX-2 by MMC. Furthermore, NS-398, a selective COX-2 inhibitor, significantly enhanced

MMC-induced apoptosis by fivefold from $4 \pm 2\%$ (MMC alone) to $20 \pm 2\%$ (MMC plus NS-398). There was no discernible change in COX-2 mRNA levels after a 2-h exposure to MMC but a twofold increase after a 24-h exposure. **Conclusions:** MMC upregulates COX-2 expression, which appears to be an antiapoptotic signal downstream of PKC. Selective inhibition of COX-2 can therefore provide a novel way to enhance MMC-induced apoptosis independent of inhibiting PKC.

Key words Gene expression · Safingol · Protein kinase C · Phorbol esters · Bcl-2

Abbreviations COX cyclooxygenase · PKC protein kinase C · SAF safingol · PMA 3-phorbol 12-myristate 13-acetate · MMC mitomycin-C

Introduction

COX-1 and COX-2 are the rate-limiting enzymes involved in the conversion of arachidonic acid to prostanooids [11, 53]. COX-1 is considered a housekeeping gene responsible for various physiological functions. In contrast, COX-2 is normally undetectable in most tissues, but can be rapidly induced by proinflammatory or mitogenic stimuli, including cytokines, growth factors, oncogenes, carcinogens and phorbol esters, and by overexpression or activation of PKC [7, 18, 26, 29, 35, 52]. It is noteworthy that COX-2 is also involved in tumorigenesis [10, 26, 38, 62], angiogenesis [33, 59] and metastasis [58] of cancer. Increased expression of COX-2 has been demonstrated in colorectal adenoma and carcinoma [12], gastric cancer [44], Barrett's esophagus and associated adenocarcinomas [63], esophageal carcinoma [64], pancreatic cancer [60], lung cancer [19], breast cancer [54], and cancer of the head and neck [4].

Forced expression of the COX-2 gene in rat intestinal epithelial cells results in an increased level of Bcl-2 protein and resistance to apoptosis induction [57]. Prostaglandin E₂, a major product of COX-2, has been

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shown to inhibit apoptosis and increase Bcl-2 expression in a human colon cancer cell line [51]. Liu et al. have recently reported that NS-398, a selective COX-2 inhibitor, induces apoptosis and downregulates Bcl-2 expression in LNCaP prostate cancer cells [30]. In addition, COX-2 inhibitors have been shown to cause suppression of tumor growth in nude mice bearing gastric cancer xenografts by induction of apoptosis [48]. These findings indicate that COX-2 is involved in anti-apoptosis signaling and could be a target for apoptosis modulation in cancer chemotherapy.

PKC, a family of serine and/or threonine protein kinases, has been shown to play a major role in anti-apoptosis signaling [8, 24, 31, 50]. We have previously reported that SAF, a PKC inhibitor, enhances the cytotoxic effect of MMC in human gastric cancer cells by promoting drug-induced apoptosis [50]. Further study in this laboratory has suggested that activation of PKC α may be responsible for the resistance of MMC-induced apoptosis in MKN-74 gastric cancer cells, and SAF can block the activation of PKC α [8]. These studies have also demonstrated that short (i.e. 1- to 2-h) exposures to PMA, which activates PKC, can abrogate SAF-mediated enhancement of MMC-induced apoptosis and restore the activation of PKC α .

Activation of PKC has been shown to be required for induction of COX-2 [2, 32, 35, 46, 52]. In human normal and malignant cells, several studies have demonstrated that PKC α is involved in the induction of COX-2 expression [29, 32]. Using an antisense oligomer targeted against PKC α , the induction of COX expression by interleukin-1 α can be prevented in human endothelial cells [32]. Moreover, further study has demonstrated that both interleukin-1 α and PMA can induce COX-2 but not COX-1 in human endothelial cells, and the PKC inhibitors can block the COX-2 induction by interleukin-1 α and PMA [3]. Given these observations, we elected to examine the role of COX-2 in the resistance of MMC-induced apoptosis in MKN-74 gastric cancer cells. We found that MMC induces COX-2, which appears to be an antiapoptotic signal downstream of PKC. Therefore, selective inhibition of COX-2 may provide a novel way to enhance MMC-induced apoptosis independent of inhibiting PKC.

Materials and methods

Cell culture and drug treatment

Early-passage human gastric cancer MKN-74 cells were established and characterized as described previously [37, 39]. All the cultures were maintained in standard MEM supplemented with 100 units/ml penicillin, 100 μ g/ml streptomycin and 20% heat-inactivated normal calf serum (Intergen) at 37 °C in a humidified atmosphere containing 5% CO₂. MMC was purchased from Bristol Laboratories. NS-398 was purchased from Cayman. SAF was obtained from Eli Lilly. PMA was purchased from Sigma. The cytotoxicity of each agent in MKN-74 cells for a 24-h exposure was determined by the Alamar blue assay [1], and the concentrations causing less than 20% growth inhibition was used in this study. At 24 h after passage, when cells were approximately 50–60% confluent, they

were exposed to the indicated drug treatment. MMC 1 μ g/ml was used in this study, and combination treatments were set up with NS-398 (100 μ M) or SAF (50 μ M) given 1 h before the addition of MMC. Cells were checked for mycoplasma contamination at least every 6 months with a GEN-Probe mycoplasma rapid detection kit (Fischer Scientific) and consistently tested negative.

Preparation of membrane and cytosolic protein extracts

Membrane and cytosolic protein extracts were prepared based upon published methods [34] with some modifications. Briefly, 2–4 $\times 10^6$ MKN-74 cells were suspended in ice-cold lysis buffer (20 mM Tris-HCl, pH 7.5, 2 mM EDTA, 2 mM [ethylenedis(ox-yethylenitrilo)]tetraacetic acid, 10 mM β -mercaptoethanol, 0.5 mM phenylmethylsulfonyl fluoride, 10 μ g/ml leupeptin, 10 μ g/ml soybean trypsin inhibitor and 10 μ g/ml aprotinin) at a concentration of 10⁷ cells/ml. Cells were lysed by passing through a 27-gauge needle three times, and further homogenized by a motorized pestle for 50 strokes. The extent of cell lysis was examined under a microscope throughout the homogenization, and consistent results with more than 95% cell lysis were obtained. Cell homogenates were centrifuged at 27,000 g for 30 min at 4 °C. The supernatants were collected as cytosolic protein extracts. The pellets were resuspended in ice-cold lysis buffer plus 1% Triton-X for 30 min at 4 °C, and intermittently homogenized by a motorized pestle every 10 min. The undissolved debris was removed after centrifugation at 12,000 g for 10 min, and the clarified supernatants were collected as membrane protein extracts. Protein concentration was determined by Bio-Rad protein assay. For Western blot analysis, 30 μ g of protein from each extract was used.

Preparation of whole cell lysates and Western blot analysis

Cells were washed twice with cold phosphate-buffered saline, and then lysed by scraping into a radioimmunoprecipitation assay buffer (phosphate-buffered saline containing 1% Nonidet P-40, 0.5% sodium deoxycholate and 0.1% SDS) containing the protease inhibitors (100 μ g/ml phenylmethylsulfonyl fluoride, 25 μ g/ml aprotinin, 25 μ g/ml leupeptin, 10 μ g/ml soybean trypsin inhibitor and 1 mM sodium orthovanadate). The lysate was left on ice for 30 min, passed through a 21-gauge needle twice, and then centrifuged at 15,000 g for 20 min in a microfuge at 4 °C. The clarified supernatant was collected and protein concentration was determined by the Bio-Rad protein assay. Whole cell lysate containing 50 μ g protein from each sample was used in immunoblotting as previously described [17, 21]. The gels were then electroblotted onto PVDF membranes (Immobilon-P, Millipore). Ponceau S (Sigma) staining of the membranes was performed to assess the equivalence of sample loading and gel transfer followed by destaining with water as previously described [47].

Antibodies purchased from Santa Cruz Biotechnology (unless otherwise specified) were used to detect the proteins of interest: monoclonal PKC α (Upstate Biotechnology), goat polyclonal COX-2, and monoclonal Bcl-2. The horseradish peroxidase-conjugated antibodies against mouse and goat IgG were used as secondary antibodies. The detection of antibody binding was performed by using Pierce SuperSignal chemiluminescent detection reagents with the protocols recommended by the manufacturer, and blots were exposed to NEN Renaissance X-ray film with intensifying screens. The linear range signal intensity of each specific band on the fluorogram was quantitated by a densitometric scanning system and comparison of proteins of interest was performed after normalization to the densitometric scanning of the ponceau S staining.

Quantitative fluorescent microscopy

The quantitative fluorescent microscopy method for apoptosis determination involves staining with bisbenzimid trihydrochloride (Hoechst-33258) of condensed chromatin, which characterizes the cells undergoing apoptosis [15, 50]. After trypsinization, adherent

and non-adherent cells were washed with PBS, fixed in 3% para-formaldehyde, and then incubated at room temperature for 10 min. The fixative was removed and the cells were washed with PBS, resuspended in 20 μ l PBS containing 8 μ g/ml of bisbenzamide trihydrochloride, and incubated at room temperature for 15 min. Aliquots of the cells (10 μ l) were placed on glass slides coated with 3-amino-propyl-triethoxysilane, and duplicate samples of 400 cells each were counted and scored for the incidence of apoptotic chromatin condensation using an Olympus BH-2 fluorescence microscope equipped with a BH2-DM2U2UV Dichromatic mirror cube filter.

Northern blot analysis

Total cellular RNA preparation, Northern blot analysis and preparation of prehybridization and hybridization buffers were carried out as previously described [20]. To assess the equivalence of sample loading and gel transfer, 30 μ g RNA from each sample was treated with ethidium bromide prior to loading [45]. Samples were then visualized by UV illumination of both the gels after electrophoresis and the nylon filters after capillary transfer. RNA blots were prehybridized at 42 °C for 12 h, then hybridized to COX-2 32 P-labeled cDNA probe of specific activity greater than 10^9 cpm/ μ g at 42 °C for 12–16 h. A 1.2-kbp COX-2 cDNA fragment (purchased from Cayman) was used in preparing 32 P-labeled probes by a Multiprime DNA labeling system (Amersham). Unbound probe was removed by washing blots with two changes of a solution containing $2 \times$ SSC and 0.2% SDS for 30 min each at room temperature, and with two changes for 30 min each of $0.2 \times$ SSC and 0.2% SDS at 60 °C. Blots were exposed to Kodak X-OMAT AR film with intensifying screens. Specific bands of interest (about 4.5-kb COX-2 mRNA) were quantitated with a Fuji BAS 2500 Phosphor Imaging System.

Statistical analysis

All experiments were performed at least twice with similar results, and the results of one representative experiment are shown. The statistical significance (*P*-value) of the experimental results was determined by the two-sided Student's *t*-test.

Results

MMC and PMA activate PKC α and induce the protein expressions of COX-2 and Bcl-2

Exponentially growing MKN-74 cells were exposed to 1 μ g/ml MMC, and at different time-points cells were collected and fractionated into membrane and cytosolic extracts. Western blots were performed using PKC α , COX-2 and Bcl-2 antibodies. As shown in Fig. 1, after a 1-h exposure to MMC, there was activation of PKC α , which was demonstrated by translocation of PKC α from the cytosolic to the membrane fraction. COX-2 is a membrane-bound protein residing at both the endoplasmic reticulum and the nuclear envelope [36]. COX-2 protein expression was gradually upregulated to about five- to eightfold after a 2-h exposure to MMC when compared to basal expression, and remained persistently induced after a 27-h exposure. COX-1 protein expression was not increased after MMC exposure (data not shown). The expression of Bcl-2 protein, an antiapoptotic protein residing mainly in the outer membrane of mitochondria [5, 25], was increased two- to threefold by

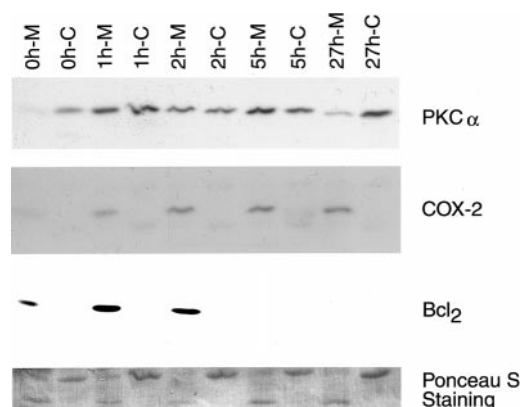


Fig. 1 Effects of MMC on the membrane translocation of PKC α and expression of COX-2 and Bcl-2 proteins. MKN-74 cells were treated with 1 μ g/ml MMC for 0 (control), 1, 2, 5 and 27 h, and subsequently membrane (M) and cytosolic (C) lysates were prepared and Western blot analysis performed as described in Materials and methods. Ponceau S staining of the membrane is displayed in the lower panel to demonstrate equal loading and even transfer of the gel

MMC after the initial 1–2-h exposure, and the expression of Bcl-2 was no longer detectable after prolonged exposure.

Similar results on the activation of PKC α , and induction of COX-2 and Bcl-2 protein expression were observed when MKN-74 cells were exposed to the PKC activator PMA (Fig. 2). After the short (1- to 2-h) exposure to PMA, PKC α was activated, and the protein expression of COX-2 and Bcl-2 was induced. With the prolonged (24-h) exposure to PMA, there was depletion of activated PKC α and loss of COX-2 induction, as opposed to persistent COX-2 induction after prolonged exposure to MMC as shown in Fig. 1. These results indicate that after cellular exposure to MMC or PMA, the levels of COX-2 and Bcl-2 proteins are temporally

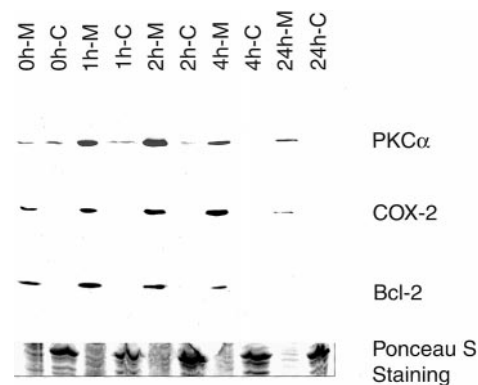


Fig. 2 Effects of PMA on the membrane translocation of PKC α and expression of COX-2 and Bcl-2 proteins. MKN-74 cells were treated with 10 nM PMA for 0 (control), 1, 2, 4 and 24 h, and subsequently membrane (M) and cytosolic (C) lysates were prepared and Western blot analysis performed as described in Materials and methods. Ponceau S staining of the membrane is displayed in the lower panel to demonstrate equal loading and even transfer of the gel

up-regulated following activation of PKC α . The induction of COX-2 protein may be due to the activation of PKC α .

Inhibition of PKC suppresses the induction of COX-2 by MMC

To further confirm that COX-2 is a downstream anti-apoptotic signal for PKC, we examined the expression of COX-2 in MKN-74 cells after inhibition of PKC by SAF. SAF, the *L-threo* enantiomer of dihydrosphingosine, is a PKC-specific inhibitor that inhibits PKC enzyme activity at micromolar concentrations [49, 50]. Whole-cell lysates from cells exposed for 24 h to no drug, 1 μ g/ml MMC, 50 μ M SAF, and 50 μ M SAF plus 1 μ g/ml MMC were used for immunoblotting analysis of COX-2 protein levels (Fig. 3). SAF alone suppressed COX-2 expression by about 80% when compared to the control cells. MMC alone induced COX-2 by five- to eightfold, and cotreatment with SAF and MMC suppressed the COX-2 induction by about 80%. These results further substantiate the notion that PKC is an upstream regulator of COX-2 expression.

Selective inhibition of COX-2 enhances MMC-induced apoptosis

To further characterize the role of COX-2 in apoptosis signaling, NS-398, a selective COX-2 inhibitor, was used in combination with MMC to determine whether MMC-induced apoptosis could be enhanced by inhibition of COX-2. NS-398 is a sulfonamide derivative that inhibits COX-2 with an IC_{50} of as low as 30 nM, and does not affect COX-1 activity at concentrations exceeding 100 μ M [14]. MKN-74 cells were exposed to the following conditions for 24 h: no drug, 100 μ M NS-398,

1 μ g/ml MMC, and 100 μ M NS-398 in combination with 1 μ g/ml MMC. Apoptosis was evaluated by quantitative fluorescent microscopy of the nuclear changes induced by apoptosis, as determined by bisbenzimidazole trihydrochloride (Hoechst-33258) staining of condensed nuclear chromatin (Fig. 4). Minimal apoptosis induction was observed when cells were exposed to NS-398 ($2 \pm 1\%$) or MMC ($4 \pm 2\%$) alone. However, significant enhancement of apoptosis induction was noted in the NS-398 and MMC cotreatment group ($20 \pm 2\%$) when compared to either NS-398 ($P < 0.02$) or MMC ($P < 0.03$) alone.

MMC induces COX-2 mRNA expression only after prolonged exposure

To further examine the molecular mechanism responsible for the induction of COX-2 expression by MMC, Northern blot analysis for COX-2 mRNA expression was performed in MKN-74 cells after exposure to 1 μ g/ml MMC for different times. As shown in Fig. 5, there was about a twofold increase in COX-2 mRNA level after a 24-h exposure to MMC. However, COX-2 mRNA levels remained relatively unchanged for the first 2 h of exposure to MMC. In conjunction with Western blot analysis results shown in Fig. 1, these results imply that the induction of COX-2 expression by short (e.g. 1- to 2-h) exposures to MMC is mediated at the level of posttranscription and/or translation. The upregulation of COX-2 expression after prolonged (e.g. 24-h) exposure to MMC occurs at the level of posttranscription and/or transcription.

Discussion

The current study demonstrates that COX-2 is induced by MMC in MKN-74 cells. A similar COX-2 induction has been observed when a different DNA alkylating agent such as cisplatin, or a different cell line such as human breast cancer MCF-7, was used [5]. Upon exposure of cells to DNA-damaging agents, induction of COX-2, which appears to be triggered by activation of PKC, contributes to the cellular resistance to apoptosis induction. Previously, we have shown potentiation of apoptosis by treatment with the PKC-specific inhibitor SAF in MMC-treated MKN 74 cells [50]. Here we demonstrated that, independently of inhibition of PKC, selective inhibition of COX-2 significantly enhances MMC-induced apoptosis. A preliminary report by Nokihara et al. also indicates that COX-2 is induced after exposure to anticancer drugs (etoposide, doxorubicin and vincristine) in human lung cancer cells, and a selective inhibitor of COX-2 increases the sensitivity to these anticancer agents [41]. Taken together, selective inhibition of COX-2 can potentially provide a novel way to enhance chemosensitivity in the treatment of solid tumor malignancies. In further studies it is planned to use

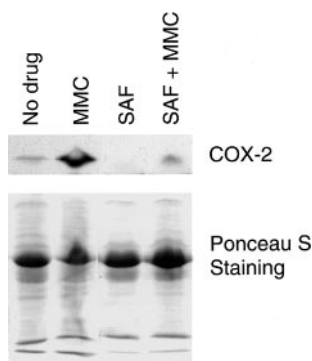


Fig. 3 Effects of MMC and SAF on COX-2 protein expression. MKN-74 cells were exposed to no drug (control), 1 μ g/ml MMC, 50 μ M SAF, and the combination of 50 μ M SAF plus 1 μ g/ml MMC for 24 h, and subsequently whole cellular lysates were prepared and Western blot analysis performed as described in Materials and methods. Ponceau S staining of the membrane is displayed in the lower panel to demonstrate equal loading and even transfer of the gel

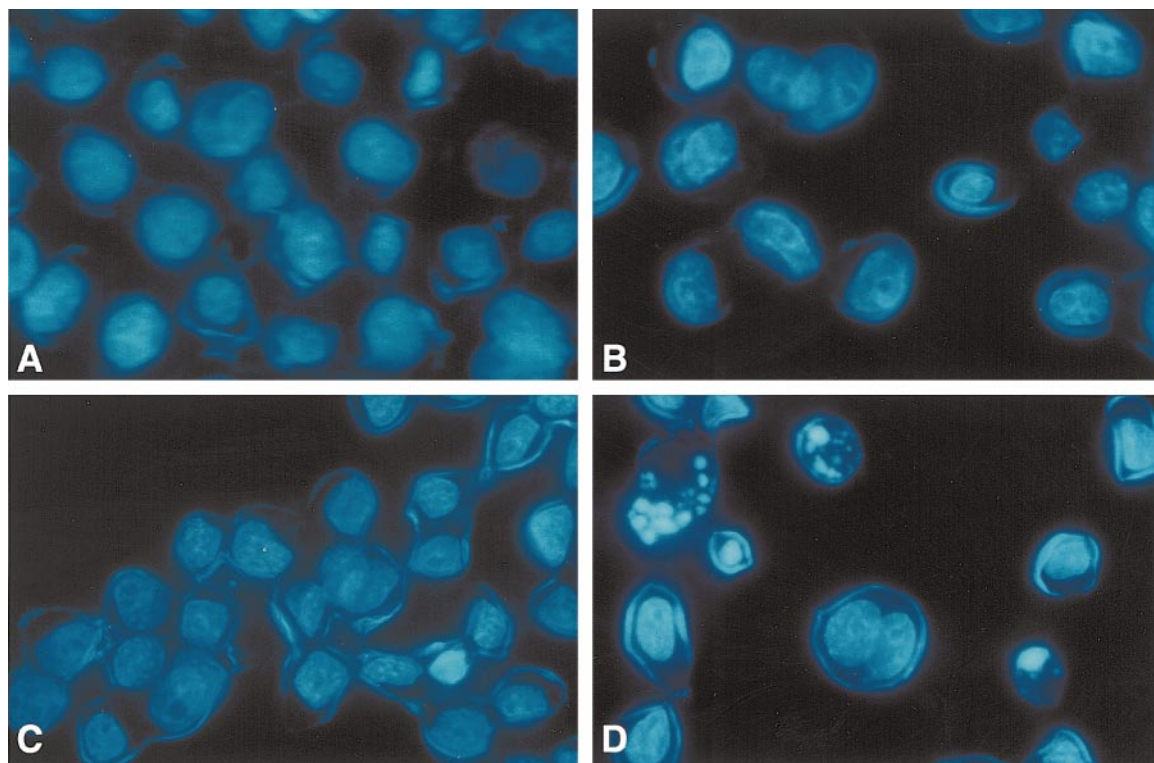


Fig. 4A–D Effects of NS-398 on apoptosis induction by MMC. The photomicrographs show representative fields of MKN-74 cells stained with bisbenzimidazole trihydrochloride (Hoechst-33258) to evaluate nuclear chromatin condensation (i.e. apoptosis induction) after a 24-h treatment with no drug (A), 100 μ M NS-398 (B), 1 μ g/ml MMC (C), and the combination of 100 μ M NS-398 plus 1 μ g/ml MMC (D)

similar schema in a panel of solid tumor cell lines with a wide variety of chemotherapeutic agents and combinations.

Activation of PKC has been shown to be required for induction of COX-2 [2, 32, 35, 46, 52]. An antisense oligomer targeted against PKC α has been shown to prevent induction of COX expression by interleukin-1 α in human endothelial cells [32]. Additionally, both interleukin-1 α and PMA can induce COX-2 but not COX-1 in human endothelial cells, and the PKC inhibitors can block COX-2 induction by interleukin-1 α and PMA [3]. Liu and Rose have reported their preliminary findings that PMA induces COX-2 expression in the human breast cancer cell line, MDA-MB-231 [29]. In the same study, calphostin-C, a PKC inhibitor, was shown to suppress basal COX-2 expression at certain concentrations. It has previously been shown in our laboratory that the activation of PKC α might be responsible for the resistance of MMC-induced apoptosis in MKN-74 cells, and that abolishing the activation of PKC α by SAF leads to significant enhancement of MMC-induced apoptosis [8, 50]. In the current study, we have identified that the activation of PKC α precedes COX-2 induction after treatment with MMC or PMA. SAF alone represses basal COX-2 expression, and cotreatment of SAF and MMC suppresses COX-2 induction by MMC.

It is very likely that PKC, especially PKC α , is the upstream regulator of COX-2 expression. Although COX-2 exhibits consensus sequences for PKC phos-

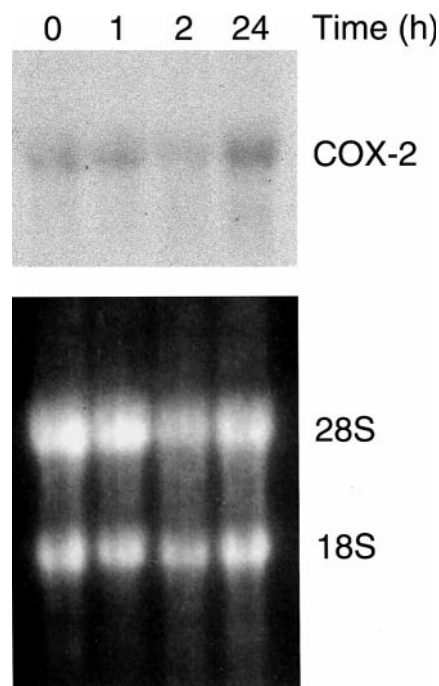


Fig. 5 Effects of MMC on COX-2 mRNA expression. COX-2 mRNA levels in MKN-74 cells exposed to 1 μ g/ml MMC for 0, 1, 2 and 24 h were determined by Northern blot analysis as described in Materials and methods. The photograph of the nylon filter exhibiting ethidium bromide fluorescence of 28 S and 18 S ribosomal RNAs is displayed in the lower panel, demonstrating equal loading and even transfer of the gel

phorylation, direct interaction between PKC and COX-2 has not been identified [61]. Moreover, overexpression of PKC ζ , an atypical isoform lacking the phorbol ester binding site, has been shown to induce COX-2 expression in rat mesangial cells [35]. To better understand the interaction between various PKC isoforms and COX-2, experiments will be carried out using an antisense approach to suppress the gene expression of different PKC isoforms. The effects on COX-2 induction after exposure to MMC or PMA will be examined under these circumstances.

Although in this study, we were not able to identify any significant apoptosis induction by COX-2 inhibitor alone, COX-2 inhibitors have been shown to cause suppression of tumor growth in nude mice bearing gastric cancer xenografts by induction of apoptosis [48]. Several lines of evidence suggest that COX-2 is an upstream regulator of Bcl-2 [30, 51, 57]. Liu et al. have reported that NS-398 induces apoptosis and downregulates the expression of the active Bcl-2 protein in human prostate cancer cells, LNCaP [30]. It has also been shown that prostaglandin E₂, which is a main product of COX-2, can induce Bcl-2 expression and prevent apoptosis induction by COX-2 inhibitor in human colon cancer cells [51]. In the present study, we showed Bcl-2 induction in conjunction with COX-2 induction within 1 to 2 h of exposure to MMC or the PKC activator PMA. Moreover, selective inhibition of COX-2 leads to enhancement of MMC-induced apoptosis. The signal cascade between the COX-2 and the apoptosis-related signals such as Bcl-2 and Bax remains to be established. We are planning a series of studies using COX-2 inhibitor, COX-2 antisense oligomer and overexpression of COX-2 by a gene transfer technique to further characterize the role of COX-2 in apoptosis signaling.

COX-2 is an intermediate early response gene to various stimuli such as growth factors, cytokines, tumor promoters, hormones and bacterial endotoxin. In response to various stimuli, COX-2 gene expression can be regulated at different levels [53]. Many studies have identified upregulation of COX-2 expression caused by enhanced transcription in carcinoma and normal cells [23, 27, 28, 55]. However, regulation of COX-2 gene expression at posttranscriptional or translational levels has been uncovered by discordant expression levels of COX-2 mRNA and protein under certain circumstances such as nitric oxide production and chronic hypoxia [6, 22, 56]. Dean et al. have reported that p38 mitogen-activated protein kinase regulates COX-2 mRNA stability in lipopolysaccharide-treated human monocytes [9]. Several studies have demonstrated that dexamethasone suppresses COX-2 expression by destabilizing its mRNA [13, 40, 43]. Moreover, IL-1 α has been shown to prolong COX-2 mRNA half-life in human endothelial cells [42].

Our present study suggests that the upregulation of COX-2 expression by a short exposure to MMC is mediated at posttranscriptional/translational level in conjunction with PKC α activation. Interestingly, PKC α recently has been shown to regulate I κ B α expression

posttranscriptionally by facilitating its mRNA export from the nucleus [16]. Our findings also indicate that prolonged exposure to MMC increases COX-2 mRNA expression, which may very well contribute to the persistently elevated COX-2 protein levels despite the depletion of activated PKC α . Further study is warranted to fully characterize the molecular mechanisms responsible for upregulation of COX-2 expression by MMC and the role of PKC α .

Increased expression of COX-2 has been demonstrated in many solid tumor malignancies. Based on the findings presented here and the preliminary findings of Nokihiro et al. [41], it is conceivable that induction of COX-2 plays an important role in the resistance to chemotherapy-induced apoptosis in most of the solid tumor malignancies. COX-2 is also involved in cancer angiogenesis [33, 59] and metastasis [58]. Therefore, clinical use of COX-2 inhibitors in combination with chemotherapy may not only enhance chemosensitivity but also inhibit the angiogenic and metastatic potential of cancer. With these rationales, we are currently planning clinical trials to incorporate COX-2 inhibitors into chemotherapeutic regimens for the treatment of solid tumor malignancies.

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