ORIGINAL ARTICLE

Celecoxib inhibits MDR1 expression through COX-2-dependent mechanism in human hepatocellular carcinoma (HepG2) cell line

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Abstract The role of COX-2 in the regulation of the expression of MDR1, a P-glycoprotein involved in hepatocellular carcinoma cell line, HepG2, was studied in the present investigation. Celecoxib, a selective inhibitor of COX-2, at 25 µM concentration increased the accumulation of doxorubicin in HepG2 cells and enhanced the sensitivity of the cells to doxorubicin by tenfold. The induction of MDR1 expression by PGE₂ and its downregulation by celecoxib or by COX-2 knockdown suggests that the enhanced sensitivity of HepG2 cells to doxorubicin by celecoxib is mediated by the downregulation of MDR1 expression, through COX-2-dependent mechanism. Further studies revealed the involvement of AP-1 in the celecoxib-induced downregulation of MDR1 expression. These experimental studies correlated well with in silico predictions and further suggested the inactivation of the signal transduction pathways involving ERK, JNK and p38. The present study thus demonstrates the usefulness of COX-2 intervention in overcoming the drug resistance in HepG2 cells.

Keywords AP-1 · Celecoxib · COX-2 · HepG2 cells · MDR1 · Simulation

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Introduction

The development of hepatocellular carcinoma (HCC) is a common feature during the natural history of cirrhosis and in advanced chronic liver disease. It has been calculated that 3–5% cases of cirrhosis evolve into HCC. In addition to an early diagnosis, surgery and chemotherapy are the usual methods adopted to reduce the growth of HCC and improve life expectancy of HCC patients. The development of multidrug resistance is the major limitation in chemotherapy of HCC. The most important form of drug resistance is the over-expression of the membrane-associated P-glycoprotein (P-gp), MDR1.

Intrinsic upregulation of MDR1 gene expression has been observed to be associated with primary resistance in untreated HCC of human and rodent origin [5, 16]. It manifests during inflammation-associated processes such as cholestasis [29] as well as in liver regeneration [1]. It was shown that regulation of MDR1 expression was dependent on COX-2 activity [26]. Cyclooxygenase (COX) or prostaglandin H₂ synthase (PGHS) is the enzyme that catalyzes the biosynthesis of prostaglandins (PGs) from the substrate arachidonic acid (AA). Several studies demonstrated elevated levels of COX-2 in different types of human cancer [11, 35, 38]. Celecoxib, a selective COX-2 inhibitor, is being used as an anti-inflammatory agent. Similarly, NSAIDs were shown to enhance the cytotoxic effects of doxorubicin in T98G human malignant glioma cells [28].

Simultaneous over-expression of the COX-2 and MDR1, reported in the regenerative nodules of cirrhotic livers as well as in well-differentiated HCC [20, 23], suggests a possible role for COX-2 in multidrug resistance. Present study is to understand the molecular mechanisms involved in the regulation of MDR1 expression by COX-2.



Materials and methods

Chemicals

PBS, RPMI 1640 medium and fetal bovine serum (FBS) were purchased from Gibco BRL (California, USA). Nitrocellulose membrane was from Millipore (Bangalore, India). Phosphatase inhibitor cocktail 1 and 2 and β-actin antibodies were purchased from Sigma-Aldrich (Bangalore, India). Polyclonal antibodies to MDR1 were from Santa Cruz Biotechnology (California, USA). Single-step RT-PCR kit was from AB Gene Technologies (Surrey, UK). Monoclonal COX-2 anti body, PGE₂ estimation kit and PGE₂ were from Cayman Chemical Co., USA. SiRNA for COX-2 was from Santa Cruz Biotechnologies Inc., USA. Celecoxib was a generous gift from Unichem Laboratories, India. Doxorubicin was a generous gift from Dabur Pharma, India. All the other chemicals and reagents were purchased from local companies and are of molecular biology grade.

Cell culture and treatment

Hepatocellular carcinoma (HepG2) cells, expressing MDR1 and COX-2 constitutively, were grown in RPMI 1640 medium supplemented with 10% heat inactivated FBS, 100 IU/ml penicillin, 100 µg/ml streptomycin and 2 mM L-glutamine and maintained in a humidified atmosphere with 5% CO₂ at 37°C. The cultured cells were sub-cultured twice each week and the exponentially growing cells were used for all treatments. Celecoxib dissolved in DMSO and doxorubicin dissolved in PBS were used for the treatments. 40 mM stock of celecoxib and 5 mM stock of doxorubicin were employed in this study. At the time of treatment, working solutions were diluted accordingly in RPMI 1640 medium. The drugs were added to the cells, 6 h after the sub-culture. Stock of celecoxib was freshly prepared before every treatment. The final concentration of the vehicle (DMSO) never exceeded 0.1%. HepG2 cells exposed to 0.1% DMSO served as controls.

Effect of celecoxib or doxorubicin on proliferation of HepG2 cells

Cell proliferation was determined by MTT [3-{4,5-dimethylthiazol-2yl}-2,5-diphenyltetrazolium bromide] assay [6]. HepG2 cells (5 \times 10 3 cells/well) were seeded to 96-well culture plate in the presence or absence of celecoxib (1, 10, 25, 50 and 100 μM) or doxorubicin (100 nM, 500 nM, 1 μM , 10 μM , 25 μM and 50 μM) for 12, 24 and 48 h in a final volume of 100 μl . After treatment, the medium was removed and 20 μl of MTT (5 mg/ml of PBS) was added to the fresh medium. After 2 h incubation at 37 °C, 100 μl of DMSO was added to each well and plates were agitated for

1 min. Absorbance was read at 570 nm on a multi-well plate reader. Percent inhibition of proliferation was calculated as a fraction of control (control was without celecoxib or doxorubicin).

Synergistic effect of celecoxib and doxorubicin on proliferation of HepG2 cells

HepG2 cells (5×10^3 cells/well) were seeded to 96-well culture plate. Doxorubicin (100 nM, 500 nM, $1 \mu\text{M}$, $10 \mu\text{M}$, $25 \mu\text{M}$ and $50 \mu\text{M}$) was added in the presence or absence of celecoxib ($25 \mu\text{M}$) for 24 h in a final volume of $100 \mu\text{L}$. After treatment, the medium was removed and $20 \mu\text{l}$ of MTT (5 mg/ml of PBS) was added to the fresh medium. After 2 h incubation at 37°C , $100 \mu\text{l}$ of DMSO was added to each well and plates were agitated for 1 min. Absorbance was read at 570 nm on a multi-well plate reader. Percent inhibition of proliferation was calculated as a fraction of control. (Cells treated with $25 \mu\text{M}$ celecoxib were taken as control for determining the synergistic effects of doxorubicin and celecoxib.)

Intracellular drug accumulation assays

HepG2 cells (1 \times 10⁶ cells/well) were seeded into 6-well culture plates. Cells were incubated with celecoxib at concentrations of 10 and 25 μM for 24 h. To determine intracellular drug accumulation, 50 μM of doxorubicin was added to HepG2 cells and incubated for 2 h. Then, the cells were trypsinized and the final doxorubicin accumulated in HepG2 cells was analyzed using flow cytometer [7]. When cells were incubated with doxorubicin, they take up the drug and kinetics of doxorubicin efflux is dependent on the expression of MDR1. So, if the expression of MDR1 is inhibited, there is more accumulation of doxorubicin, which can be quantified on flow cytometer.

RT-PCR analysis

HepG2 cells were seeded at a density of 5×10^6 in 90 mm culture dishes. Cells were treated with celecoxib (1, 10 and 25 μ M) or PGE2 (6 μ g/ml) for 24 h. Cells were harvested and total RNA was extracted using TRIzol reagent from control and treated HepG2 cells. Semi-quantitative RT-PCR was performed with 5 μ g total RNA, isolated from HepG2 cells, using one-step RT-PCR kit. Primers used were as follows—human MDR1: forward, 5'-TGA CTA CCA GGC TCG CCA A-3'; reverse, 5'-TAG CGA TCT TCC CAG CAC CTT-3', which yields 252 bp product [22], actin: forward, 5'-GTT TGA GAC CTT CAA CAC CCC-3', reverse, 5'-GTG GCC ATC TCC TGC TCG AAG TC-3', which yields 318 bp product [15]. Reverse transcription was performed at 47°C for 30 min. Subsequent to inactivation



of reverse transcriptase (2 min, 94°C), the samples were subjected to 25 amplification cycles, each consisting of 20 s at 94°C, 1 min at 54°C, and 1 min at 72°C, followed by 5 min at 72°C after the last cycle. The products were analyzed on 1% agarose gel.

COX-2 and MDR1 knockdown analysis

HepG2 cells (1×10^6 cells/well) were seeded into 6-well culture plates. After overnight incubation, cells were transfected with siRNA for COX-2 (Santacruz:sc-44256) and MDR1 (Santacruz:sc-29395) at concentration of 100 nM for 48 h. Total RNA was isolated and RT-PCR analysis (procedure described in "RT-PCR analysis") was performed to estimate the expression of MDR1 in control, COX-2 siRNA transfected, MDR1 siRNA transfected and PGE₂ ($6 \mu g/ml$) treated cells.

Preparation of whole-cell extracts and immunoblot analysis

HepG2 cells at a density of 5×10^6 were seeded in 90 mm culture dishes. They were incubated with celecoxib (1, 10 and 25 μ M) and PGE₂ (6 μ g/ml). Cells harvested were used for preparation of whole-cell extract. The harvested, control and treated, HepG2 cells were washed with PBS and suspended in lysis buffer (20 mM Tris, 1 mM EDTA, 150 mM NaCl, 1% NP-40, 0.5% sodium deoxycholate, 1 mM β -glycerophosphate, 1 mM sodium orthovanadate, 1 mM PMSF, 10 µg/ml leupeptin, 20 µg/ml aprotinin and phosphatase inhibitor cocktail 1 and 2 with 100-fold dilution). After 30 min of shaking at 4°C, the mixtures were centrifuged $(10,000 \times g)$ for 10 min, and the supernatants were used as the whole-cell extracts. The protein content was determined according to the Bradford method [4]. 100 µg of protein from each treatment was resolved on 10% gels along with protein molecular weight standards, and then transferred onto nitrocellulose membranes. Membranes were stained with 0.5% Ponceau S in 1% acetic acid to check the transfer. The membranes were blocked with 5% (w/v) non-fat dry milk and then incubated with the primary antibodies (COX-2 and MDR1, 1:500 dilution) in 10 ml of antibody-diluted buffer (1× Tris-buffered saline and 0.05% Tween-20 with 1% milk) with gentle shaking at 4°C for 8– 12 h and then incubated with peroxidase-conjugated secondary antibodies. Signals were detected using peroxidase substrate, TMB/H₂O₂. Equal protein loading was confirmed by reprobing the nitrocellulose membranes with β -actin antibodies (1:500 dilution).

Electrophoretic mobility shift assay (EMSA)

HepG2 cells at a density of 5×10^6 were seeded in 90 mm culture dishes. Cells were incubated with celecoxib (10 and

25 μ M) for 6 h and PGE₂ (6 μ g/ml) for 1, 2 and 6 h. Cells were harvested and then used for nuclear protein extraction. The cells were washed with PBS and 200 µl of ice cold lysis buffer (20 mM Tris-HCl, pH 7.5, 10 mM magnesium acetate, 1% NP-40, 1 mM PMSF) was added, and incubated for 5 min on ice with 3-4 vortexings of 10 s each. The nuclei were then harvested by centrifugation at 16,000 rpm for 1 min. The nuclear pellet was resuspended in 40 µl of nuclear protein extraction buffer (420 mM NaCl, 10 mM HEPES, 10 mM MgCl₂, 1 mM EDTA, 0.1 mM DTT and 25% glycerol) and incubated on ice for 30 min with intermittent vortexing of 10 s each. The sample was then centrifuged at 13,000 rpm for 30 min at 4°C. The supernatant collected was used for the mobility shift assay after protein estimation using Bradford assay [4]. Nuclear extracts (8 µg) were incubated with γ -32P-labeled doublestranded oligonucleotide with specific AP-1 binding sequence (5'-CTG AAT CAA CTG CTT CAA-3') for 30 min at 37°C. DNA-protein complex formed was separated from free oligonucleotides on 6.6% native acrylamide gel. The dried gel was exposed to X-ray film. The specificity of binding was examined by competition with unlabeled oligonucleotide (cold competition).

PGE₂ estimation

HepG2 cells at a density of 5×10^6 were seeded in 90 mm culture dishes. They were incubated with celecoxib (1, 10, 25 μ M) for 24 h. At the end of the treatment period, culture medium was collected to determine the amount of PGE₂ secreted by these cells and stored at -80° C. The quantitative analysis of PGE₂ released into the medium was assessed using PGE₂ immunoassay kit as per manufacturer's instructions (Cayman Chemical Company, USA).

In silico studies

Model overview

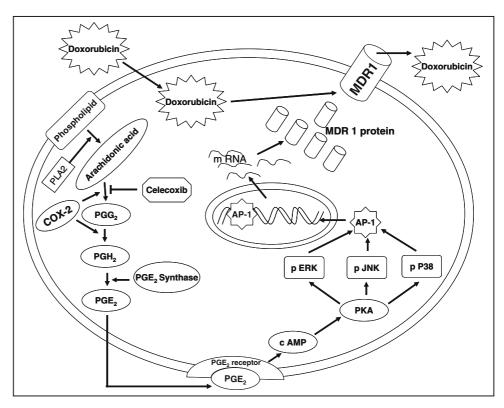
The model was developed using Teranode's Biological Modeler, which uses MML (Mathematical Modeling Language, developed by the National Simulation Resource at the University of Washington) and allows creation of kinetic equations. The TeranodeTM software was used to create and integrate the pathway with ODEs (ordinary differential equations) solved numerically by the Radau method [14]. A scheme of the elements of the model and their connections are shown in Fig. 1.

Model structure and description

Celecoxib-mediated regulation of MDR1 expression has been modeled as follows: (1) COX-2 catalyzes the conversion



Fig. 1 Schematic representation of the model showing the regulation of MDR1 expression by COX-2 and site of interference by celecoxib



of AA to prostanoids by a two-step process. In the first step, two molecules of O2 are added to form a short-lived, unstable intermediate prostaglandin G₂ (PGG₂). PGG₂ is then converted to PGH₂ by shedding of single oxygen [37]. (2) PGE₂ synthase catalyzes conversion of COX-derived PGH₂ to PGE₂ through an isomerization reaction [24, 34, 39]. PGE₂ bound prostaglandin (EP2/4) receptor [18, 21] mediates signal transduction by activating PKA pathway [24]. (3) ERK, p38 and JNK in turn are activated by phosphorylation mediated by PKA [9, 13]. (4) The phosphorylated MAPKs subsequently activate the protein c-Jun and c-Fos. Together these two proteins form an active AP-1 transcription complex [8, 27]. AP-1 is the transcription factor regulating the expression of MDR1 [31–33]. MDR1 mRNA is translated to MDR1 protein in the cytoplasm. (5) Doxorubicin is a drug that acts at the level of Topoisomerase II. With the expression of MDR1, there is a rapid extrusion of the drug out of the cell and hence resistance to this chemotherapeutic agent [25]. (6) Celecoxib selectively inhibits COX-2 thereby regulating MDR1 protein levels and increasing the overall doxorubicin retention in the cell. Further details on the model description were included in Supplementary information.

Statistical analysis

Data were reported as the mean \pm SE of three independent experiments. Statistical analysis of differences was carried out by one-way analysis of variance (ANOVA).

 Table 1
 Effect of celecoxib and doxorubicin on the growth of HepG2 cells

Celecoxib	Doxorubicin	IC-50
+	_	35 μΜ
_	+	5 μΜ
+	+	500 nM (for doxorubicin)

The percent viable cells were calculated in comparison to control cells. (Control was without doxorubicin or celecoxib for the determination of IC $_{50}$ for celecoxib or doxorubicin. Cells treated with 25 μM celecoxib were taken as control for determining the synergistic effects with both doxorubicin and celecoxib)

A *P* value less than 0.05 was considered to indicate significance.

Results

Celecoxib and doxorubicin showed synergistic effects on the proliferation of HepG2 cells

HepG2 cells were treated with celecoxib (1–100 μ M) and doxorubicin (100 nM to 50 μ M) separately for 12, 24 and 48 h and cell proliferation was determined by MTT assay. Under these experimental conditions, a dose-dependent decrease in proliferation of HepG2 cells was observed with an IC₅₀ of 35 μ M for celecoxib and 5 μ M for doxorubicin at 24 h exposure (Table 1).



In order to test the combination effects, HepG2 cells were treated with varying concentrations of doxorubicin (100 nM, 500 nM, 1 μ M, 10 μ M, 25 μ M and 50 μ M) and fixed concentration of celecoxib (25 μ M) for 24 h and cell proliferation was determined by MTT assay. In the presence of 25 μ M celecoxib, the percent inhibition in the growth of HepG2 cells was much higher at all the concentrations of doxorubicin studied. As a result, the IC₅₀ of doxorubicin for HepG2 cells was reduced from 5 μ M in the absence of celecoxib to 500 nM in the presence of 25 μ M celecoxib (Table 1), i.e. a tenfold reduction.

Celecoxib treatment increased the accumulation of doxorubicin in HepG2 cells

HepG2 cells treated with 25 μ M celecoxib (less than its IC₅₀ value) for 24 h and then incubated with 50 μ M doxorubicin for 2 h showed 56.7% more doxorubicin accumulation compared to the cells without celecoxib treatment (Fig. 2a). In silico predictions and analysis also showed dose-dependent increase in doxorubicin accumulation with celecoxib treatment (Fig. 2b).

Celecoxib regulates MDR1 expression by inhibition of COX-2 enzyme activity

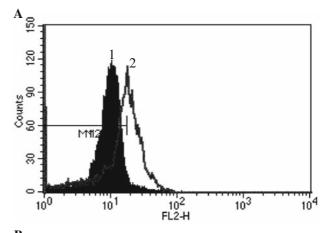
Treatment of HepG2 cells with celecoxib (1, 10 and 25 μ M) for 24 h resulted in a dose-dependent reduction of MDR1 expression at mRNA (Fig. 3a) and protein levels (Fig. 3b). Celecoxib inhibited the expression of MDR1 starting from 12 to 48 h time point (data not shown). Addition of PGE₂ (6 μ g/ml) to the medium, on the other hand, induced the expression of MDR1 compared to untreated controls. In silico predictions were aligned with experimental trends (bar diagrams in Fig. 3a, b). Experimental and in silico results of celecoxib treatment (1, 10 and 25 μ M) for 24 h showed a dose-dependent decrease in levels of PGE₂ (Fig. 3c).

COX-2 knockdown reduced the expression of MDR1

As inhibition of COX-2 activity inhibited the expression of MDR1, the effect of COX-2 depletion on MDR1 expression was tested. Knockdown of COX-2 by siRNA reduced the expression of MDR1 (Fig. 3d). PGE₂ treatment, on the other hand, increased the expression of MDR1 compared to the untreated control cells (Fig. 3d).

Celecoxib-induced inhibition of MDR1 expression is mediated by signal transduction pathway involving MAP kinases and AP-1

Nuclear levels of AP-1, a positive regulator of MDR1 expression, were reduced in a dose-dependent manner in



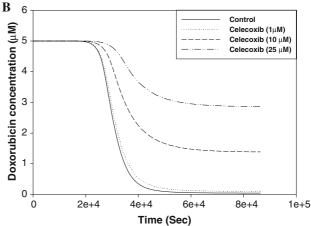


Fig. 2 Measurement of intracellular doxorubicin accumulation by flow cytometer. **a** HepG2 cells were treated with 25 μM of celecoxib for 24 h and then incubated with 50 μM doxorubicin for 2 h. The fluorescence of doxorubicin retained in HepG2 cells was measured with FL2 filter. *Histogram 1* (doxorubicin retained in control cells exposed to 50 μM doxorubicin) overlaid with *histogram 2* (doxorubicin retained in cells treated with 25 μM of celecoxib and exposed to 50 μM doxorubicin). Greater the FL2-Height, greater is the drug retention. **b** *Line plot* showing simulation data of doxorubicin accumulation with celecoxib treatment. Concentration of doxorubicin accumulated in μM on *Y*-axis against time (s) on *X*-axis. This was obtained by running the simulation model with celecoxib concentrations of 0, 1, 10, 25 μM

HepG2 cells treated with celecoxib (10 and 25 μ M) for 6 h. Treatment with PGE₂ (6 μ g/ml) for 1, 2 and 6 h, on the other hand, showed an increase in the levels of AP-1 in HepG2 cells (Fig. 4). Simulation data of AP-1 translocation correlated well with the experimental data (bar diagrams in Fig. 4). In silico studies showed a dose-dependent decrease in phosphorylated levels of JNK, ERK and p38 with celecoxib treatment (Fig. 5a–c).

Discussion

Over-expression of MDR1, a drug transporter protein, is the primary impediment in cancer chemotherapy. The role



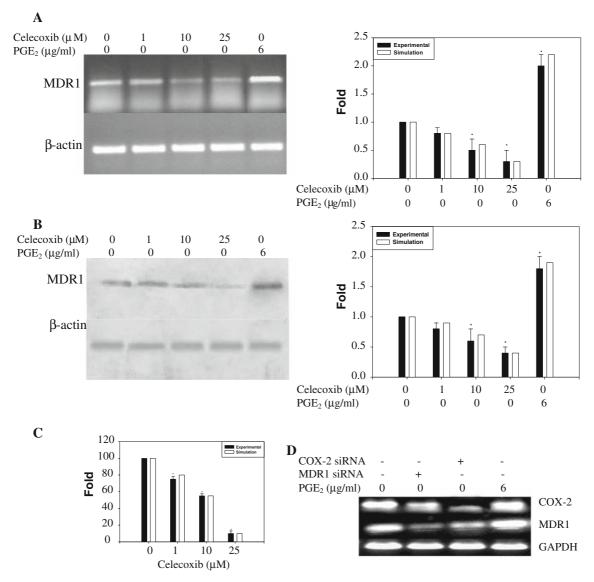


Fig. 3 Effect of celecoxib and COX-2 knockdown on MDR1 expression and PGE_2 release in HepG2 cells. **a** RT-PCR analysis of celecoxib and PGE_2 mediated effect on MDR1 mRNA expression in HepG2 cells. Bar graphs denote the fold difference in the expression levels of MDR1 mRNA obtained by experimental and simulation data. **b** Western blot analysis of celecoxib and PGE_2 mediated effect on MDR1 protein expression in HepG2 cells. Bar graphs denote the fold difference

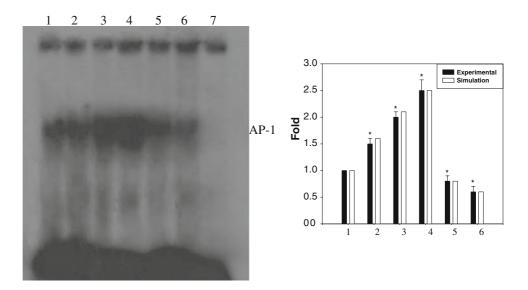
in the expression levels of MDR1 protein obtained by experimental and simulation data. **c** *Bar graphs* showing the fold difference in the release of PGE₂ in HepG2 cells with celecoxib treatment (1, 10 and 25 μ M) obtained by experimental and simulation data. **d** RT-PCR analysis of COX-2 and MDR1 knockdown and PGE₂ mediated effect on MDR1 and COX-2 mRNA expression in HepG2 cells. *Asterisk* denotes statistical significance over control (P < 0.05)

of MDR1 in protecting cells from apoptosis induced by chemotherapy has been demonstrated in several cellular systems [17]. Recent studies indicate that the activation of the cyclooxygenase system might be critical event in the development of MDR1-mediated drug resistance [11]. Selective COX-2 inhibitors have been shown to have strong chemopreventive actions against colon cancers in animals and patients with familial adenomatous polyposis [2, 19]. In the present study, treatment of HepG2 cells with celecoxib, a selective COX-2 inhibitor, showed an increased doxorubicin accumulation. Similar increase in

the accumulation of doxorubicin with celecoxib treatment was shown in MDA-MB231 cell line, independent of COX-2 and MDR1 but dependent on NF- κ B inhibition [36]. Enhanced accumulation of rhodamine 123 was shown in rat glomerular mesangial cells treated with NS-398, a selective COX-2 inhibitor [11]. In the present study also, celecoxib enhanced the accumulation of doxorubicin in HepG2 cells in a dose-dependent manner. As a result of this enhanced accumulation of doxorubicin in the presence of celecoxib, the sensitivity of HepG2 cells to doxorubicin was enhanced by tenfold.



Fig. 4 Effect of PGE, and celecoxib on nuclear translocation of AP-1 in HepG2 cells. Electrophoretic mobility shift assay (EMSA) of nuclear extracts using specific AP-1 binding probe in cells treated with celecoxib and PGE₂. Lane 1 control, lane 2 PGE₂ (6 µg/ml) 1 h, lane 3 PGE₂ (6 μg/ml) 2 h, lane 4 PGE₂ (6 μg/ml) 6 h, lane 5 celecoxib (10 µM) 6 h, lane 6 celecoxib (25 μM) 6 h, lane 7 cold competition. Bar graphs denote the fold difference in the AP-1 translocation obtained by experimental and simulation data. Asterisk denotes statistical significance over control (P < 0.05)



The present study demonstrates the downregulation of MDR1 expression in HepG2 cells, when treated with celecoxib, in COX-2-dependent mechanism. Similar observations were reported in rat glomerular mesangial cells, where in the transfection of COX-2 expression vector resulted in increased expression of MDR1 and its expression was decreased with NS-398 treatment [11]. It was also shown that addition of PGE₂ to the culture medium of rat primary hepatocytes upregulated MDR1b mRNA expression and MDR1-dependent transporter activity [40]. In addition, structurally different cyclooxygenase inhibitors (Indomethacin, Meloxicam, NS-398) were shown to inhibit EGF-induced MDR1 mRNA over-expression, leading to the accumulation rhodamine 123 in rat primary hepatocyte cultures [3]. But the effect of celecoxib on PGE₂ release might be influenced to certain extent on other parameters such as PLA₂ expression [30]. The specific role of COX-2 in MDR1 expression was further supported by COX-2 knockdown experiments. Knockdown of COX-2 by siRNA reduced the expression of MDR1. PGE2, the enzymatic product of COX-2, binds to prostaglandin receptor [18, 21] and mediates signal transduction by activating PKA pathway [12]. ERK, p38 and JNK in turn are activated by phosphorylation mediated by PKA [9, 13]. These MAP kinases activate c-fos and c-jun, promoting the formation of AP-1 [8, 27]. AP-1 is the key molecule in the regulation of expression of drug transporters [3, 10]. Treatment with celecoxib reduced the nuclear levels of AP-1 in a dosedependent manner while treatment with PGE2 showed an increase in the formation of AP-1 in HepG2 cells. The combination of experimental and in silico studies helped in dissecting the signaling pathway involved in the COX-2dependent mechanism in the regulation of MDR1 protein.

In silico simulation studies utilized the initial levels of components of the pathway, which were calibrated to match the levels obtained via experimental data. The predicted levels of MDR1, COX-2 and AP-1 obtained by in silico simulation studies with celecoxib and PGE₂ treatment corroborated with the experimental results. A gradual increase in doxorubicin retention with increase in celecoxib concentration was observed in both in silico and in experimental studies. Using in silico experiments when K_i values of celecoxib were varied within a range of 300- $1 \times 10^{-2} \,\mu\text{M}$, reduction in MDR1 expression (RNA and protein levels) and AP-1 levels was observed with the decrease in K_i values (data not shown). In silico studies further revealed the reduction in the activation of ERK, JNK and p38 by \sim 1.3-fold with celecoxib (25 μ M) treatment when compared to the untreated cells. This decrease in the activation of protein MAP kinases might also be responsible, to a certain extent, for the decrease in MDR1 expression in celecoxib-treated cells.

The experimental and in silico data presented in this study strongly suggest that celecoxib regulates the expression of MDR1 in a COX-2-dependent manner and potentiates the effects of doxorubicin in HepG2 cells. Further, AP-1-mediated signal transduction pathway is involved in the regulation of MDR1 expression by COX-2 in HepG2 cells, whose activity is inhibited by celecoxib treatment. The schematic representation of the model showing the regulation of MDR1 expression by COX-2 and site of interference by celecoxib is shown in Fig. 1. In conclusion, the foregoing studies clearly demonstrate the role of COX-2 in the development of drug resistance and usefulness of COX-2 inhibitor, celecoxib, in overcoming drug resistance in HepG2 cells.



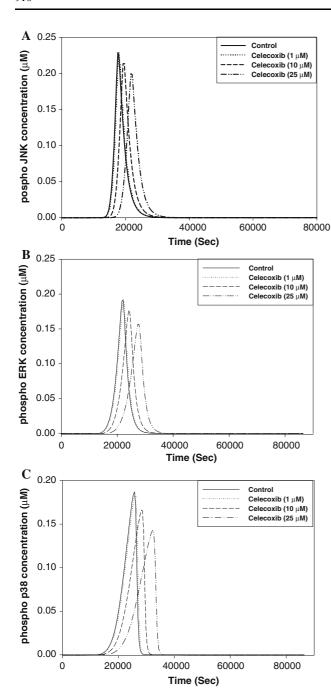


Fig. 5 In silico simulation data on the effect of celecoxib on phosphorylation of JNK, ERK and p38 in HepG2 cells. *Line plot* showing simulation data of phospho JNK (**a**), phospho ERK (**b**) and phospho p38 (**c**) concentration in μM on *Y*-axis against time (s) on *X*-axis with celecoxib treatment. This was obtained by running the simulation model with celecoxib concentrations of 0, 1, 10, 25 μM. At 25 μM of celecoxib concentration, the levels of phosphorylated forms of JNK, ERK, p38 were decreased by \sim 1.3-fold

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