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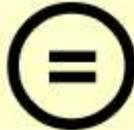
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5-Fluorouracil 내성 대장암 세포에서
cyclooxygenase 2 에 의해 유도된
prostaglandin E₂ 의 upregulation

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5-Fluorouracil 내성 대장암 세포에서
cyclooxygenase 2 에 의해 유도된
prostaglandin E₂ 의 upregulation

- Upregulation of PGE₂ by cyclooxygenase 2
in colon cancer cells resistant to 5-fluorouracil -

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의 학 과

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5-Fluorouracil 내성 대장암 세포에서
cyclooxygenase 2 에 의해 유도된
prostaglandin E₂ 의 upregulation

지도교수 민 영 돈

이 논문을 의학 박사학위신청 논문으로 제출함

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ABSTRACT

5-Fluorouracil 내성 대장암 세포에서 cyclooxygenase 2 에 의해 유도된 prostaglandin E₂ 의 upregulation

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이 연 아

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서론: 5-Fluorouracil (5-FU)은 결장직장암의 항암제로 가장 많이 사용되고 있으나, 그 효과는 내인성 또는 획득 내성 때문에 여전히 만족스럽지 못하다. 암세포에서 cyclooxygenase (COX)-2 의 발현은 세포고사에 저항을 보이는 것으로 알려져 있다. 이런 세포고사에 대한 저항은 내성세포에서 흔히 보이는 현상이다. 또한, COX-2 외에 microsomal prostaglandin (PG) E₂ synthase 1 (mPGES1)이 COX-2 와 연관되어 PGE₂ 합성에 중요하며, PGE₂를 주로 분해하는 효소로 알려진 15-PG dehydrogenase (15-PGDH)이 결장직장암의 병인에 중요한 역할을 하는 것으로 알려지고 있다. 따라서 본 연구는 대장암세포에서 COX-2 와 PGE₂ 가 5-FU 에 대한 획득 내성에 중요한 역할을 하는지 알아보려고 하였다.

방법: 대장암세포주인 SNU-C5/WT 에 5-FU 의 농도를 14 μ M 에서부터 140 μ M 까지 점차 증량하면서 세포 배양하여 5-FU 에 내성을 보이는 대장암세포(SNU-C5/5FUR)을 배양하였다. 여러 약물에 대한 세포독성 실험을 MTT assay 을 이용하여

시행하였다. SNU-C5/WT 과 SNU-C5/5FUR 사이의 유전자의 발현 차이를 cDNA mircoarray assay 를 이용하여 비교하였다. COX-2, mPGES1, 15-PGDH, vascular endothelial growth factor (VEGF)의 발현은 real-time RT-PCR, RT-PCR, Western blot assays 등을 사용하였다. PGE₂의 농도는 enzyme-linked immunosorbent assay (ELISA) 방법을 이용하여 측정하였다.

결과: SNU-C5/5FUR 세포주는 모세포주인 SNU-C5 (SNU-C5/WT)보다 5-FU 에 대해 6.7 배 더 내성을 보였다. COX-2 mRNA 와 단백질은 SNU-C5/WT 에서 보다 SNU-C5/5FUR 에서 더 높게 발현되었다. PGE₂ 농도는 SNU-C5/5FUR 에서 유의하게 증가되었다(P < 0.01). 그리고 meloxicam 투여 후에 PGE₂ levels 은 용량 의존적으로 감소되었다(P < 0.01). 그러나 SNU-C5/WT 에서는 이러한 현상이 관찰되지 않았다. 또한 mPGES1 과 15-PGDH 발현은 SNU-C5/WT 에서 보다 SNU-C5/5FUR 에서 더 증가된 것이 관찰되었다. VEGF mRNA 의 발현은 SNU-C5/WT 에서 보다 SNU-C5/5FUR 에서 더 증가 되었으며, 이러한 up-regulation 은 meloxicam 투여 후 감소 되는 것이 관찰되었다.

결론: 이러한 결과는 대장암세포에서 5-FU 의 획득내성과 관련하여 COX 2-derived PGE₂ 가 관여한다는 것을 시사한다. 또한 대장암세포에서 PGE₂ 합성을 감소시키는 약물 등은 혈관생성 억제 기전에 의해 5-FU 에 대한 내성 극복에 도움이 될 것으로 기대된다.

I . Introduction

5-Fluorouracil (5-FU) is a widely used chemotherapeutic agent that inhibits cancer cell growth and initiates apoptosis by targeting thymidylate synthase (TS) and by direct incorporation of 5-FU metabolites into DNA and RNA [Longley DB et al. 2003]. 5-FU-based chemotherapy improves overall and disease-free survival of patients with solid cancers, including colorectal cancer. De novo and acquired chemoresistance is the major obstacle for the success of 5-FU-based chemotherapy. Overexpression of TS has been shown to be a major 5-FU resistance-inducing factor [Popat S, 2004].

However overexpression of TS does not account for all non-responding tumors in colorectal cancer patients treated with 5-FU [Johnston PG et al. 2004, Salonga D et al. 2003, Sobrero A et al. 2000]. Besides the overexpression of TS, high expression levels of dihydropyrimidine dehydrogenase (DPD) [Salonga D et al. 2003, Ishibiki Y et al. 2003], the genetic status of p53 [Boyer J et al. 2004, Bunz F et al. 1999], NF- κ B [Wang W et al. 2004, Wang W et al. 2003], DNA mismatch-repair genes [Meyers M et al. 2001], and cell cycle disturbance [Longley DB et al. 2003, Mirjolet JF et al. 2002] have been reported to be associated with 5-FU resistance. Thus, the resistant mechanisms of 5-FU have been thought to be multi-factorial and have not yet been fully understood.

Up-regulation of cyclooxygenase (COX)-2 expression is an early and key oncogenic event in human colon neoplasia, typifying 85% of colon cancers and 50% of colon adenomas [Brown JR & DuBois RN, 2005].

It has also been suggested that the overexpression of COX-2 in colorectal cancer is associated with tumor growth, angiogenesis, lymphatic invasion, and metastasis [Yamauchi T et al. 2002]. Nonsteroidal anti-inflammatory drugs (NSAIDs) targeting COX-2 have been shown to directly shrink the size of colon adenoma in some patients and mediate apoptosis in cancer cells [Williams CS et al. 1999, Fosslie E. 2000]. In mice, genetic inactivation of COX-2 similarly blocks development of murine intestinal adenomas [Subbaramaiah K & Dannenberg AJ. 2003, Jacoby RF et al. 2000].

Most actions of COX-2 are mediated by prostaglandin E₂ (PGE₂). COX-2 produces prostaglandin H₂ (PGH₂), and PGH₂ is converted to PGE₂ by cytosolic or membrane-associated PGE₂ synthase (PGES). The inducible form of PGES is microsomal PGES1 (mPGES1; gene symbol PTGES), which has a marked affinity for coupling with COX-2. Induced expression of mPGES1 is observed in inflammatory conditions and cancers of the stomach, colon, endometrium, lung, and skin [Kamei D et al. 2003, Yoshimatsu K et al. 2001]. PGE₂ levels are regulated not only by its synthesis but also by its degradation. The key enzyme responsible for the biological inactivation of prostaglandins is NAD⁺-linked 15-PGDH. And recent studies identified a tumor suppressor activity of 15-PGDH in various cancers [Backlund MG et al. 2005, Myung SJ et al. 2006].

Some studies reported that antitumor effect of 5-FU was increased with the combination treatment of COX-2 inhibitors [Mizutani Y et al. 2002, Wilgus TA et al. 2004]. However, little is known about the role of COX-2 in the mechanisms of the acquired resistance to 5-FU in colon cancer cells.

In the present study, I therefore investigated whether COX-2 might contribute to the acquired resistance to 5-FU in colon cancer cells. Furthermore, I examined whether mPGES-1 and 15-PGDH have been involved in colon cancer cells with acquired 5-FU resistance.

II. Materials and Methods

Chemicals and antibodies

5-FU and meloxicam were purchased from Sigma Co. (ST. Louis, MO, USA). The primary antibodies for Western blotting assay were followings: COX-2 mouse monoclonal (1:500, Cayman, Ann Arbor, MI, USA); mPGES1 mouse monoclonal clone 6C6, (1:500, Cayman Chemical); 15-PGDH rabbit polyclonal (1:500, Nobus Biologicals, Littleton, CO, USA).

Cell culture

SNU C5 cell lines from the Cancer Research Center in Seoul National University (South Korea) were cultured at 37°C in a 5% CO₂ atmosphere using RPMI1640 medium (GibcoBRL, Gland Island, NY, USA) with 10% heat inactivated fetal bovine serum (Sigma). The cells were maintained as a suspension culture and then subcultured. The 5-fluorouracil-resistant SNU C5 subline SNU C5/5FUR was selected from the parental cell line, SNU C5, after chronic exposure to an intermittent dose schedule of 5-fluorouracil in order to allow the expression of the resistance phenotype. 5-fluorouracil was added starting from 1 x IC₅₀ (The 50% inhibitory concentration), and the concentration was increased at a rate of 50%. Finally, the cells were cultured in a fixed 5-fluorouracil concentration (140 μM).

Cytotoxicity assay

The in vitro cytotoxicity of the drugs was determined by using the MTT assay [Pieters R et al. 1988]. Ninety-μl aliquots of the cell suspensions, at 1 x 10⁵

cells/ml in a RPMI1640 medium containing 10% FBS, were seeded into a 96-well microplate which already contained 10 μ l of a drug. The wells containing no drugs were used as a control of cell viability. A stock solution of 5 mg/ml of MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide, Sigma) was prepared in normal saline and then stored at -20 °C. After incubation of the cells at 37°C for 3 days, an aliquot of 10 μ l of MTT solution was added to each well, shaken for 1 min, and the microplates were incubated for 5 hr. Formazan crystals were dissolved with dimethylsulfoxide (DMSO). The optical density of the wells was measured with a microplate reader at a wavelength of 540 nm. IC₅₀ of a particular agent was defined as that drug concentration that causes a 50% reduction in the cell number versus the untreated control. The IC₅₀ values were directly determined from the semilogarithmic dose-response curves. All experiments were carried out at least in triplicate.

cDNA microarray assay

TwinChipTM Human-8K (Digital Genomics, Seoul, Korea) was used for this study. The total RNA was prepared from the cells by using a RNeasy midi kit (Quiagen, Hilden, Germany). The quality and integrity of the prepared total RNAs were confirmed with the use of an Agilent 2100 bioanalyzer (Agilent, Palo Alto, CA, USA), and by spectrophotometry. Fluorescent labeled cDNA for the cDNA microarray analysis was prepared by the reverse transcription of the total RNA in

the presence of aminoallyl-dUTP. This was followed by the coupling of the Cy3 and Cy5 dyes (Amersham Pharmacia, Uppsala, Sweden) for SNU C5 and SNU C5/5FUR cells, respectively. The TwinChip™ Human-8K cDNA microarray was hybridized with a mixture of the fluorescent labeled cDNAs from SNU C5 and SNU C5/5FUR cells at 58 °C for 16 hr and then they were washed. After the washing procedure, the DNA chips were scanned using a ScanArray Lite (Perkin-Elmer Life Sciences, Billerica, MA). The scanned images were analyzed with GenePix 3.0 software (Axon Instruments, Union City, CA) to obtain the gene expression ratio [Yang YH et al. 2002]. Logged gene expression ratios were normalized by a LOWESS regression. The genes were considered differentially expressed when the logarithmic gene expression ratios in two independent hybridizations were more than a 2-fold difference in the expression level.

Determination of mRNA levels by quantitative reverse transcription - Polymerase Chain Reaction (RT-PCR)

Quantitative Real-time RT-PCR

Extraction of mRNA from the colorectal cancer tissues and the corresponding normal tissues was performed according to the RNeasy protocol (Qiagen, Hilden, Germany). One microgram of total RNA was reversely transcribed into cDNA in a volume of 20µ l with avian myeloma leukemia virus (AMV) reverse transcriptase and oligo dT primers (Promega, Madison, USA) according to the manufacture' s manual. Real-time PCR measurement of COX-2, mPGES1, and 15-PGDH cDNA

was performed with the Light Cycler Instrument (Roche) using the Fast Start DNA Master SYBR Green I Kit (Roche Diagnostics, Mannheim, Germany). [Schulz C et al. 2003] For verification of the correct amplification product, PCRs were analyzed on a 2% agarose gel stained with ethidium bromide. The sequences of the primers are as follows: for β -actin, 5'-GACTATGACTTAGTTGCGTTA-3' and 5'-GTTGAACTCTCTACATACTTCCG-3'; for COX-2, 5'-ATGATCTACCCTCCTCAA-3' and 5'-GAACAACCTGCTCATCAC-3'; for mPGES1, 5'-CAT CAA GAT GTA CGT GGT -3' and 5'-GGA GTA GAC GAA GCC C -3'; for 15-PGDH, 5'-TCT GTT CAT CCA GTG CGA TGT -3' and 5'-ATA ATG ATG CCG CCT TCA CCT -3'. Each reaction (20 μ l) contained 4 μ l cDNA (10 fold dilution), 2.5mM MgCl₂, 10 pmol of each primer and 2 μ l of Fast Starter Mix (containing buffer, dNTPs, SYBR Green dye and Tag polymerase). The amplification of target genes were as follows: pre-denaturing at 95 °C for 10 min, 40 cycles of denaturing at 95 °C for 15 sec, annealing for COX-2 at 65°C; mPGES-1, cPGES-1 and 15-PGDH at 57°C; β -actin at 55°C for 5 sec, and extension at 72°C for 7 sec (β -actin for 21 sec). Melting curve analysis was performed to confirm production of a single product. Negative controls without template were produced for each run. Gene expression values (relative mRNA levels) are expressed as ratios (difference between the Ct values) between the gene of interest (COX-2, mPGES-1, cPGES-1 and 15-PGDH mRNA) and an internal reference gene (β -actin) that provide a normalization

factor for the amount of RNA isolated from a specimen. Analysis of data was performed using Light Cycler software version 4.0.

RT-PCR analysis

RT-PCR was used to analyze the expression of mRNA for VEGF and β -actin (internal control). One microgram of total RNA was reversely transcribed into cDNA in a volume of 20 μ l with Taq polymerase and 10 pmole of each primer in a GeneAmp PCR2400 (Perkin-Elmer, Boston, MA, USA). For verification of the correct amplification product, PCRs were analyzed on a 2% agarose gel stained with ethidium bromide. For verification of the correct amplification product, PCRs were analyzed on a 2% agarose gel stained with ethidium bromide. The gels were documented using a Kodak Image Station 4000MM (Eastman Kodak, Rochester, NY, USA) and digitized using UN-SCAN-IT software (SilK scientific, Orem, UT). The sequences of the primers are as follows: for β -actin, 5'-GACTATGACTTAGTTGCGTTA-3' and 5'-GTTGAACTCTCTACATACTTCCG-3'; for VEGF, 5'-AYGCGGATCAAACCTCACCAAG-3' and 5'-ACAGCAGCGGGCACCAAC-3'. Each reaction (20 μ l) contained 1.25 μ l cDNA, 2.5mM MgCl₂, 10 pmol of each primer and Taq polymerase (Perkin-Elmer-Cetus, Norwalk, CT, USA). The amplification of target genes were as follows: pre-denaturing at 94°C for 5 min, 35 cycles of denaturing at 94°C for 30 sec, annealing for VEGF at 62°C (β -actin at 55°C) for 30 sec, and extension at 72°C for 1 min (β -actin for 21 sec).

Western blot analysis

Proteins were solubilized and then fractionated by SDS-PAGE. Western blotting was performed by a slight modification of the method first described by Towbin et al. [Towbin H et al. 1972]. Proteins were transferred onto a polyvinylidene fluoride (PVDF) membrane by electroblotting at a current of 60 V overnight. The membrane was incubated in 5% skim milk solution in TBST buffer for 2 hr at room temperature, washed, and then incubated with primary antibodies. The membrane was washed, and incubated with horseradish peroxidase-conjugated rabbit-antimouse IgG (diluted 1:2000, Sigma, ST. Louis, MO, USA) for 1 hr. The membrane was then stained using the detection reagent of the ECL detection kit (Amersham, Piscataway, NJ, USA). Protein concentration was determined with a Bio-Rad protein assay kit and standardized with bovine serum albumin.

Determination of PGE₂ levels by enzyme-linked immunosorbent assay (ELISA)

Prostaglandin E₂ levels in the culture medium were measured by radioimmunoassay using a general assay procedure adapted from Cetta and Goetz (Cetta F & Goetz FW, 1982). In preliminary studies, prostaglandin was recovered from culture medium with extraction fluid (ethyl acetate : isopropanol : 0.05 N HCl = 3 : 3 : 1) and the recovery rate was relatively constant (92 ± 3%, N = 9). When PGE₂ was assayed in increasing aliquots of unextracted medium (25, 50 and 100 μ L), potency estimates were parallel to a linearly transformed dose response

curve. Thus, the medium samples were assayed directly without extraction. Each sample was quantified using a liquid scintillation analyzer. Duplicate hormone standards (5 to 1000 pg) were included in each assay. The between and within assay coefficient of variants for PGE₂ were 7.3% and 6.5%, respectively.

Statistical analysis

Statistically significant difference among data sets of multiple groups were analyzed using ANOVA followed by Fisher' s protected least significant difference. The SPSS version 12.0 software package (SPSS Inc., Chicago, IL, USA) was used for statistical analysis.

III. Results

1. Sensitivity of SNU-C5/WT and SNU-C5/5FUR cells to 5-FU

The sensitivity of 5-FU on SNU-C5/WT and SNU-C5/5FUR cells was determined using MTT assay (Fig. 1). IC₅₀ values against 5-FU of SNU-C5/WT and SNU-C5/5FUR cells were 17.8 μ M and 118.8 μ M, respectively, resulting in 6.7 times more resistant to 5-FU in SNU-C5/5FUR cells as compared with that in SNU-C5/WT cells.

2. mRNA expression profiles altered in SNU-C5/5FUR cells

The microarray data were classified into four categories by their function; signal transduction, immune response, transcription, and response to stress (Table 1 - 4). As shown in Table 1, interferon receptor 1 and prostaglandin E synthase were significantly increased, while vascular endothelial growth factor B, fibroblast growth factor binding protein 1, BRCA 1 associated gene, tumor necrosis factor receptor superfamily member 8 and 21 were significantly decreased. As shown in Table 2, leukotriene A4 hydrolase and Inhibitor of kappa light polypeptide gene enhancer in B-cells were significantly decreased. As shown in Table 3, transforming growth factor beta 1 induced transcript 4 was significantly increased, and Methyl CpG binding protein 2 (Rett syndrome), cyclin-dependent kinase 7 were significantly decreased. As shown in Table 4, kallikrein 6 and interferon

receptor 1 were significantly increased, while ubiquitin-like domain member 1, B-cell CLL/lymphoma 6 (BCL6) were significantly decreased.

3. Expression levels of COX-2, mPGES1, and 15-PGDH in SNU-C5/WT and SNU-C5/5FUR cells

On quantitative RT-PCR analyses, the expression levels of COX-2, mPGES1, and 15-PGDH were significantly increased in SNU-C5/5FUR than in SNU-C5/WT. On Western blotting assay, COX-2 expression was higher in SNU-C5/5FUR than in SNU-C5, whilst mPGES1 and 15-PGDH expression seemed similar in both cell lines (Fig. 2)

4. Effect of meloxicam on PGE₂ levels and sensitivity to 5-FU in SNU-C5/WT and SNU-C5/5FUR cells

PGE₂ levels present in the supernatant of the culture medium after incubation for 12 hours were determined using ELISA method. In the basal condition, PGE₂ levels were significantly higher in SNU-C5/5FUR than in SNU-C5 ($p < 0.01$).

Furthermore, PGE₂ levels were significantly decreased in SNU-C5/5FUR cells in a dose-dependent manner ($P < 0.01$), but not in SNU-C5/WT with treatment of the COX-2 inhibitor meloxicam (Fig. 3).

To investigate whether or not meloxicam can overcome 5-FU resistance in SNU-C5/5FUR cells, MTT assay was carried out. Although at the concentration of 500

μ M meloxicam enhanced sensitivity to 5-FU in both cell lines, at the lower concentration meloxicam did not show any effect on 5-FU sensitivity in both cell lines (Fig. 4).

5. VEGF mRNA expression in SNU-C5/WT and SNU-C5/5FUR cells

In spite of up-regulation of PGE₂ levels in SNU-C5/5FUR cells, meloxicam showed little effect on overcoming the resistance to 5-FU under the circumstances of cell culture medium. Next, I investigated the expression of VEGF, which is the most powerful stimulator for angiogenesis that is important in tumor growth and metastasis. VEGF mRNA levels in SNU-C5/5FUR cells were higher than that in SNU-C5/WT cells. Meloxicam of 10 μ M to 500 μ M decreased VEGF mRNA levels in SNU-C5/5FUR cells in a dose-dependent manner, but paradoxically increased those in SNU-C5/WT cells in a dose-dependent fashion (Fig. 5).

IV. Discussion

In the current study, I demonstrate that the expression of COX-2, its main product, PGE2 and VEGF are up-regulated in SNU-C5/5FU cells as compared with those in SNU-C5/WT. Furthermore, COX-2 inhibitor shows anti-angiogenic effect by blocking the levels of VEGF mRNA in the resistant cell, but not in the wild type colon cancer cells.

TS, thymidylate phosphorylase, DPD suggested to be a resistance mechanism to 5-FU were not significantly changed in the microarray analysis of the present study. Also, NF- κ B was not significantly changed in our microarray analysis. However, we used the microarray analysis as a screening method to detect the differential genes correlated with 5-FU resistance. So we believed that the results on the microarray analysis were not confirmative. It has been suggested that wild type p53 significantly improves response to 5-FU both in vitro and in vivo [Arango D, 2001]. In the present study, we used the colon cancer cell lines, SNU-C5 and its 5-FU resistant cell line, of which the former is known to have mutated p53 and complete loss of p53 function [Rand A, et al.1996].

It is known that COX-2 could be induced by a variety of stimuli including oncogenes (HER-2/neu), growth factors (EGF), tumor promoters (phorbol esters and bile acid), and chemotherapy [Subbaramaiah K, 2003]. Of various chemotherapeutic agents, microtubule-interfering agents (paclitaxel, vincristine,

etc) are known to induce COX-2 in cancer cells [Subbaramaiah K, 2000, Mathieu A, 2004]. However, it is yet inconclusive whether COX-2 is induced by 5-FU in 5-FU-resistant cancer cells. It has been reported that expression of COX-2 mRNA was increased by exposure to 5-FU or 5-FU combination chemotherapy in human solid tumors including esophageal, breast, ovarian, and colorectal tumors [Mercer SJ. et al. 2005]. In addition, significant increase of COX-2 has been reported in rectal cancer after preoperative chemoradiation [Debusquoy A, et al. 2006]. In the present study, I also demonstrate that COX-2 and its main product, PGE₂ levels are up-regulated in the colon cancer cell with acquired resistance to 5-FU (in SNU-C5/5FUR cells). This finding suggests that COX-2 inhibitors may play a beneficial role in overcoming the resistance of SNU-C5/5FUR cells to 5-FU.

Clinically, 5-FU is the main drug in the first line or in the second line or even in the third line chemotherapy of patients with colorectal cancer (CRC). In the first line chemotherapy or adjuvant therapy, 5-FU usually used combined with folic acid (leukovorin) in patient with CRC. In case of recurrent disease after treating with this regimen, 5-FU also used in combination with oxaliplatin (FOLFOX regimen) or irinotecan (FOLFIRI regimen). Theoretically, in that case it is likely to have little effect of 5-FU on the chemotherapy. So, it is needed something different to try to overcome the acquired resistance to 5-FU.

NSAIDs, targeting COX-2, is commonly prescribed drug in patients with colorectal cancer as well as in patient with other diseases such as arthritis and other inflammatory diseases. Although it has been well known that COX-2 inhibitors induce apoptosis in cancer cells and reduce the growth rate of established tumor, tumor regression is rarely observed. Hence, it is reasonable that COX-2 inhibitors are given in conjunction with standard anti-cancer agents rather than monotherapy. Irie et al. [Irie T et al. 2007] reported that celecoxib, selective COX-2 inhibitor synergistically potentiated the antitumor effect of 5-FU depending on IFN-gamma in vivo study with colon cancer cells. Similar finding has been reported in the Ultraviolet light B-induced skin tumors of mice [Wilgus TA et al. 2004]. Inconsistent those findings, we could not demonstrated that meloxicam, which is commonly used COX-2 inhibitor, exactly preferential COX-2 inhibitor, synergistically potentiated the antitumor effect of 5-FU in both the chemo-naive colon cancer cells and acquired 5-FU resistant colon cancer cells.

Angiogenesis, the sprouting of capillaries from preexisting vasculature, occurs during embryonic development, wound repair, and tumor growth. Because it is thought to play a central role in human tumor development, inhibition of tumor-associated angiogenesis has been touted as a promising therapeutic strategy. In fact, it is generally believed that neovascularization is required for tumor to grow > 2-3 mm in size [Wang D and DuBois RN, 2004]. Chang et al. [Chang SH, 2004] reported that PGE₂ stimulated that the expression angiogenic regulatory genes in

mammary tumor cells isolated from COX-2 transgenic mice, defining COX-2-derived PGE₂ as a potent inducer of angiogenic switch during mammary cancer progression. In the present study, consistent to that report, up-regulation of VEGF mRNA was observed in the colon cancer cell with the acquired resistance to 5-FU and this up-regulation was recovered with the treatment of COX-2 inhibitor, suggesting that COX-2 derived PGE₂ may also play an important role in angiogenic switch during the acquired resistance of colon cancer to 5-FU. Furthermore, in the present study, we demonstrated that meloxicam exerted anti-angiogenic effect through inhibition of PGE₂ synthesis at a low dose (10 μ M), which is comparable to clinically therapeutic levels.

In this study, however, there was an unexpected result. In SNU-C5, which is chemonaive colon cancer cell and is little expressing VEGF and COX-2 in the basal state, up-regulation of VEGF was observed after treatment of meloxicam. We could not interpret this result exactly. Similar to this result, Ueno et al. [Ueno T et al. 2006] reported that treatment with COX-2 inhibitor, celecoxib, decreased serum VEGF levels at an early time and increased VEGF levels in serum and plasma at a late time in breast cancer patients. So further studies are necessary to elucidate how COX-2 inhibitors play a role in production of VEGF in COX-2 not expressing cancer cells or tissues.

V. Conclusions

These results suggest that upregulation of COX-2 derived PGE₂ may be involved in the acquired 5-FU resistance in colon cancer cells. Targeting to decrease PGE₂ level may benefit in overcoming 5-FU resistance through the anti-angiogenic effect in colon cancer cells.

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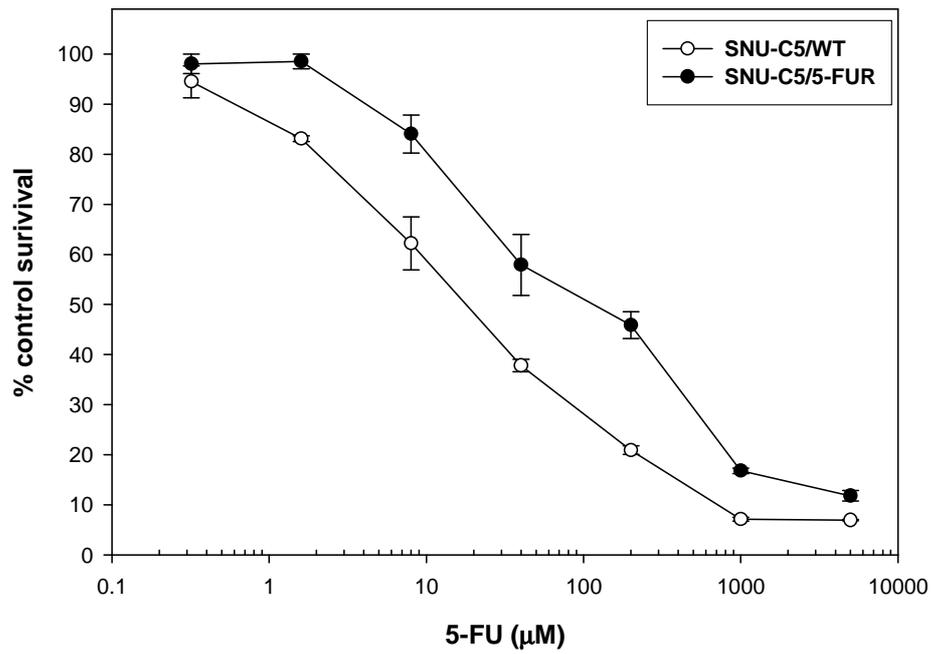


Figure1. Cytotoxic effect of 5-FU in SNU-C5 and SNU-C5/5FUR. Cells were pretreated with various concentrations of 5-FU for 3 days, and then cell viability was measured by MTT assay.

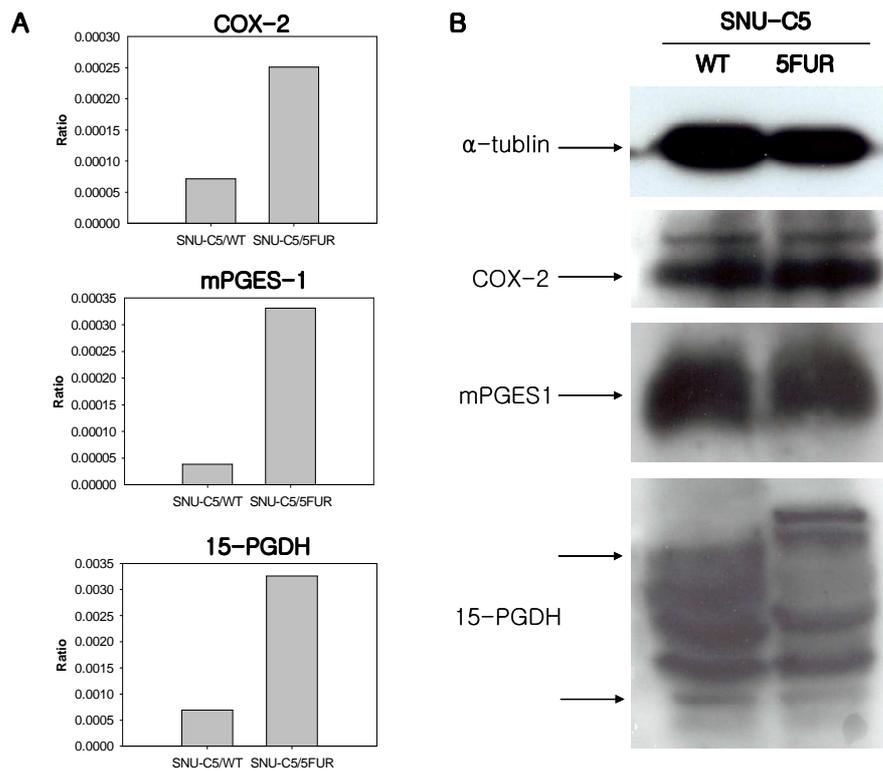


Figure2. (A) mRNA expression patterns of COX-2, mPGES1, and 15-PGDH in SNU-C5 and SNU-C5/5FUR determined by quantitative RT-PCR. (B) Protein expression patterns of COX-2, mPGES1, and 15-PGDH in the two cells determined by Western blott assay. Equivalent amounts (100 μ g) of total protein extract from the both cells were separated by SDS-PAGE and immunoblotted with each antibody described in “ Materials and methods” .

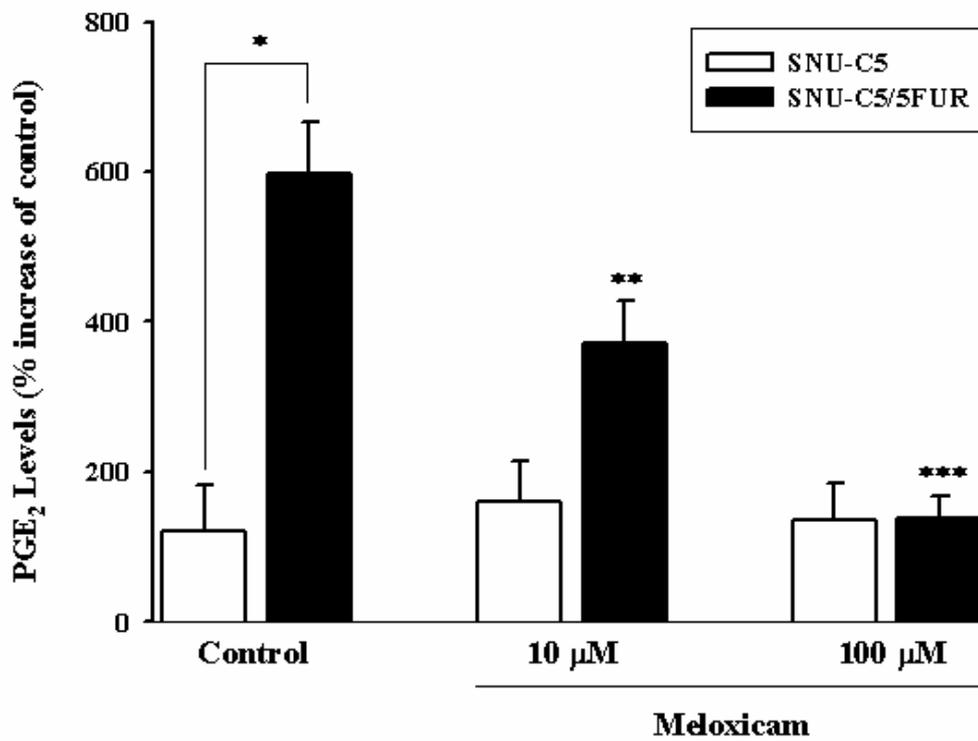


Figure3. Comparison of PGE₂ levels between SNU-C5 and SNU-C5/5FUR. PGE₂ levels present in the supernatant of the culture medium were determined by ELISA using PGE₂ monoclonal antibody (* compare PGE₂ levels between SNU-C5 and SNU-C5/5FUR at basal state; ** compare PGE₂ levels after 12hours treatment of meloxicam (10 μ M) with control in SNU-C5/5FUR. *** compare PGE₂ levels after meloxicam (100 μ M) with control in SNU-C5/5FUR, all of which P value are less than 0.01.)

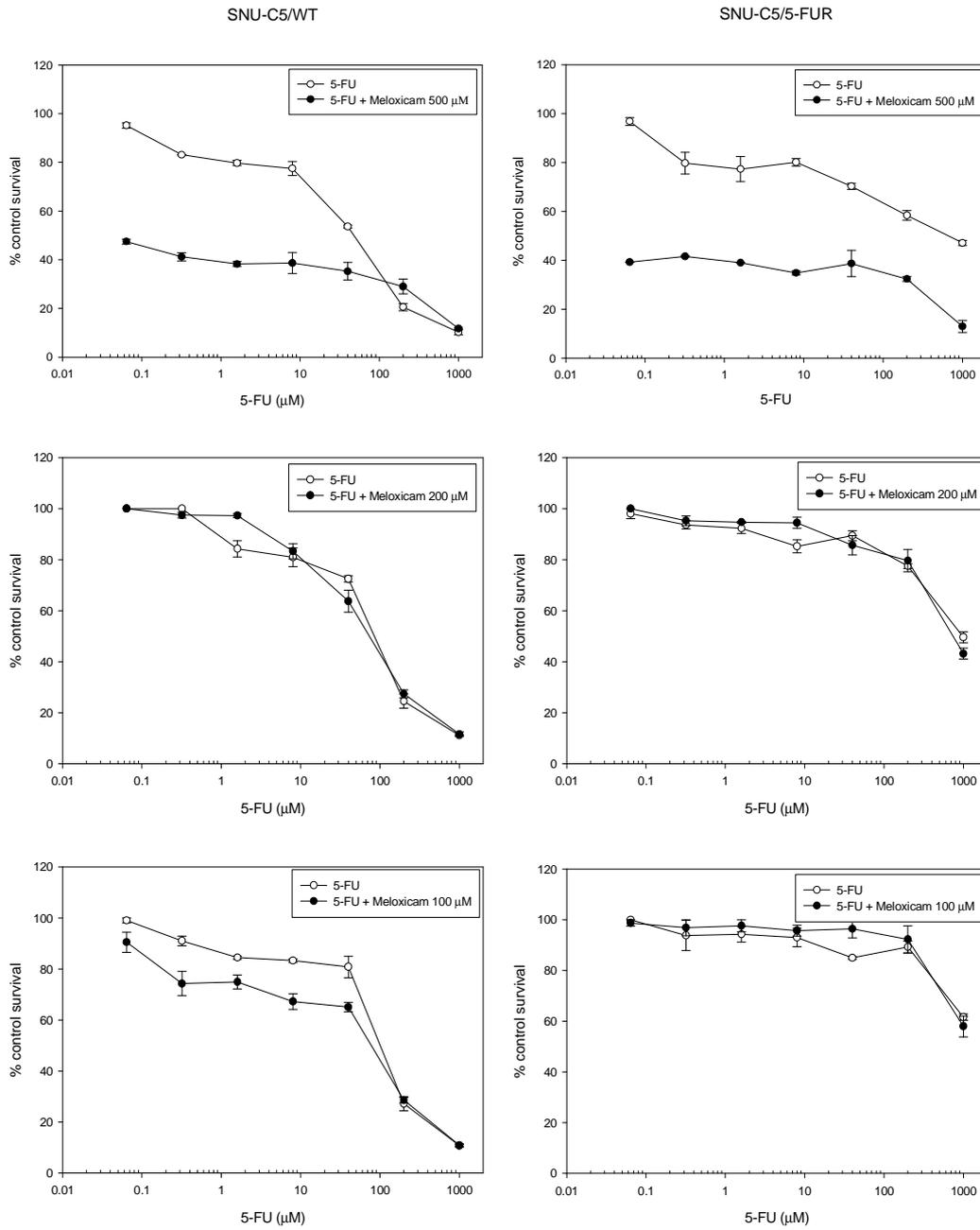


Figure 4. Cytotoxic effect of 5-FU alone and/or in combination with meloxicam in SNU-C5 and SNU-C5/5FUR. MTT assay was used to analyze cell viability.

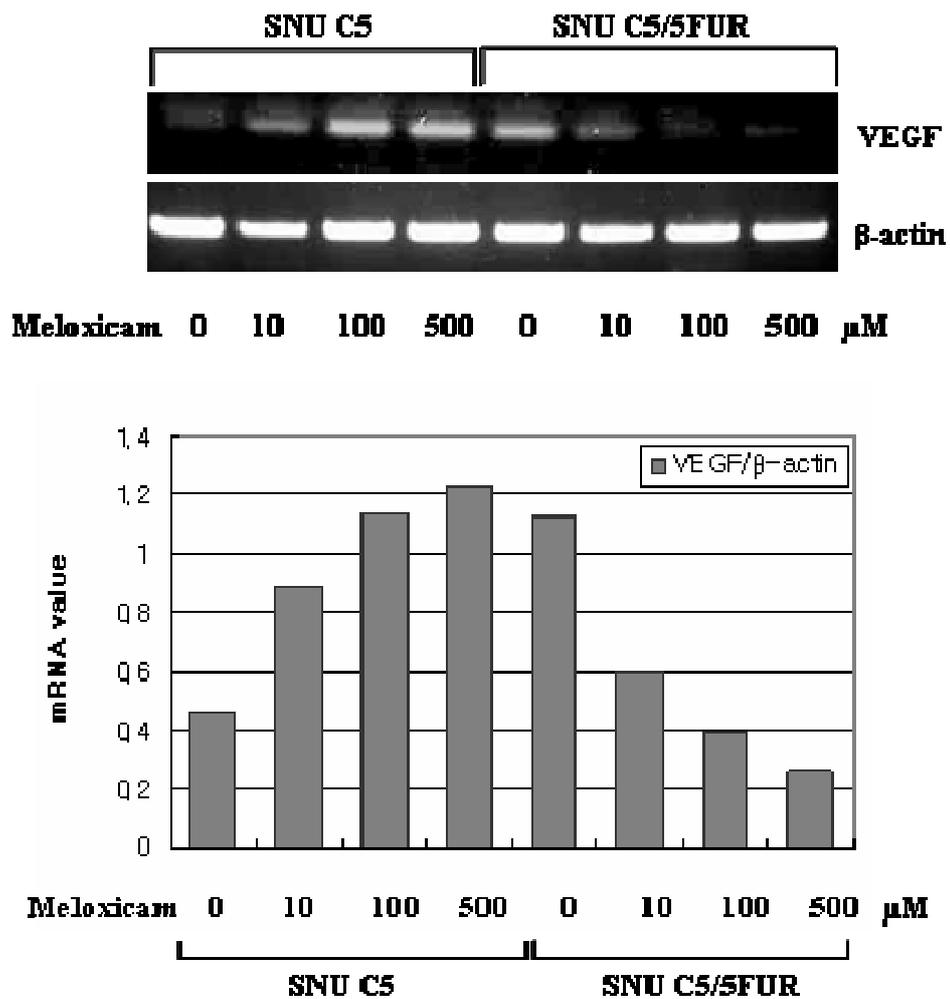


Figure5. Expression patterns of VEGF mRNA in SNU-C5 and SNU-C5/5FUR at basal state and after treatment of meloxicam (10, 100 and 500 μ M) for 24 hours by RT-PCR method.

Table1. Significantly affected genes related to the signal transduction in SNU-C5/5FUR

| Title | Gene. Symbol | Fold | Cytoband |
|---|--------------|------|----------------|
| Increased genes | | | |
| Corticotropin releasing hormone receptor 1 | CRHR1 | 2.4 | 17q12-q22 |
| Regulator of G-protein signalling 2, 24kDa | RGS2 | 2.2 | 1q31 |
| Interferon (alpha, beta and omega) receptor 1 | IFNAR1 | 2.2 | 21q22.1 |
| Rho guanine nucleotide exchange factor (GEF) 7 | ARHGEF7 | 2.0 | 13q34 |
| A kinase (PRKA) anchor protein (gravin) 12 | AKAP12 | 2.0 | 6q24-q25 |
| Prostaglandin E synthase | PTGES | 2.0 | 9q34.3 |
| Dimethylarginine dimethylaminohydrolase 1 | DDAH1 | 2.0 | 1p22 |
| Decreased genes | | | |
| Lymphotoxin beta receptor (TNFR superfamily, member 3) | LTBR | 2.0 | 12p13 |
| Glutamate receptor, ionotropic, N-methyl D-aspartate 2D | GRIN2D | 2.0 | 19q13.1-qter |
| Gamma-aminobutyric acid (GABA) A receptor, beta 1 | GABRB1 | 2.0 | 4p12 |
| Ribosomal protein L17 | RPL17 | 2.0 | 18q21 |
| Rho GTPase activating protein 4 | ARHGAP4 | 2.0 | Xq28 |
| Epithelial cell transforming sequence 2 oncogene | ECT2 | 2.0 | 3q26.1-q26.2 |
| EPH receptor B2 | EPHB2 | 2.0 | 1p36.1-p35 |
| Nuclear receptor subfamily 4, group A, member 1 | NR4A1 | 2.1 | 12q13 |
| Vascular endothelial growth factor B | VEGFB | 2.1 | 11q13 |
| Receptor (calcitonin) activity modifying protein 1 | RAMP1 | 2.2 | 2q36-q37.1 |
| Tumor-associated calcium signal transducer 2 | TACSTD2 | 2.2 | 1p32-p31 |
| Fibroblast growth factor binding protein 1 | FGFBP1 | 2.3 | 4p16-p15 |
| Rho family GTPase 3 | ARHE | 2.5 | 2q23.3 |
| BRCA1 associated protein | BRAP | 2.5 | 12q24 |
| TXK tyrosine kinase | TXK | 2.8 | 4p12 |
| Fibroblast growth factor receptor 4 | FGFR4 | 2.9 | 5q35.1-qter |
| Endothelin 1 | EDN1 | 3.1 | 6p24.1 |
| A disintegrin and metalloproteinase domain 9 (meltrin gamma) | ADAM9 | 3.1 | 8p11.23 |
| Tumor necrosis factor receptor superfamily, member 8 | TNFRSF8 | 3.2 | 1p36 |
| Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon | IKBKE | 3.3 | 1q32.1 |
| Tumor necrosis factor receptor superfamily, member 21 | TNFRSF21 | 3.6 | 6p21.1-12.2 |
| Transmembrane 4 superfamily member tetraspan NET-5 | NET-5 | 6.5 | 12p13.33-13.32 |

Table2. Significantly affected genes related to the immune response in SNU-C5/5FUR

| Title | Gene Symbol | Fold | Cytoband |
|---|-------------|------|-----------|
| Increased genes | | | |
| Corticotropin releasing hormone receptor 1 | CRHR1 | 2.4 | 17q12-q22 |
| Hypothetical protein FLJ35429 | FLJ35429 | 2.4 | 6p21.32 |
| Keratin 1 (epidermolytic hyperkeratosis) | KRT1 | 2.0 | 12q12-q13 |
| Prostaglandin E synthase | PTGES | 2.0 | 9q34.3 |
| Decreased genes | | | |
| Lymphotoxin beta receptor (TNFR superfamily, member 3) | LTBR | 2.0 | 12p13 |
| CCAAT/enhancer binding protein (C/EBP), beta | CEBPB | 2.0 | 20q13.1 |
| Leukotriene A4 hydrolase | LTA4H | 2.3 | 12q22 |
| Proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) | PSME1 | 2.6 | 14q11.2 |
| Dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing protein 2) | DPP4 | 2.6 | 2q24.3 |
| Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon | IKBKE | 3.3 | 1q32.1 |
| B-cell CLL/lymphoma 6 (zinc finger protein 51) | BCL6 | 3.4 | 3q27 |

Table3. Significantly affected genes related to the transcription in SNU-C5/5FUR

| Title | Gene. Symbol | Fold | Cytoband |
|---|-------------------|------|-------------------|
| Increased genes | | | |
| Oligodendrocyte lineage transcription factor 2 | OLIG2 | 2.9 | 21q22.11 |
| Regulatory factor X, 2 (influences HLA class II expression) | RFX2 | 2.7 | 19p13.3- p13.2 |
| Snf2-related CBP activator protein | SRCAP | 2.5 | 16p11.2 |
| SPTF-associated factor 65 gamma | STAF65 (gamma) | 2.4 | 2pter-p25.1 |
| Transforming growth factor beta 1 induced transcript 4 | TGFB114 | 2.0 | 13q14 |
| Decreased genes | | | |
| Chromobox homolog 7 | CBX7 | 2.0 | 22q13.1 |
| Activating transcription factor 2 | ATF2 | 2.0 | 2q32 |
| Telomeric repeat binding factor (NIMA-interacting) 1 | TERF1 | 2.0 | 8q13 |
| CCAAT/enhancer binding protein (C/EBP), beta | CEBPB | 2.0 | 20q13.1 |
| Nuclease sensitive element binding protein 1 | NSEP1 | 2.0 | 1p34 |
| Nuclear receptor subfamily 4, group A, member 1 | NR4A1 | 2.1 | 12q13 |
| Transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor | TCF2 | 2.1 | 17cen- q21.3 |
| High-mobility group box 2 | HMGB2 | 2.1 | 4q31 |
| Methyl CpG binding protein 2 (Rett syndrome) | MECP2 | 2.1 | Xq28 |
| Protein phosphatase 1, regulatory subunit 10 | PPP1R10 | 2.2 | 6p21.3 |
| Transcription factor binding to IGHM enhancer 3 | TFE3 | 2.5 | Xp11.22 |
| SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1 | SMARCB1 | 2.5 | 22q11.23 |
| Cyclin-dependent kinase 7 (MO15 homolog, <i>Xenopus laevis</i> , cdk-activating kinase) | CDK7 | 2.6 | 5q12.1 |
| Zinc finger protein 45 | ZNF45 | 2.6 | 19q13.2 |
| BTB and CNC homology 1, basic leucine zipper transcription factor 1 | BACH1 | 2.8 | 21q22.11 |
| B-cell CLL/lymphoma 6 (zinc finger protein 51) | BCL6 | 3.4 | 3q27 |
| Sterol regulatory element binding transcription factor 2 | SREBF2 | 5.6 | 22q13 |

Table4. Significantly affected genes related to the response to stress in SNU-C5/5FUR

| Title | Gene. Symbol | Fold | Cytoband |
|--|-----------------|------|---------------|
| Increased genes | | | |
| Kallikrein 6 (neurosin, zyme) | KLK6 | 3.8 | 19q13.3 |
| Interferon (alpha, beta and omega) receptor 1 | IFNAR1 | 2.2 | 21q22.1 |
| Keratin 1 (epidermolytic hyperkeratosis) | KRT1 | 2.0 | 12q12-q13 |
| Prostaglandin E synthase | PTGES | 2.0 | 9q34.3 |
| Decreased genes | | | |
| RAD21 homolog (S. pombe) | RAD21 | 2.0 | 8q24 |
| CCAAT/enhancer binding protein (C/EBP), beta | CEBPB | 2.0 | 20q13.1 |
| Nuclease sensitive element binding protein 1 | NSEP1 | 2.0 | 1p34 |
| Homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 | HERPUD1 | 2.1 | 16q12.2-q13 |
| High-mobility group box 2 | HMGB2 | 2.1 | 4q31 |
| Serine (or cysteine) proteinase inhibitor, clade D (heparin cofactor), member 1 | SERPIND1 | 2.2 | 22q11.2 |
| Leukotriene A4 hydrolase | LTA4H | 2.3 | 12q22 |
| Putative translation initiation factor | SUI1 | 2.3 | 17q21.2 |
| Cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase) | CDK7 | 2.6 | 5q12.1 |
| Polymerase (DNA directed), delta 1, catalytic subunit 125kDa | POLD1 | 2.6 | 19q13.3 |
| Defensin, alpha 4, corticostatin | DEFA4 | 2.7 | 8p23 |
| Connective tissue growth factor | CTGF | 3.3 | 6q23.1 |
| B-cell CLL/lymphoma 6 (zinc finger protein 51) | BCL6 | 3.4 | 3q27 |
| Tumor rejection antigen (gp96) 1 | TRA1 | 4.0 | 12q24.2-q24.3 |

저작물 이용 허락서

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| | 영문: Upregulation of PGE ₂ by cyclooxygenase 2 in colon cancer cells resistant to 5-fluorouracil | | | | |

본인이 저작한 위의 저작물에 대하여 다음과 같은 조건 아래 -조선대학교가 저작물을 이용할 수 있도록 허락하고 동의합니다.

- 다 음 -

1. 저작물의 DB 구축 및 인터넷을 포함한 정보통신망에의 공개를 위한 저작물의 복제, 기억장치에의 저장, 전송 등을 허락함.
2. 위의 목적을 위하여 필요한 범위 내에서의 편집과 형식상의 변경을 허락함. 다만, 저작물의 내용변경은 금지함.
3. 배포·전송된 저작물의 영리적 목적을 위한 복제, 저장, 전송 등은 금지함.
4. 저작물에 대한 이용기간은 5 년으로 하고, 기간종료 3 개월 이내에 별도의 의사 표시가 없을 경우에는 저작물의 이용기간을 계속 연장함.
5. 해당 저작물의 저작권을 타인에게 양도하거나 출판을 허락을 하였을 경우에는 1 개월 이내에 대학에 이를 통보함.
6. 조선대학교는 저작물 이용의 허락 이후 해당 저작물로 인하여 발생하는 타인에 의한 권리 침해에 대하여 일체의 법적 책임을 지지 않음.
7. 소속 대학의 협정기관에 저작물의 제공 및 인터넷 등 정보통신망을 이용한 저작물의 전송·출력을 허락함.

동의여부 : 동의(○) 반대()

2007 년 8 월 일

저작자: 이 연 아 (인)

조선대학교 총장 귀하