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Proteomic Analysis for the Purpose of Understanding the Mechanisms of Benzene and X-ray Induced Leukemia Using Human Bone Marrow Cells

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Abstract

Benzene and the ionizing radiation are well known as leukemogens. There have been many studies on leukemia accumulated, but the mechanisms underlying the leukemogenicity are not fully understood. Since there are differences and similarities in leukemogenesis by benzene and radiation, comparative analysis could offer insight toward understanding basic leukemogenesis. In this study, we extracted proteins from CD34+ cells from human bone marrow, the target organ of leukemia, exposed to benzene metabolites (catechol and hydroquinone) or/and X-rays, and performed two dimensional gel image analysis. As a result, we identified 8 proteins specific to benzene metabolites exposure, and 14 to X-ray irradiation. Notably, we found 2 proteins, protein SET and cofilin-1, which showed changes in expression levels common to both benzene metabolites and X-ray exposure. These results suggest that the SET-PP2A-JNK pathway might play a key role in the mechanisms of the leukemia.

Keywords: Benzene; Human bone marrow cells; Protein SET; Proteomics; Radiation; Two-dimensional gel electrophoresis

Abbreviations: ALL: Acute Lymphocytic Leukemia; AML: Acute Myeloid Leukemia; BEIR: Committee on the Biological Effects of Ionizing Radiation; CAT: Catechol; CERI: Chemicals Evaluation and Research Institute; CC100: Cytokine Cocktail 100; CLL: Chronic Lymphocytic Leukemia; CML: Chronic Myeloid Leukemia; DDA: Data Dependent Analysis; HQ: Hydroquinone; IEF: Isoelectric Focusing; IPCS: International Programme on Chemical Safety; IPG: Immobilized PH Gradient; JNK: Jun N-terminal Kinase; LC: Liquid Chromatography; LET: Linear Energy Transfer; MALDI-TOF: Matrix-Assisted Laser Desorption/Ionization Time-Of Flight; MS: Mass Spectrometry; PAGE: Polyl-Acrylamide Gel Electrophoresis; PP2A: Protein Phosphatase 2A; ROSs: Reactive Oxygen Species; SDS: Sodium Dodecyl Sulfate; SFEM: Serum-Free Expansion Medium; 2DE: Two Dimensional gel Electrophoresis

Introduction

Benzene (C_6H_6) is an important industrial chemical. It is commonly used as an industrial solvent and synthetic material, and the main sources of exposure are cigarette smoke and exhaust gas of gasoline (Chemicals Evaluation and Research Institute (CERI), 1997). Benzene is known to cause adverse health effects on humans such as acute myelogenous leukemia. Epidemiological studies of benzene-exposed workers have demonstrated a causal relationship between benzene exposure and the induction of myelogenous leukemia (International Programme on Chemical Safety (IPCS), 1993). Among them, Pliofilm cohort study from 1970 is a sufficiently large well-studied cohort with enough benzene exposure to lead benzene risk estimation statistically. When benzene is taken into the body, it is metabolized to various metabolites by the action of metabolic enzymes such as cytochrome P-450 and myeloperoxidase (Parke, 1996). Benzene itself is a stable substance, but some of these metabolites have cytotoxicity and mutagenicity, and they are thought to contribute to the development of benzene-induced leukemia (Sammett et al., 1979). Among various metabolites, catechol (CAT) and hydroquinone (HQ) are reported to have an especially close connection with the leukemogenesis of benzene (Robertson et al., 1991). There have been many studies on benzene-induced leukemia accumulated, but the mechanisms underlying benzene-induced leukemogenicity are still not fully understood. The analysis of the effects of CAT and HQ on human bone marrow, which is the target organ of leukemia, is beneficial for getting better understanding on the mechanisms of benzene-induced leukemogenicity. In such analysis, the synergistic effects of CAT and HQ should be considered because CAT and HQ are simultaneously in bone marrow of humans and because it has reported that the combination exposure of CAT and HQ showed stronger toxicity than the individual exposure of CAT of HQ (Roberston et al., 1991; Igarashi, 2004, Kyoto University, Japan, unpublished observation; Levay and Bodell, 1991; Stillman et al., 1999).

As well as benzene, the radiation exposure causes various health effects including leukemia. It has been reported that the exposure to 1Gy of radiation leads to an increasing incidence of cancers by 0.05-0.16% (Bertell, 1984). 0.1Gy of low Linear En-

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ergy Transfer (LET) radiation has also been estimated to increase the carcinogenic rate by 0.5-1.4% (Committee on the Biological Effects of Ionizing Radiation (BEIR), 1980). In addition, it was shown that gene mutations could be induced artificially by X-ray exposure (Muller, 1927). X-ray is a form of electromagnetic radiation with a wavelength in the range of 0.01 to 10 nanometers. It is primarily used for medical diagnostics with the help of its high penetration. Today the exposure from medical X-rays has the highest percentage of exposure from man-made radiation. X-ray has been frequently used for biological study because the X-ray machines are easier to handle than other radiation sources.

Both benzene and radiation are similarly known to induce leukemia. They induce in common some DNA damages to human bone marrow cells, resulting in the induction of leukemia. For example, it was reported that benzene and radiation induced same kinds of chromosome aberrations such as t(8;21) and the losses of long arms or whole chromosome 5 and 7, which were thought to have some connections with leukemogenesis (McHale et al., 2008; Deininger et al., 1998; Domracheva et al., 2002). These results suggested that the inductions of leukemia by benzene and radiation exposure might have some similar mechanisms of action. However, there are also some differences. At first, there is a difference on the subtypes of leukemia induced by benzene and radiation. The relationship of benzene with acute myeloid leukemia (AML) is already proven, but there was no persuasive evidence the link of benzene to other subtypes including acute lymphocytic leukemia (ALL), chronic myeloid leukemia (CML), and chronic lymphocytic leukemia (CLL) (Schnatter et al., 2005). On the other hand, there was strong evidence of radiation-induced risks for all subtypes of leukemia (Preston et al., 1994). In addition, there have been another differences in the mechanisms of leukemia by them. In radiation-induced leukemia, DNA damages of bone marrow cells, which are the primary steps of leukemogenesis, is inducted mainly by two kinds of actions: one is the direct action in which the exposed radiation ionizes or excites the atoms constituting DNA and DNA damages are directly generated, and the other is the indirect action in which water molecules are ionized or excited by radiation and free radicals are produced, then these radicals induce DNA damages (Iida, 2009). On the other hand, in benzene-induced leukemia, DNA damages are mainly induced by binding of benzene metabolites such as CAT and HQ to intracellular molecules or by reactive oxygen species (ROSs) generated by the oxidation of benzene metabolites (Irons, 1985). It has also reported that benzene metabolites inhibit enzymes involved in DNA replication and maintenance such as topoisomerases, which are likely to contribute to benzene-induced leukemias (Eastmond et al., 2005; Lindsey et al., 2005).

Since there are differences and similarities in leukemogenesis by benzene and radiation described above, comparative analysis could give the insight of understanding basic leukemogenesis. As this comparative analysis, we conducted a comprehensive proteomic analysis by two-dimensional gel electrophoresis (2DE) using $CD34^+$ cells from human bone marrow, which are hematopoietic stem cells and thought to be the target of leukemia.

Proteins are involved with various cancers including leukemia. Mutations on a gene level are very important as the first steps in carcinogenesis. However, the change in protein expression alters more directly biological process than gene expressions and the essence of carcinogenesis is that mutant genes produce abnormal proteins and these proteins can not fulfill their original functions (Hirai, 1994). A translocation t(8;21) is one of the high frequency chromosome aberrations observed in acute myeloid leukemia. In this aberration, the AML1 gene on chromosome 21 and the MTG8 gene on chromosome 8 fuse together, and formed the chimera gene AML1/MTG8. The fusion protein produced by this chimera gene is regarded as a protein involved in leukemogenesis by disturbing the differentiation of myeloid cells to mature granulocytes. Additionally, one group recently reported that the primary target of radiation-induced leukemia might be not DNA itself but rather proteins (Kumagai et al., 2003; Suzuki et al., 2005; Urushibara et al., 2004). Therefore, monitoring the change of proteins may be useful as a means of getting better understanding the mechanisms underlying leukemia. Combined with the progress of analysis technology, recent researchers have actively analyzed the protein expression profile in cancers, and tumor markers are often used for the diagnosis and cure (Honda et al., 2005).

2DE is a form of gel electrophoresis commonly used for protein analysis. Using this method, we can analyze the changes of so many kinds of proteins at a time comprehensively. So, 2DE must be helpful for shedding light on the similarities and differences in leukemogenesis by benzene and radiation. Hence, we applied 2DE in this study to find proteins specific to benzene metabolites (CAT and HQ) or/and X-ray irradiation in human bone marrow cells.

Materials and Methods

Reagents and cells

Reagents were obtained from WAKO (Osaka, Japan) unless otherwise stated.

$CD34^+$ cells used here were purchased from Lonza. (Hispanic, female, twenty six years old).

$CD34^+$ cells were cultured at 1.3 to 2.0×105 cells/mL in StemSpan® Serum-Free Expansion Medium (SFEM) (StemCell Technolgies, Inc.) supplemented with 1% StemSpan® Cytokine Cocktail 100 (CC100) (StemCell Technologies, Inc.). The cultures were incubated in a humidified atmosphere of 5% CO_2 in air at 37 degrees C for 6 days until cultures reach early- or mid-log phase.

Chemical treatment and X-ray irradiation

For chemical treatment, the half amount of medium was exchanged for new medium after 6 days of culture, and cells were seeded at a density of 5.0×10^4 cells/mL in a 100-mm dish and treated for 30 hr with CAT or HQ dissolved in dH_2O at the concentrations of 6 μM, or 1% of dH_2O. Cells were also treated with the mixture of CAT and HQ at the concentration of 6 μM (CAT 2 μM + HQ 4 μM). This ratio was determined according to literature, which reported the median values of CAT and HQ in the urine of exposed workers (1 to 25 ppm, n=20) were 7.2 and 16.4, 25 percentile values were 5.2 and 9.8, and 75 percentile values were 14.6 and 31.9, respectively (Rothman et al., 1998).

For X-ray irradiation, cells were re-seeded at a density of

1.0×10^5 cells/mL in a 50-mm dish. An X-ray exposure machine, Radioflex 350 (Rigaku, Tokyo, Japan) was used for the X-ray irradiation (5 Gy/min, 250 kV, 15 mA, Al 2 mm filter). The irradiated doses were 0, 0.5, 1 and 1.5 Gy. After irradiation, cells were cultured in the same medium for 30 hr.

Cytotoxicity analysis

Harvested cells of each treatment condition or X-ray irradiation were counted in a hematocytometer by using a phase-contrast microscope (Axiovert 25 ,Carl Zeiss, Germany). The survival rate was defined as the cell number ratio between treated cells and non-treated (control) cells. The Student's t-test was applied to test the difference of the survival rates between each dose and control.

Protein extraction

Proteins were extracted from $CD34^+$ cells by ultrasonication using SONIFIER150 (BRANSON, Japan) directly in 100 mL of cellular lysis buffer containing 8 M urea, 4% CHAPS (GE healthcare bioscience, UK), and 40 mM Tris. Ultrasonication was conducted at 4 W for 20 sec, and after that, solutions were set on ice for 30 sec. This process was repeated five times. The suspension was centrifuged at 15000 rpm for 10 min at 4 °C. For 2-DE, interfering components were removed using the 2-D Clean-Up Kit (GE healthcare bioscience), and proteins were diluted in cellular lysis buffer described above. The protein concentration was determined using the 2-D Quant Kit (GE healthcare bioscience). The coefficients of variation of these extraction processes were less than 15% (n = 5 per exposure condition).

2DE

For 2DE, we used 50 µg of proteins per gel. 2DE was performed in the following method.

Proteins were resuspended in 450 µL of buffer containing 8 M urea, 4% CHAPS, 40 mM Tris, 0.28% DTT (GE healthcare bioscience), and 0.5% immobilized pH gradient (IPG) buffer (GE healthcare bioscience). IPG gel strips (24 cm, pH 4-7, GE healthcare bioscience) were rehydrated with samples for 2DE using Immobiline DryStrip Reswelling Tray (GE healthcare bioscience) for 16 hr at room temperature. In order to avoid drying during the rehydration, DryStrip cover fluid (GE healthcare bioscience) was piled up on the strips. After the rehydration, isoelectric focusing (IEF) was performed with an Ettan IPGphor II electrophoresis unit (GE healthcare bioscience) for a total of 46.9 kVh at room temperature. The detailed conditions for IEF is 1 hr at 100 V, 1 hr at 500 V, gradually increased to 1000 V over 7 hr, then gradually increased to 8000 V over 3 hr, and finally run at 8000 V for 3.45 hr.

Before the second dimensional separation, each focused IPG strip was equilibrated, firstly in a buffer (50mM Tris-HCl, 6M urea, 30% glycerol, 2% SDS, 0.002% bromophenol blue (MP biomedicals), pH8.8) containing 1% DTT for 15 min, and then in the same equilibration buffer containing 2.5% iodoacetamide for another 15 min. Both incubations were carried out at room temperature with gentle shaking using MULTI SHAKER MMS (EYELA, Japan). In this equilibration process, DTT cut the disulfide bindings in proteins, and iodoacetamide protected the exposed cysteine residues to hold primary structures of proteins. The second dimension, sodium dodecyl sulfate - poly-acrylamide gel electrophoresis (SDS-PAGE), was carried out using an Ettan Dalt six (GE healthcare bioscience). The upper buffer chamber of Ettan Dalt six was filled with a SDS buffer I containing 50 mM Tris, 384 mM Glycine (MP Biomedicals), and 0.2% SDS. The lower buffer chamber was filled with a SDS buffer II containing 25 mM Tris, 192 mM Glycine, and 0.1% SDS. The equilibrated IPG strips were loaded on 12.5% gels (255 mm × 205 mm × 1 mm) at 10 °C, which contained 25% 40(w/v)%-Acrylamide/Bis Mixed Solution (37.5:1) (nacalai tesque, Kyoto, Japan), 375 mM Tris-HCl, 0.1% SDS, 0.05% ammonium persulphate (nacalai tesque), and 0.33 µL/mL TEMED (nacalai tesque). The agarose solution (0.5% agarose and 0.002% bromophenol blue in a SDS buffer II described above) was applied to seal the IPG strips, then SDS-PAGE was run at 2.5 W/gel for 30 min, followed by 25 W/gel until the bromophenol blue reached the bottom of the gel. A constant-temperature unit, NCB-2500 (EYELA) was used in order to keep the gels and buffers at 10 °C. After SDS-PAGE, analytic gels were stained by silver staining using 2-D silver staining kit II (Daiichi, Japan).

Identification of specific proteins

For image analysis, all the silver-stained gels were scanned by image scanner GT-X 8000 (SEIKO EPSON Corporation, Japan). Electronic gel images were exported as tagged image format (TIF) in 8-bit black-and-white color with 160 µm of pixels. Images were analyzed using the PDQuest software (Bio-Rad Laboratories, Inc., USA). Twenty-four TIF images obtained from experiments (2 images from 2 treatment conditions as 0.5 Gy and 1.0 Gy, and 3 images from other 6 treatment conditions, i.e., control, CAT, HQ, CAT+HQ, 0Gy, 1.5 Gy) were loaded into the program and grouped. Spot detections were carried out automatically, followed by the manual editing of each image to remove artifacts such as streaks and splotches. All the spots on the gels were matched either automatically or manually. After each matching, the background subtraction and spot volume normalization were performed. We used the local regression model for the normalization because it is not easily affected by abnormal values. In this normalization method the variance of each spot volume was minimized. Using normalized volume as a parameter, the spots showing at least twofold changes in expression levels were identified.

For the spots specific to benzene metabolites exposure, mass spectrometric identification of proteins was performed as previously described (Jensen et al., 1996). Briefly, after SDS-PAGE, proteins were visualized by silver staining and excised separately from gels, followed by the in-gel digestions with trypsin (Promega Corporation) in a buffer containing 50mM ammonium bicarconate (pH 8.0) and 2% acetonitrile overnight at 37 degrees C. Molecular mass analyses of triptic peptides were performed by matrix-assisted laser desorption/ionization time-of flight mass spectrometry (MALDI-TOF/MS) using an ultraflex TOF/TOF (Bruker Daltonics). Proteins were identified by comparison between the molecular weights determined by MALDI-TOF/MS and theoretical peptide masses from the proteins registered in NCBInr.

For the spots specific to X-ray irradiation, mass spectrometric identification of proteins was performed as follows. The gels were subjected to in-gel tryptic digestion essentially as described (Wilm et al., 1996). Briefly, the gel pieces were destained and washed, and, after dithiothreitol reduction and iodoacetamide alkylation, the proteins were digested with porcine trypsin (mass spec grade) overnight at 37 degrees C. The resulting tryptic peptides were extracted from the gel pieces with 30% acetonitrile, 0.3% trifluoroacetic acid and 100% acetonitrile. The extracts were evaporated in a vacuum centrifuge to remove organic solvent, then desalted and concentrated on reversed-phase C18 StageTips as previously described (Rappsilber et al., 2003). Then, Nanoflow-Liquid Chromatography (LC)-MS and MS/MS experiments were performed on HITACHI Nano LC (HITACHI, Tokyo, Japan) and Q-Tof Ultima API (Waters, Milford, USA). Chromatographic separation of the peptides took place in a 10 cm fused silica column (50 µm inner diameter) in-house packed with reversed-phase ReproSil-Pur C_{18}-AQ 3 µm resin (Dr. Maisch GmbH, Ammerbuch-Entringen, Germany). Peptide mixtures were injected onto the column with a flow of 200 nl/min and subsequently eluted with a flow of 200 nl/min from 3.8% to 11.6% acetonitrile in 0.5% acetic acid, in a 5 min gradient, from 11.6 % to 26 %, in a 15 min gradient, and from 26% to 69.2%, in a 10 min gradient. Data were acquired in MS mode and data-dependent analysis (DDA) mode using MassLynx software (Waters, Milfold, USA). Proteins were identified via automated database searching (Mascot; Matrix Science, London, United Kingdom) of all tandem mass spectra against an MSIPI database (versions 3.53; European Bioinformatics Institute, www.ebi.ac.uk/IPI/msipi.html). Carbamidomethyl cysteine was set as fixed modification, and oxidized methionine and deamidation of asparagine and glutamine were searched as variable modifications. Initial mass tolerances for protein identification on MS peaks were 100 ppm and on MS/MS peaks were 0.3 Da. Two "missed cleavages" were allowed. The instrument setting for the Mascot search was specified as "ESI-QUAD-TOF". Peptides and proteins were identified using criteria as follows. Peptides which MS2 scores were above the 95th percentile of significant (Mascot score > XX). Only fully tryptic peptides with 6 amino acids or longer were accepted for identification. Proteins were considered positively identified when they were identified with at least two fully tryptic peptides.

Results

Cytotoxicity analysis

Figure 1 shows the survival rates of cells in each treatment condition. The experiments on benzene metabolites were performed thrice, and those on X-ray were performed five times. In Figure 1, error bars were set based on the standard deviations. For chemical exposure, CAT treatment lowered the survival rate to 83.9%, HQ to 84.9%, and CAT+HQ to 69.2%, respectively. CAT and CAT+HQ showed significant decrease in the survival rate of cells ($P < 0.05$), but HQ did not show significant decrease ($P = 0.106$). The X-ray irradiation induced dose-response decrease in the survival rate significantly ($P < 0.01$). 0.5 Gy X-ray lowered the survival rate to 78.9%, 1.0 Gy to 65.2%, and 1.5 Gy to 49.0%, respectively.

2D gel image analysis

Figure 2 shows representative image (control) of silver stained 2D gels obtained from benzene metabolites treatment, and Figure 3 shows representative image (1.5 Gy) of 2D gels from X-ray irradiation. By the image analysis software, over thousand spots per gel were detected in samples, but some of them were too small or faint to be identified, so we manually selected spots enough large and deep to be quantified and identified. As a result, 692 spots per gel were detected in chemical exposure samples and 412 spots per gel were detected in X-ray irradiation samples.

Before the differential analysis, the correlation coefficients between gels were calculated based on normalized volume of each spot in order to check the reproducibility of 2DE. The Calculated values of correlation coefficients are shown in Table 1 and Table 2. Since the total amount of proteins in every gel is equal (50 mg) and the expression levels of most of the proteins remain constant across treatments, so the correlation coefficients between gels are expected to be high. As shown in Table 1 and Table 2, calculated coefficients were large enough (0.695 to 0.930) to enable us to perform differential analysis and to confirm the reproducibility of the experiments.

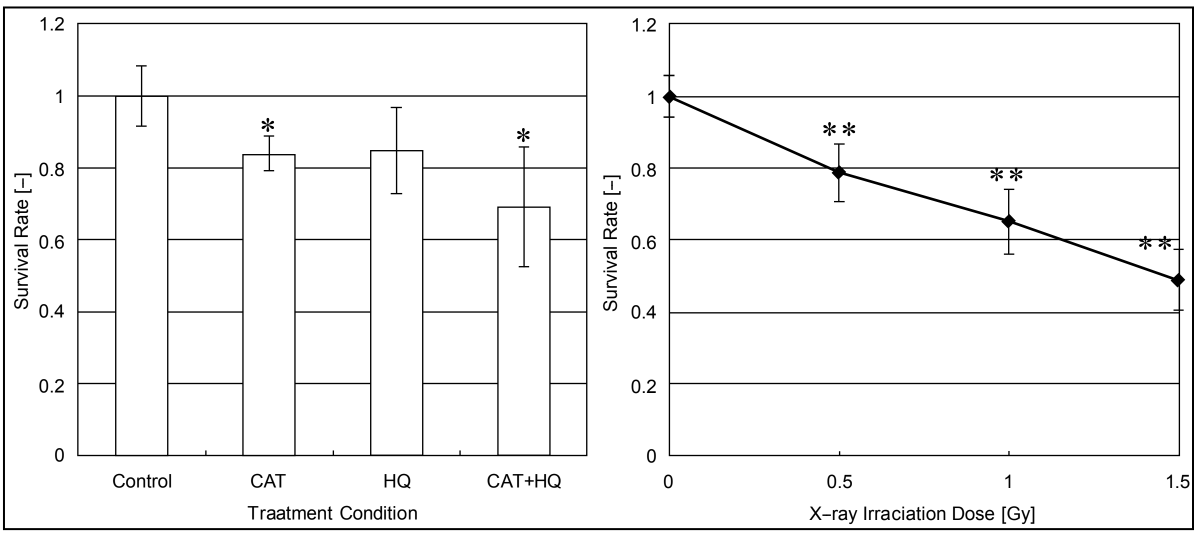

Figure 1: The survival rates of cells in chemical treatment (left) and X-ray irradiation (right).
The marks * and ** mean the significance of difference (*: $P < 0.05$, **: $P < 0.01$) between control and each treatment tested by the Student's t-test.

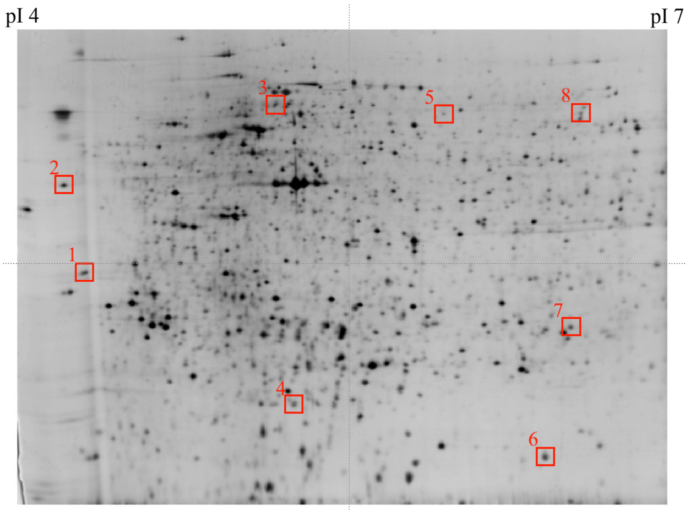

Figure 2: Representative image of gels from benzene metabolites exposure (control). Fifty micrograms of proteins were applied to a pH 3-7 IPG strip (24cm), and with 12.5% constant vertical SDS-PAGE as the second dimension. The gel was visualized by silver staining, and the resulting image was analyzed by PDQuest software. Marked squares show specific spots to exposure.

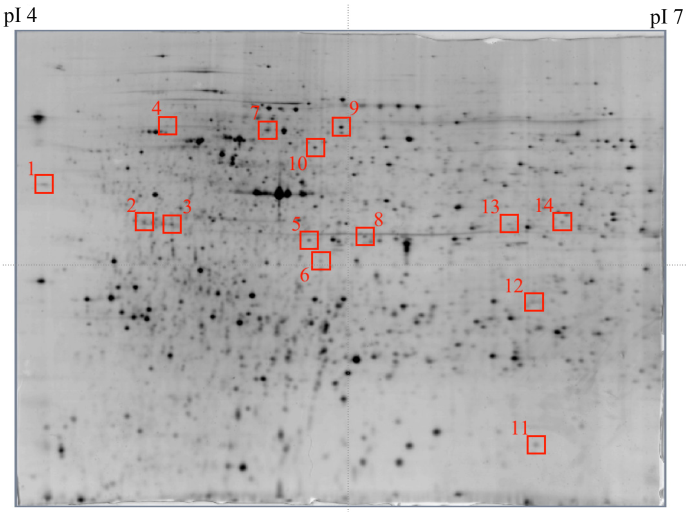

Figure 3: Representative image of gels from X-ray irradiation (1.5Gy). Fifty micrograms of proteins were applied to a pH 3-7 IPG strip (24cm), and with 12.5% constant vertical SDS-PAGE as the second dimension. The gel was visualized by silver staining, and the resulting image was analyzed by PDQuest software. Marked squares show specific spots to exposure.

For the chemical exposure samples, the comparison was performed between the expression levels of proteins in control gels and those in treated gels. For the X-ray irradiation samples, the comparison was performed between the expression levels in 0 Gy gels and those in irradiated gels. The expression levels used for the comparison were the average of expression levels in two or three gels of the same treatment. As a result of differential analysis, we found 8 spots showing at least twofold changes in expression levels by treatment of CAT, HQ or the mixture of them. Also, 14 spots showed more than twofold changes in expression levels by X-ray irradiation. These spots were labeled in Figure 2 and Figure 3. Their expression ratios to control were shown in Table 3. We could not identify some spots specific to X-ray shown as "not identified" in Table 3 because the amounts of these proteins were too low.

Among these specific spots, two proteins, protein SET and cofilin-1, changed their expression levels by both benzene metabolites exposure and X-ray irradiation. The expression of protein SET was decreased by HQ and X-ray exposure, and that of cofilin-1 was decreased by CAT and X-ray exposure.

Discussions

In this study, we extracted proteins from human bone marrow $CD34^+$ cells and performed 2-D gel image analysis. As a result, we found 8 proteins specific to benzene metabolites exposure, and 14 to X-ray irradiation. Especially, we found 2 proteins, protein SET and cofilin-1, where changes common to both benzene metabolites and X-ray exposure were identified. The expression of protein SET was decreased by HQ and X-ray exposure, and that of cofilin-1 was decreased by CAT and X-ray exposure.

Cofilin-1, 18 kD phosphoprotein (p18), controls reversibly actin polymerization and depolymerization. In benign prostatic hyperplasia cells (BPH), LIM kinase 1 (LIMK1) was reported to inactivate phosphorylation of cofilin and result in chromosomal abnormalities, which indicated carcinogenicity in prostate (Davila et al., 2007; Nakano et al., 2003; Pope et al., 2004; Sumi et al., 2006).

Protein SET is a multitasking protein, involved in apoptosis, transcription, nucleosome assembly and histone binding. SET also works as a stimulator for DNA replication of the adenovirus genome complexed with viral core proteins. SET is known as a myeloid leukemia-associated protein, and it was reported that a fusion-protein, SET-CAN, was found in cases of acute undifferentiated leukemia (Adachi et al., 1994; Nagata et al., 1995; Tsujio et al., 2005; von Lindern et al., 1992). In addition, this protein is an inhibitor of protein phosphatase 2A (PP2A) and is thought to play a key role in leukemogenesis by its nuclear localization, protein-protein interactions and PP2A inhibitory activity (Minakuchi et al., 2001). PP2A is a serine/threonine phosphatase and it was reported that the activation of PP2A inhibited the activity of c-Jun N-terminal kinase (JNK), which is thought to play a key role in the control of apoptotic cell death (Shanley et al., 2001). It was also suggested that PP2A be involved in the function of cyclin G which controls the cell cycle and is known to be regulated at the transcriptional level by p53 (Li et al., 2009). Therefore, the decrease of the expression level of SET in this study might imply the excess expression of PP2A, resulting in some troubles in cell cycle such as apoptotic process. Moreover, it was reported that SET suppressed activation of ERK following EGF stimulation, which suggested that SET negatively regulates cell growth by inhibiting the G1/S transition and inhibiting the MEK/ERK pathway stimulated by external stimuli and that SET potentially functions as a tumor suppressor (Fukukawa et al., 2005). Hence, we think that there might be some problems in the control of cell cycle of bone marrow cells because of the decrease of SET by benzene metabolites and X-ray exposure, which suggests that the SET-PP2A-JNK pathway might play an important role in basic leukemogenicity.

In addition, we should pay attention to another two proteins. One is the serine/threonine-protein kinase PAK2, which was specific to the exposure of benzene metabolites, and the other is the COP9 signalosome subunit 5 (COPS5), which was specific to the X-ray exposure. PAK2 is an activated kinase acts on a variety of targets such as phosphorylates ribosomal protein S6, histone H4

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gels	CON1	CON2	CON3	CAT1	CAT2	CAT3	HQ1	HQ2	HQ3	MIX1	MIX2	MIX3
CON1		0.796	0.799	0.743	0.802	0.729	0.781	0.704	0.695	0.834	0.815	0.768
CON2			0.874	0.780	0.878	0.826	0.813	0.807	0.789	0.867	0.857	0.855
CON3				0.846	0.883	0.848	0.830	0.841	0.804	0.868	0.851	0.912
CAT1					0.802	0.784	0.747	0.783	0.754	0.775	0.749	0.829
CAT2						0.847	0.829	0.821	0.788	0.877	0.861	0.858
CAT3							0.792	0.855	0.770	0.831	0.798	0.829
HQ1								0.764	0.776	0.851	0.836	0.824
HQ2									0.808	0.779	0.758	0.825
HQ3										0.777	0.763	0.797
MIX1											0.907	0.857
MIX2												0.839
MIX3												

* 'CON' means control (non-treated), 'MIX' means CAT+HQ.

Table 1: Correlation coefficients between gels of chemical exposure samples.

gels	CON1	CON2	CON3	CAT1	CAT2	CAT3	HQ1	HQ2	HQ3	MIX1	MIX2	MIX3
CON1		0.796	0.799	0.743	0.802	0.729	0.781	0.704	0.695	0.834	0.815	0.768
CON2			0.874	0.780	0.878	0.826	0.813	0.807	0.789	0.867	0.857	0.855
CON3				0.846	0.883	0.848	0.830	0.841	0.804	0.868	0.851	0.912
CAT1					0.802	0.784	0.747	0.783	0.754	0.775	0.749	0.829
CAT2						0.847	0.829	0.821	0.788	0.877	0.861	0.858
CAT3							0.792	0.855	0.770	0.831	0.798	0.829
HQ1								0.764	0.776	0.851	0.836	0.824
HQ2									0.808	0.779	0.758	0.825
HQ3										0.777	0.763	0.797
MIX1											0.907	0.857
MIX2												0.839
MIX3												

Table 2: Correlation coefficients between gels of X-ray irradiation samples.

Spot in Fig 2	Spot in Fig 3	Protein	ratio of expression level							
			CON	CAT	HQ	MIX	0Gy	0.5Gy	1.0Gy	1.5Gy
1	-	Clathrin, light polypeptide A	1	0.50	0.55	0.75	1	not specific		
2	1	Protein SET	1	0.71	0.38[c]	0.80	1	0.47	0.46	0.44
3	-	Keratin-9	1	3.06	2.42	1.50	1	not specific		
4	-	Chromobox homolog 3	1	0.79	0.23[b]	0.81	1	not specific		
5	-	Serine/threonine-protein kinase PAK2	1	1.84	4.47	1.43	1	not specific		
6	11	Cofilin-1	1	0.51	0.85	1.62	1	1.21	0.93	0.32
7	-	Proteasome subunit alpha type-6	1	1.71	2.58[c]	1.38	1	not specific		
8	-	T-complex protein 1 subunit zeta	1	1.81	2.58[a]	0.98	1	not specific		
-	2	Isoform 1 of Protein SET	1	not specific			1	0.49	0.70	0.52
-	3	40s ribosomal protein SA	1	not specific			1	0.99	0.70	0.54
-	4	not identified	1	not specific			1	0.48	0.56	0.49
-	5	highly similar to Actin, cytoplasmic 1	1	not specific			1	0.60	0.55	0.55
-	6	not identified	1	not specific			1	0.36	0.30	0.43
-	7	not identified	1	not specific			1	0.73	0.34[d]	0.69
-	8	CAPZA2 20kDa protein	1	not specific			1	0.56	0.50	0.32[c]
-	9	not identified	1	not specific			1	1.08	0.89	0.38
-	10	not identified	1	not specific			1	1.37	2.04	4.08[a]
-	12	not identified	1	not specific			1	0.33	0.72	0.44
-	13	COP9 signalosome subunit 5 variant	1	not specific			1	0.43	0.36	0.65
-	14	not identified	1	not specific			1	0.69	0.72	0.67

* 'CON' means control (non-treated), 'MIX' means CAT+HQ.

** a, b, c and d mean the significance of difference (a: $P < 0.01$, b: $P < 0.02$, c: $P < 0.05$, d: $P < 0.1$) between control and each treatment tested by the Student's t-test.

*** 'not identified' means the spots which we could not identify because the expression levels of them were too low.

Table 3: Expression levels of specific proteins and results of identification.

and myelin basic protein. This protein stimulates cell survival and cell growth. The process is, at least in part, mediated by phosphorylation and inhibition of pro-apoptotic BAD. Caspase-activated PAK2 is involved in cell death response, probably involving the JNK signaling pathway (Benner et al., 1995; 38. Rudel and Bokoch, 1997; Jakobi et al., 2003; Vilas et al., 2006). COPS5 is a probable protease subunit of the COP9 signalosome complex (CSN), a complex involved in various cellular and developmental processes. The CSN complex is an essential regulator of the ubiquitin (Ubl) conjugation pathway by mediating the deneddylation of the cullin subunits of the SCF-type E3 ligase complexes, leading to decrease the Ubl ligase activity of SCF-type complexes sugh as SCF, CSA or DDB2. The complex is also involved in phosphorylation of p53/TP53, c-jun/JUN, IkappaBalpha/NFKBIA, ITPK1 and ICSBP, possibly via its association with CK2 and PKD kinases. CSN-dependent phosphorylation of TP53 and JUN promotes and protects degradation by the Ubl system, respectively (Dechend et al., 1999; Bech-Otschir et al., 2001; Groisman et al., 2003; Uhle et al., 2003; Kim et al., 2004; Fang et al., 2008). As above, both PAK2 and COPS5 have a possible connection with the JNK signaling pathway as well as SET. Therefore, the changes of their expression levels might also suggest an important role of the SET-PP2A-JNK pathway in leukemogenicity.

While we obtained some proteins that might shed light on the leukemogenesis and might be candidates for biomarkers of leukemia, there were also some problems to be solved. Some of specific proteins detected did not show significant difference of expression levels. Moreover, in X-ray irradiated samples, there were no dose-response decrease of expression levels of proteins detected. These problems occurred mainly because the sample size was small and the variability was still a little large. To solve these problems, additional experiments with larger sample size should be conducted. Besides, more quantitative analysis such as Western blot helps to validate the change of protein expression.

Conclusions

In this study we performed 2-D gel electrophoresis using human bone marrow $CD34^+$ cells for the purpose of finding proteins specific to benzene metabolites and/or X-ray. As a result, we found 8 proteins specific to benzene metabolites exposure, and 14 to X-ray irradiation, which suggest that the SET-PP2A-JNK pathway might play a key role in the mechanisms of the leukemia.

Indeed comprehensive proteomic analyses using 2DE such as this study are useful in obtaining information for the better understanding of the unclear mechanisms of various diseases. However, it is also true that 2DE lacks the quantitative accuracy and that the validation of the results is necessary. Therefore, more quantitative analyses such as Western blot are needed in order to validate the changes of protein expressions identified in this study. In addition, further approaches such as dose-response analysis designed to include more than two exposure conditions, proteomic analysis on other leukemogens, and gene analysis as represented by DNA microarray will shed more light on the leukemogenesis.

References

1. Adachi Y, Pavlakis GN, Copeland TD (1994) Identification and characterization of SET, a nuclear phosphoprotein encoded by the translocation break point in acute undifferentiated leukemia. J Biol Chem 269: 2258-62. » CrossRef » PubMed » Google Scholar
2. Bech-Otschir D, Kraft R, Huang X, Henklein P, Kapelari B, et al. (2001) COP9 signalosome-specific phosphorylation targets p53 to degradation by the ubiquitin system. EMBO J 20: 1630-9. » CrossRef » PubMed » Google Scholar
3. BEIR (1980) The effects on populations of exposure to low levels of ionizing radiation. Washington D. C., USA: National Academy Press. » CrossRef » PubMed » Google Scholar
4. Benner GE, Dennis PB, Masaracchia RA (1995) Activation of an S6/H4 kinase (PAK 65) from human placenta by intramolecular and intermolecular autophosphorylation. J Biol Chem 270: 21121-8. » CrossRef » PubMed » Google Scholar
5. Bertell R (1984) Handbook for estimation health effects from exposure to ionizing radiation. Toronto, Canada: Institute of Concern for Public Health. » CrossRef » PubMed » Google Scholar
6. CERI (1997) Chemical Substances Hazard Assessment Report: Benzene. Available at: http://qsar.cerij.or.jp/SHEET/F96_01.pdf. Accessed on 6 October, 2009. » CrossRef » PubMed » Google Scholar
7. Davila M, Jhala D, Ghosh D, Grizzle WE, Chakrabarti R (2007) Expression of LIM kinase 1 is associated with reversible G1/S phase arrest, chromosomal instability and prostate cancer. Mol Cancer 6: 40. » CrossRef » PubMed » Google Scholar
8. Dechend R, Hirano F, Lehmann K, Heissmeyer V, Ansieau S, et al. (1999) The Bcl-3 oncoprotein acts as a bridging factor between NF-kappaB/Rel and nuclear co-regulators. Oncogene 18: 3316-23. » CrossRef » PubMed » Google Scholar
9. Deininger MW, Bose S, Gora-Tybor J, Yan XH, Goldman JM, et al. (1998) Selective induction of leukemia-associated fusion genes by high-dose ionizing radiation. Cancer Res 58: 421-5. » CrossRef » PubMed » Google Scholar
10. Domracheva EV, Aseeva EA, Udovichenko AI, Obukhova TN, Ol'shanskaia IuV, et al. (2002) Induced leukemias and their connection with radiation exposure. Radiats Biol Radioecol 42: 715-9. » CrossRef » PubMed » Google Scholar
11. Eastmond DA, Mondrala ST, Hasegawa L (2005) Topoisomerase II inhibition by myeloperoxidase-activated hydroquinone: a potential mechanism underlying the genotoxic and carcinogenic effects of benzene. Chem Biol Interact 153-4: 207-16. » CrossRef » PubMed » Google Scholar
12. Eastmond DA, Mondrala ST, Hasegawa L (2008) Characterization of the human COP9 signalosome complex using affinity purification and mass spectrometry. J Proteome Res 7: 4914-25. » CrossRef » PubMed » Google Scholar
13. Fukukawa C, Shima H, Tanuma N, Okada T, Kato N, et al. (2005) The oncoprotein I-2PP2A/SET negatively regulates the MEK/ERK pathway and cell proliferation. Int J Oncol 26: 751-6. » CrossRef » PubMed » Google Scholar
14. Groisman R, Polanowska J, Kuraoka I, Sawada J, Saijo M, et al. (2003) The ubiquitin ligase activity in the DDB2 and CSA complexes is differentially regulated by the COP9 signalosome in response to DNA damage. CELL 113: 357-67. » CrossRef » PubMed » Google Scholar
15. Hirai H (1994) Hakketsubyo no Bunshiigaku. Tokyo, Japan: Yodosha. » CrossRef » PubMed » Google Scholar
16. Honda T, Tamura G, Endoh Y, Nishizuka S, Kawata S, et al. (2005) Expression of Tumor Suppressor and Tumor-related Proteins in Differentiated Carcinoma, Undifferentiated Carcinoma with Tubular Component and Pure Undifferentiated Carcinoma of the Stomach. Jpn J Clin Oncol 35: 53. » CrossRef » PubMed » Google Scholar
17. Iida H (2009) Hoshasen Gairon. Tokyo, Japan: Tsusyo Sangyo Kenkyusha. » CrossRef » PubMed » Google Scholar
18. IPCS (1993) Environmental Health Criteria 150: Benzene. Available at: http://www.inchem.org/documents/ehc/ehc/ehc150.htm. Accessed on 1 May, 2009. » CrossRef » PubMed » Google Scholar
19. Irons RD (1985) Quinones as toxic metabolites of benzene. J Toxicol Environ Health 16: 673-8. » CrossRef » PubMed » Google Scholar
20. Jakobi R, McCarthy CC, Koeppel MA, Stringer DK (2003) Caspase-activated PAK-2 is regulated by subcellular targeting and proteasomal degradation. J Biol Chem 278: 38675-85. » CrossRef » PubMed » Google Scholar

21. Jensen ON, Podtelejnikov A, Mann M (1996) Delayed extraction improves specificity in database searches by matrix-assisted laser desorption/ionization peptide maps. Rapid Commun Mass Spectrom 10: 1371-8. » CrossRef » PubMed » Google Scholar

22. Kim BC, Lee HJ, Park SH, Lee SR, Karpova TS, et al. (2004) Jab1/CSN5, a component of the COP9 signalosome, regulates transforming growth factor beta signaling by binding to Smad7 and promoting its degradation. Mol Cell Biol 24: 2251-62. » CrossRef » PubMed » Google Scholar

23. Kumagai J, Masui K, Itagaki Y, Shiotani M, Kodama S, et al. (2003) Long-lived mutagenic radicals induced in mammalian cells by ionizing radiation are mainly localized to proteins. Radiat Res 160: 95-102. » CrossRef » PubMed » Google Scholar

24. Levay G, Bodell WJ (1992) Potentiation of DNA adduct formation in HL-60 cells by combinations of benzene metabolites. Proc Natl Acad Sci USA 89: 7105-9. » CrossRef » PubMed » Google Scholar

25. Li H, Okamoto K, Peart MJ, Prives C (2009) Lysine-independent turnover of cyclin G1 can be stabilized by B'alpha subunits of protein phosphatase 2A. Mol Cell Biol 29: 919-28. » CrossRef » PubMed » Google Scholar

26. Lindsey RH, Bender RP, Osheroff N (2005) Stimulation of topoisomerase II-mediated DNA cleavage by benzene metabolites. Chem Biol Interact 153-4: 197-205. » CrossRef » PubMed » Google Scholar

27. McHale CM, Lan Q, Corso C, Li G, Zhang L, et al. (2008) Chromosome translocations in workers exposed to benzene. J Natl Cancer Inst Monogr 39: 74-7. » CrossRef » PubMed » Google Scholar

28. Minakuchi M, Kakazu N, Gorrin-Rivas MJ, Abe T, Copeland TD, et al. (2001) Identification and characterization of SEB, a novel protein that binds to the acute undifferentiated leukemia-associated protine SET. Eur J Biochem 268: 1340-51. » CrossRef » PubMed » Google Scholar

29. Muller HJ (1927) Artificial Transmutation of the Gene. Science 66: 84-7. » CrossRef » PubMed » Google Scholar

30. Nagata K, Kawase H, Handa H, Yano K, Yamasaki M, et al. (1995) Replication factor encoded by a putative oncogene, set, associated with myeloid leukemogenesis. Proc Natl Acad Sci USA 92: 4279-83. » CrossRef » PubMed » Google Scholar

31. Nakano K, Kanai-Azuma M, Kanai Y, Moriyama K, Yazaki K, et al. (2003) Cofilin phosphorylation and actin polymerization by NRK/NESK, a member of the germinal center kinase family. Exp Cell Res 287: 219-27. » CrossRef » PubMed » Google Scholar

32. Parke DV (1996) Personal reflections on 50 years of study of benzene toxicology. Environ Health Perspect 104: 1123-8. » CrossRef » PubMed » Google Scholar

33. Pope BJ, Zierler-Gould KM, Kühne R, Weeds AG, Ball LJ (2004) Solution structure of human cofilin: actin binding, pH sensitivity, and relationship to actin-depolymerizing factor. J Biol Chem 279: 4840-8. » CrossRef » PubMed » Google Scholar

34. Preston DL, Kusumi S, Tomonaga M, Izumi S, Ron E, et al. (1994) Cancer incidence in atomic bomb survivors. Part III. Leukemia, lymphoma and multiple myeloma, 1950-1987. Radiat Res 137: S68-97. » CrossRef » PubMed » Google Scholar

35. Rappsilber J, Ishihama Y, Mann M (2003) Stop and go extraction tips for matrix-assisted laser desorption/ionization, nanoelectrospray, and LC/MS sample pretreatment in proteomics. Anal Chem 75: 663-70. » CrossRef » PubMed » Google Scholar

36. Robertson ML, Eastmond DA, Smith M (1991) Two benzene metabolites catechol and hydroquinone produce a synergistic induction of micronuclei and toxicity in cultured human lymphocytes. Mutat Res 249: 201-9. » CrossRef » PubMed » Google Scholar

37. Rothman N, Bechtold WE, Yin SN, Dosemeci M, Li GL, et al. (1998) Urinary excretion of phenol, Catechol, hydroquinone, and muconic acid by workers occupationally exposed to benzene. Occup Environ Med 55: 705-11. » CrossRef » PubMed » Google Scholar

38. Rudel T, Bokoch GM (1997) Membrane and morphological changes in apoptotic cells regulated by caspase-mediated activation of PAK2. Science 276: 1571-4. » CrossRef » PubMed » Google Scholar

39. Sammett D, Lee EW, Kocsis JJ, Snyder R (1979) Partial hepatectomy reduces both metabolism and toxicity of benzene. J Toxicol Environ Health 5: 785-92. » CrossRef » PubMed » Google Scholar

40. Schnatter AR, Rosamilia K, Wojcik NC (2005) Review of the literature on benzene exposure and leukemia subtypes. Chem Biol Interact 153-4: 9-21. » CrossRef » PubMed » Google Scholar

41. Shanley TP, Vasi N, Denenberg A, Wong HR (2001) The serine/threonine phosphatase, PP2A: endogenous regulator of inflammatory cell signaling. J Immunol 166: 966-72. » CrossRef » PubMed » Google Scholar

42. Stillman WS, Varella-Garcia M, Irons RD (1999) The benzene metabolites hydroquinone and catechol act in synergy to incude dose-dependent hypoploidy and -5q31 in a human cell line. Leuk Lymphoma 35: 269-81. » CrossRef » PubMed » Google Scholar

43. Sumi T, Hashigasako A, Matsumoto K, Nakamura T (2006) Different activity regulation and subcellular localization of LIMK1 and LIMK2 during cell cycle transition. Exp Cell Res 312: 1021-30. » CrossRef » PubMed » Google Scholar

44. Suzuki M, Suzuki K, Kodama S, Watanabe M (2005) Interstitial chromatin alteration causes persistens p53 activation involved in the radiation-induced senescence-like growth arrest. Biochem Biophys Res Commun 340: 145-50. » CrossRef » PubMed » Google Scholar

45. Tsujio I, Zaidi T, Xu J, Kotula L, Grundke-Iqbal I, et al. (2005) Inhibitors of proteins phosphatase-2A from human brain structures, immunocytological localization and activities towards dephosphorylation of the Alzheimer type hyperohorylated tau. FEBS Lett 579: 363-72. » CrossRef » PubMed » Google Scholar

46. Uhle S, Medalia O, Waldron R, Dumdey R, Henklein P, et al. (2003) Protein kinase CK2 and protein kinase D are associated with the COP9 signalosome. EMBO J 22: 1302-12. » CrossRef » PubMed » Google Scholar

47. Urushibara A, Kodama S, Suzuki K, Desa MB, Suzuki F, et al. (2004) Involvement of telomere dysfunction in the induction of genomic instability by radiation in scid mouse cells. Biochem Biophys Res Commun 313: 1037-43. » CrossRef » PubMed » Google Scholar

48. Vilas GL, Corvi MM, Plummer GJ, Seime AM, Lambkin GR, et al. (2006) Posttranslational myristoylation of caspase-activated p21-activated protein kinase 2 (PAK2) potentiates late apoptotic events. Proc Natl Acad Sci USA 103: 6542-7. » CrossRef » PubMed » Google Scholar

49. von Lindern M, van Baal S, Wiegant J, Raap A, Hagemeijer A, et al. (1992) Can, a putative oncogene associated with myeloid leukemogenesis, may be activated by fusion of its 3' half to different genes: characterization of the set gene. Mol Cell Biol 12: 3346-55. » CrossRef » PubMed » Google Scholar

50. Wilm M, Shevchenko A, Houthaeve T, Breit S, Schweigerer L, et al. (1996) Femtomole sequencing of proteins from polyacrylamide gels by nano-electrospray mass spectrometry. Nature 379: 466-9. » CrossRef » PubMed » Google Scholar