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Role of DNA Methylation in Cell Cycle Arrest Induced by Cr (VI) in Two Cell Lines

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Abstract

Hexavalent chromium [Cr(IV)], a well-known industrial waste product and an environmental pollutant, is recognized as a human carcinogen. But its mechanisms of carcinogenicity remain unclear, and recent studies suggest that DNA methylation may play an important role in the carcinogenesis of Cr(IV). The aim of our study was to investigate the effects of Cr(IV) on cell cycle progress, global DNA methylation, and DNA methylation of p16 gene. A human B lymphoblastoid cell line and a human lung cell line A549 were exposed to 5–15 μM potassium dichromate or 1.25–5 $\mu g/cm^2$ lead chromate for 2–24 hours. Cell cycle was arrested at G_1 phase by both compounds in 24 hours exposure group, but global hypomethylation occurred earlier than cell cycle arrest, and the hypomethylation status maintained for more than 20 hours. The mRNA expression of p16 was significantly up-regulated by Cr(IV), especially by potassium dichromate, and the mRNA expression of cyclin-dependent kinases (CDK4 and CDK6) was significantly down-regulated. But protein expression analysis showed very little change of p16 gene. Both qualitative and quantitative results showed that DNA methylation status of p16 remained unchanged. Collectively, our data suggested that global hypomethylation was possibly responsible for Cr(IV) - induced G_1 phase arrest,but DNA methylation might not be related to up-regulation of p16 gene by Cr(IV).

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Introduction

Chromium (Cr) and its compounds are widely used in many industries such as chromate manufacturing, chrome plating, ferrochrome production and stainless steel welding. Chromium can also be found in the environment in the form of airborne particles from automobile catalytic converters. Hexavalent chromium [Cr (VI)] is one of two major forms of Cr, and it is recognized as a human carcinogen. It is estimated that tens of millions of people are exposed to chromium worldwide [1]. Epidemiological and risk assessment studies have indicated that inhalation exposure to Cr (VI) significantly increases the risk of respiratory cancer, especially lung cancer, in workers [2]. There are three well-accepted general carcinogenic paradigms which include multistage carcinogenesis, genomic instability and epigenetic modifications [3]. Since epigenetics was first introduced by Conrad Waddington in 1942, people are paying more and more attention to it, which plays a significant role in phenotypic expression. Epigenetic modifications are heritable changes in gene expression that occur without changes in DNA sequences [4], and DNA methylation is one of the most common and best understood epigenetic mechanisms [5]. Global DNA hypomethylation is generally associated with chromosomal instability, and hypermethylation at promoter of specific gene may silence the expression of this gene [6].

Some *in-vitro* and human investigations about Cr (VI)-induced DNA methylation have been conducted/carried out so far. It was reported that exposure to potassium chromate was able to induce promoter methylation of *gpt* transgene in Chinese hamster G12 lung cells [7]. A study about genetic and DNA methylation changes in Brassica napusL. plants showed that potassium dichromate induced genome-wide DNA hypermethylation in the CCGG-sequence and the effect was dose-dependent [8]. Meanwhile, methylation of p16 gene has been frequently found in chromate lung cancers [9,10]. More interestingly, Kondo et al. [10] found that more than 80% of the chromate lung cancers showed repression of the p16 protein. Therefore, it was suggested that methylation of p16 was closely associated with chromate lung cancers, but the question is whether the methylation of p16 is the cause of chromate lung cancer, or just the consequence of cancer? p16 is located on chromosomal arm 9p and is a tumor suppressor gene. The product of p16 gene is an inhibitor of CDK 4/6, which phosphorylates the serine/threonine residues of the tumor suppressor retinoblastoma [8], and plays an important role in inhibiting cell cycle progression [10,11].

Previous studies indicated that Cr (VI) could cause cell cycle arrest in HeLa cells, human lung epithelial A549 cells, human lymphoma U937 cells, p53 mutated cells [11], human lung epithelial H460 cells and primary human lung IMR90 fibroblasts [12]. Stanley et al. [13]reported that Cr (VI) could arrest cell cycle by down-regulating cyclin-dependent kinases (CDK4, CDK6, CDK1) and up-regulating CDK-inhibitor (p16) in both primary and immortalized granulosa cells from rats. But no study has been performed in human lymphocytes or related cell lines, and the mechanism of up-regulating p16 gene remains unclear. Also few study compared the difference of cell cycle arresting effects and the underlying mechanisms between soluble and particulate Cr (VI). Although both soluble and particulate Cr (VI) are cytotoxic and genotoxic to human lung epithelial cells [14], and human and sperm whale skin cells [15], the effects of these two types of chromate on methylation status of *gpt* gene in a transgenic Chinese hamster lung cell line with a bacterial *gpt* reporter gene were different. Partial methylation in the *gpt* gene was found after soluble Cr (VI) exposure, but no methylation changes after particulate Cr (VI) exposure [7].

In the present study, a human B lymphoblastoid cell line and a human lung cell line A549 were exposed to different concentrations of soluble ($K_2Cr_2O_7$) or particulate ($PbCrO_4$) chromate. Cell cycle progression and cell cycle regulatory gene expressions were analyzed in samples treated with Cr (VI), and the global DNA methylation level and methylation status of p16 gene were also detected. The aim of our study is to investigate the relationship between DNA methylation and cell cycle progression, and to compare the difference of cell cycle arresting effects and its possible mechanisms between soluble and particulate Cr (VI).

Materials and Methods

Cell Culture and Treatments

Human B lymphoblastoid cell line was purchased from Cell Bank, Chinese Academy of Sciences, and it was cultured in IMDM (HyClone, USA) supplemented with 10% fetal bovine serum (HyClone, USA). A549, a human lung cell line, was kindly provided by Professor Z. Y. Jia (Zhejiang Academy of Medical Sciences, P. R. CHINA) and cultured in RPMI-1640 supplemented with 10% fetal bovine serum (HyClone, USA). Cells were maintained at 37°C in a fully humidified atmosphere with 5% CO2, and they were subcultured every 2–3 days.

Cells were exposed to potassium dichromate ($K_2Cr_2O_7$, Sigma, USA) or lead chromate ($PbCrO_4$, Sigma,USA). The concentrations of potassium dichromate were 0 μM, 5.0 μM, 10 μM, and 15 μM, and the concentrations of lead chromate were 0 $\mu g/cm^2$, 1.25 $\mu g/cm^2$, 2.5 $\mu g/cm^2$, and 5 $\mu g/cm^2$. The exposure time was 2 hours or 24 hours for potassium dichromate, and 4 hours or 24 hours for lead chromate. Solutions of potassium dichromate were prepared by dissolving it in double distilled water, and then sterilized through a 10 ml syringe with a 0.2 μM filter. Suspension of lead chromate was made according to descriptions by Wise et al. [14].

Cell Cycle Analysis

Cells treated with potassium dichromate or lead chromate were collected, rinsed twice with cold PBS, and then fixed in ice cold 70% ethanol and kept at 4°C overnight. Subsequently, the cells were treated with DNase-free RNase and stained with propidium iodide in staining buffer using Cell Cycle Analysis Kit (Byotime, China) for 30 minutes at 37°C. The number of cells distributed in G1, S, and G2-M phases of the cell cycle was counted on a flow cytometer (BD, USA) using Cell Quest software.

Total RNA Extraction

Total RNA was extracted from cells using Trizol® reagent (Invitrogen, USA) according to manufacturer's protocols. The purity and concentrations of extracted RNA were determined by a NanoDrop 2000 (Thermo Scientific, USA) spectrophotometer.

DNA Extraction and Bisulfite Modification

DNA was extracted from cells using DNA extraction Kit for cells and tissues (OMEGA BioTek, USA) following the manufacturer's protocols. DNA from each sample was treated with sodium bisulfite using the EZ DNA Methylation-Gold™ Kit (Zymo Research, Orange, USA) according to manufacturer's protocol.

Detection of Global Methylation Patterns

MethylFlash™ Methylated DNA Quantification Kit (Epigentek, Brooklyn, USA) was used for detecting global methylation status of the DNA isolated from Cr (VI) treated samples. All procedures were carried out according to manufacturer's protocol. To determine the relative methylation status of two different DNA samples, simple calculation for percentage of 5-methylcytosine (5-mC) in total DNA can be carried out using the following formula:

$$5-mC\% = \frac{(SampleRFU - MF3RFU) \div S}{(MF4RFU - MF3RFU) \times 2^{*} \div P} \times 100\%$$

S is the amount of input sample DNA in ng, P is the amount of input positive control (MF4) in ng, MF3 = negative control, RFU = relative fluorescence units.

Methylation Specific PCR (MSP)

The methylation status of the promoter of the p16 gene was determined by MSP according to the description of Kondo et al. [10]. The primer sequences for detecting the methylated p16 gene were 5′-TTATTAGAGGGTGGGGCGGATCGC-3′ (forward) and 5′-GACCCCGAACCGCGACCGTAA-3′ (reverse), which amplified a 150-bp product. The primer sequence for the unmethylated reaction were 5′- TTATTAGAGGGTGGGGTGGATTGT-3′ (forward) and 5′-CCACCTAAATCAACCTCCAACCA-3′, giving an amplification product of 234 bp. MSP amplification for the p16 gene was carried out in a final volume of 25 μl, 12.5 μl Zymo *Taq*™ PreMix, 1.2 μl primers, 2 μl DNA template, 9.3 μl ddH_2O. Amplification was performed in a PTC-200 DNA Engine Thermal Cycler machine (Bio-Red, USA). The PCR conditions for MSP were as follows: hot start at 95°C for 10 min; then 35 cycles (30s at 95°C for denaturation, 30s at 68°C (methylated gene) or 64°C (unmethylated gene) for annealing, 50s at 72°C for elongation followed by 5min at 72°C for extension. The methylated (M) and unmethylated (U) control DNA (Qiagen, Germany) were used as a positive control for the methylated and unmethylated p16 gene, respectively. Five microliter of each PCR reaction was directly loaded onto a 3% agarose gel, stained with GelRed™ Nucleic Acid Gel Stain (Biotium, USA) and visualized under UV illumination using the Alpha Innotech FluorChem® FC2 Imager (Alpha Innotech, USA) to determine if there is a visible band and discriminate the size of the PCR products according to bands of the marker.

Primer Design and Pyrosequencing

Primers were designed by using the PSQ assay design program (Biotage, Charlotte, NC, USA). The primer sequences of p16 were 5′-AGGGGTTGGTTGGTTATTAG-3′ (forward) and 5′-biotin-CTACCTACTCTCCCCCTCTC-3′ (reverse) for PCR amplifying a part of CPG islands, and 5′-GGTTGGTTATTAGAGGGT-3′ for pyrosequencing. PCR reaction was performed in a volume of 25 μl with 1.5 μl converted gDNA, 12.5 μl *Taq*™ PreMix (CoWin, Beijing, China), 0.8 μl primers, 10.2 μl ddH_2O.

The amplification condition was as following: denaturating at 95°C for 10 minutes, followed by 45 cycles at 95°C for 30 seconds, at 58°C (B cells) or 62°C (A549 cells) for 40 seconds, at 72°C for 30 seconds and a final extension at 72°C for 10 minutes. Confirmation of PCR product quality was established on 1.5% agarose gel stained with GelRed. Pyrosequencing was performed using the PyroMark Q24 System (Qiagen, Germany) according to manufacturer's instructions.

mRNA Quantification by Real-time Quantitative PCR (RT-qPCR)

First-strand cDNA was synthesized by reverse transcription of total RNA with PrimeScript® RT reagent Kit (TaKaRa, China). Quantitative PCR was performed in triplicate per sample for each gene using the SYBR Green PCR system (SYBR Premix Ex Taq^{TM}, TaKaRa, China) under the following conditions: 95°C for 1 minute and immediately repetitively cycled 40 times through a denaturing step at 95°C for 5s and an annealing-elongation step at 64°C (p16 and CDK6) or 60°C (GAPDH) for 20s. The primer sequences were as follows: p16 5′-GGCACCAGAGGCAGTAACCA-3′ (forward) and 5′-CCTACGCATGCCTGCTTCTACA-3′, (reverse), CDK6 5′-GTGACCAGCAGCGGACAAATAA-3′ (forward) and 5′-AGCAAGACTTCGGGTGCTCTGTA-3′ (reverse), CDK4 5′-TTCTGCAGTCCACATATGCAACA-3′ (forward) and 5′-GGTCGGCTTCAGAGTTTCCAC -3′ (reverse), and GAPDH 5′- GAAGGTGAAGGTCGGAGTC -3′ (forward) and 5′-GAAGATGGTGATGGGATTTC -3′ (reverse). Relative fold change was determined using the comparative C_t method using GAPDH as endogenous control [16].

Western Blot

Total cell lysates were resolved by SDS-PAGE and transferred to PVDF membranes (Millipore, Billerica, USA), and membranes were blocked and incubated with primary antibodies against p16 (Epitomics, California, USA) and tublin (Huabio, Hangzhou, China) at 4°C over night. Antibody binding was detected with horseradish peroxidase-conjugated antibodies (Huabio, Hangzhou, China) and enhanced chemiluminescence (Millipore, Billerica, USA). Reactive bands were analyzed using Image-Pro Plus program (Media Cybernetics, Inc. USA), and the target protein expression was normalized with respect to tublin expression.

Statistical Analyses

One-way ANOVA was used to compare the effects among various treatment groups. Where significant differences were found, Dunnett's multiple comparison test (equal variances not assumed) or LSD (equal variances assumed) was applied to make post hoc comparison between the means of controls and treatments. Differences were considered significant at $P<0.05$ for two-tailed tests. Statistical analysis was performed with SPSS 11.0 for windows.

Results

Cell Cycle Arrest Induced by Cr (VI)

The effects of Cr (VI) on cell cycle were determined in human B lymphoblastoid cells. In 24 hours exposure group, the percentages of G_1-phase cells in samples treated with $K_2Cr_2O_7$ (Fig. 1-B) increased significantly ($p<0.01$) in a concentration dependent manner, and the percentages of G_1-phase cells in samples treated with $PbCrO_4$ were also significantly ($p<0.01$) higher than those in controls (Fig. 1-D). Conversely, the percentages of S-phase cells in samples treated with soluble or particulate chromate were significantly ($p<0.05$, $p<0.01$) lower than those in controls. No significant ($P>0.05$) changes of the percentages of G_2-phase cells were observed in both soluble and particulate chromate treatment groups (Fig. 1-B, D). In 2-hour or 4-hour exposure group, significant change was only observed in the percentages of S-phase cells in samples exposed to 5 μg/cm^2 $PbCrO_4$, which was significantly ($p<0.05$) higher than those in controls (Fig. 1-C).

The effects of Cr (VI) on cell cycle of A549 cells were similar to those of human B lymphoblastoid cells, but there were also some differences between these two cell lines. No significant ($P>0.05$) change of cell cycle of A549 cells was observed in short-term (2 hours or 4 hours) exposure group (Fig. 1-E, G). Cells were significantly ($p<0.05$, $p<0.01$) arrested at G1 phase by both chromium compounds, and the percentages of G2/M-phase cells decreased significantly ($p<0.05$, $p<0.01$) (Fig. 1-F, H).

Global Hypomethylation Induced by Cr (VI)

Global methylation status was analyzed by measuring the percentage of 5-mC in total DNA from cells treated with Cr (VI), and the change of global methylation in both cell lines was similar. The global methylation levels of DNA samples from these two cell lines without treatment were below 0.3% (Fig. 2). Both $K_2Cr_2O_7$ and $PbCrO_4$ could decrease the percentages of 5-mC in total DNA in a concentration dependent manner. Significant ($p<0.01$) decrease of global methylation levels were observed at all concentrations of both two chromate compounds, compared with that of controls, except of 5 μM of $K_2Cr_2O_7$ (Fig. 2). In human B lymphoblastoid cells, the decrease of global methylation levels was more obvious in short-term (2 or 4 hours) exposure groups than those in long-term (24 hours) exposure groups, but it was not so obvious in A549 cells.

DNA Methylation Status at the Promoter of p16 gene

The DNA methylation status of p16 was qualitatively determined with MSP. Our results indicated that the promoter of p16 gene in both cell lines was completely methylated, and neither $K_2Cr_2O_7$ nor $PbCrO_4$ could reduce the methylation level of p16 gene, even at the highest concentrations (Fig. 3). To further quantitatively analyze the effect of Cr (VI) on the methylation of p16 gene, pyrosequencing was performed after PCR amplification. The results were consistent with that of MSP, and the percentages of methylation at the promoter of p16 gene were higher than 94% in all samples treated with Cr (VI) and controls (Fig. 4).

Cr (VI) Up-regulated mRNA level of *p*16

Real-time quantitative PCR was utilized to assess the effects of Cr (VI) on mRNA expression of p16 gene. In the $K_2Cr_2O_7$ exposure group, no significant ($P>0.05$) change was observed after 2 hours exposure, but mRNA levels of p16 in human B lymphoblastoid cells increased significantly ($P<0.01$) in a concentration dependent manner when exposure time was extended to 24 hours (Fig. 5-A), and significant ($P<0.01$) increase was only observed at moderate and high exposure groups in A549 cells (Fig. 5-C). In the $PbCrO_4$ exposure group, no significant ($P>0.05$) difference of mRNA levels of p16 was found between samples treated with $PbCrO_4$ for 4 hours and controls. Significant change of mRNA levels of p16 in human B lymphoblastoid cells was only observed at 2.5 μg/cm^2 of $PbCrO_4$ after 24 hours exposure (Fig. 5-B), and significant ($P<0.01$) increase was found at moderate and high exposure groups in A549 cells (Fig. 5-D).

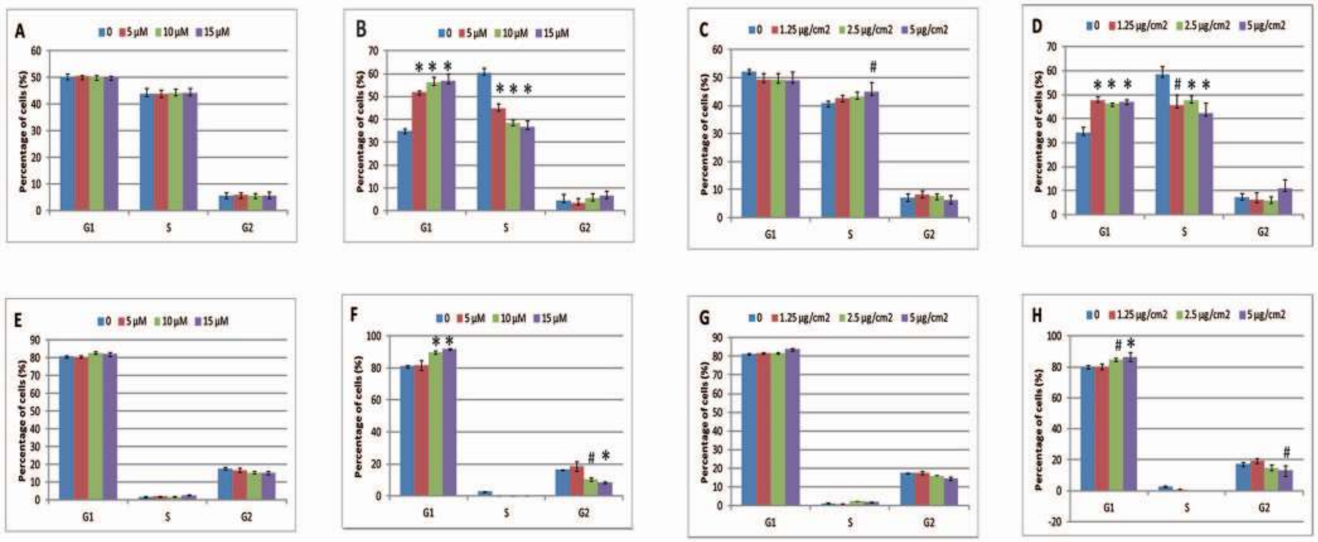

Figure 1. Cr (VI)-induced cell cycle arrest in two cell lines. The concentrations of potassium dichromate were 0, 5 μM, 10 μM, and 15 μM, and the concentrations of lead chromate were 0, 1.25 μg/cm^2, 2.5 μg/cm^2, and 5.0 μg/cm^2. A–B:Percentages of human B lymphoblastoid cells at G_1, S, and G_2 phases after being exposed to potassium dichromate for 2 hours (A) and 24 hours (B). C–D: Percentages of human B lymphoblastoid cells at G_1, S, and G_2 phases after being exposed to lead chromate for 4 hours (C) and 24 hours (D). E–F:Percentages of A549 cells at G_1, S, and G_2 phases after being exposed to potassium dichromate for 2 hours (E) and 24 hours (F). G–H: Percentages of A549 cells at G_1, S, and G_2 phases after being exposed to lead chromate for 4 hours (G) and 24 hours (H). Hash keys above the bars: $P<0.05$ as compared with control; asterisks above the bars: $P<0.01$ as compared with control.

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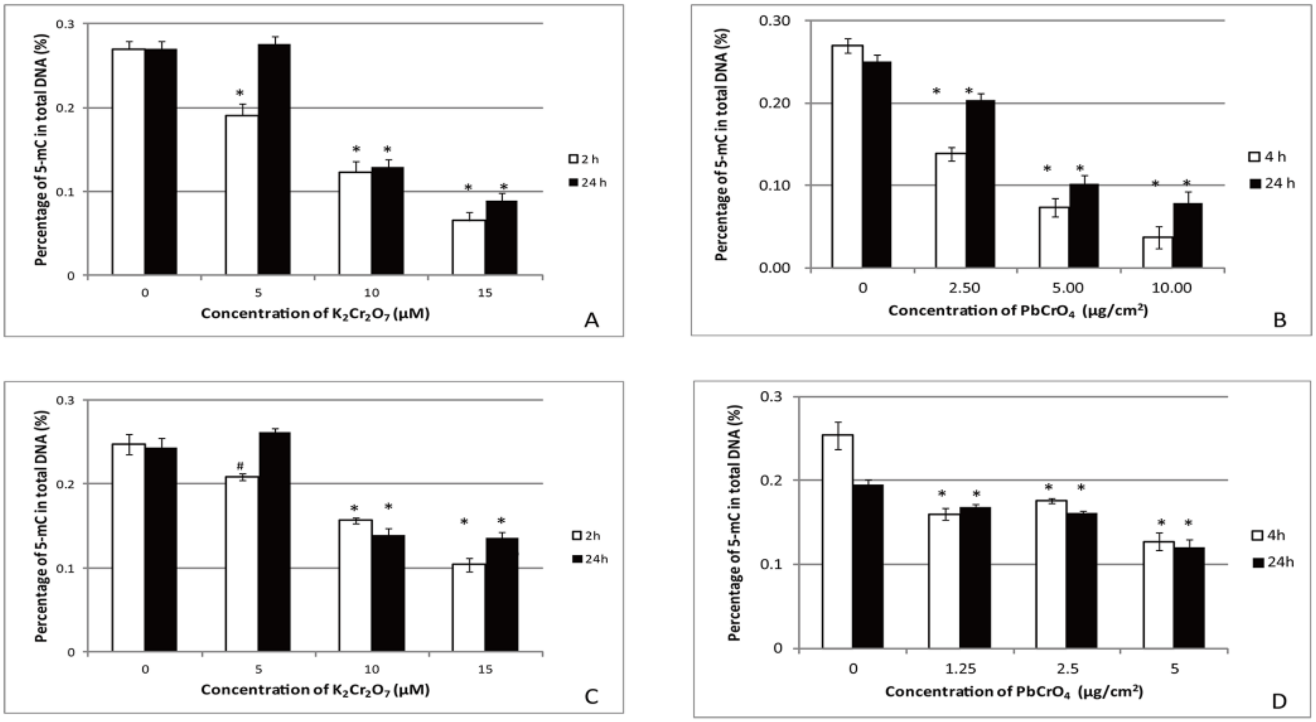

Figure 2. Global hypomethylation induced by Cr (VI) in two cell lines. A and C: Percentages of 5-methyl-cytosine (5-mC) in DNA extracted from human B lymphoblastoid cells (A) and from A549 cells (C) treated with potassium dichromate for 2 hours and 24 hours. B and D: Percentages of 5-methyl-cytosine (5-mC) in DNA extracted from human B lymphoblastoid cells (B) and from A549 cells (D) treated with lead chromate for 4 hours and 24 hours. Asterisks above the bars indicate that the difference between exposure and control was significant ($P<0.01$).

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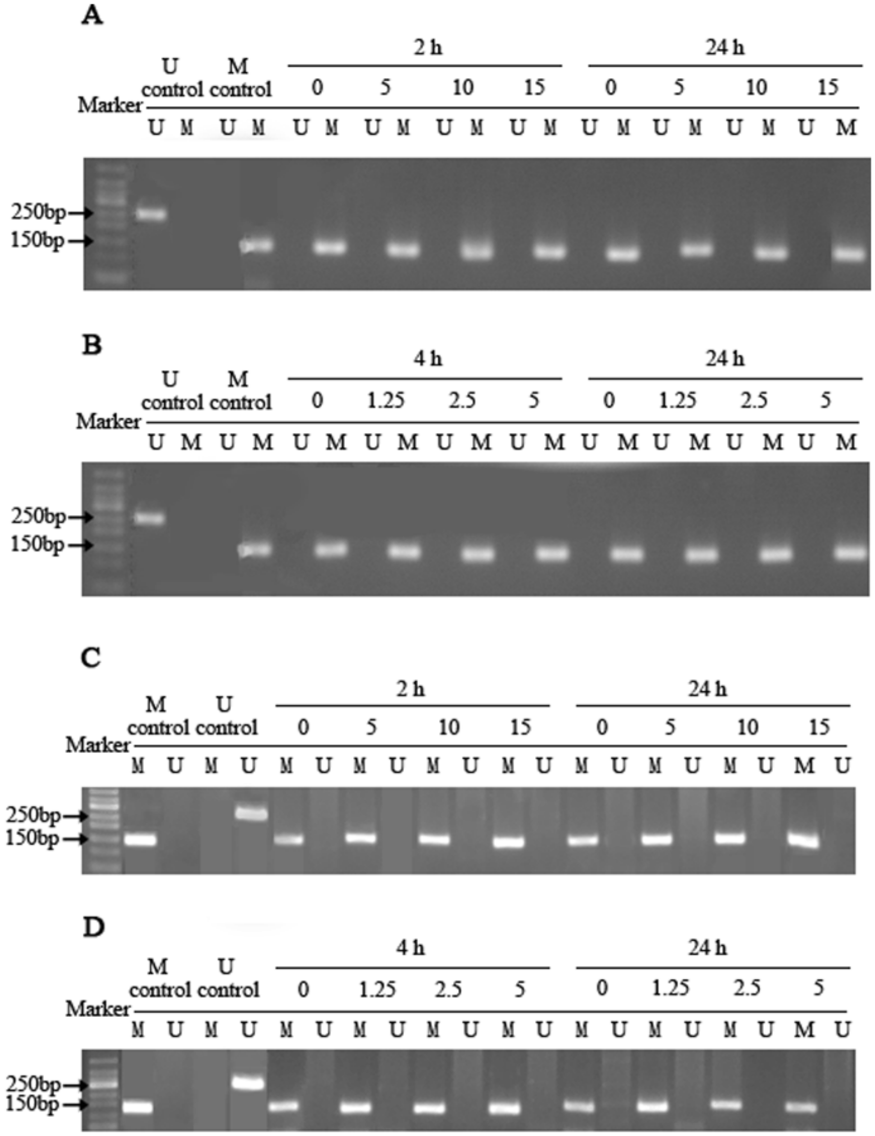

Figure 3. MSP analysis of p16 gene. Primer sets utilized for PCR amplification are designated as unmethylated (U) or methylated (M), and the amplification products were run on 3% agarose gel, stained with GelRed, and visualized under UV illumination. The methylated and unmethylated control DNA purchased from Qiagen company were used as a positive control for the methylated (M control) and unmethylated (U control) p16 gene, respectively. A and C: The results of MSP analysis of p16 gene in human B lymphoblastoid cells (A) and in A549 cells (C) treated with potassium dichromate at the concentrations of 0, 5 μM, 10 μM, and 15 μM for 2 hours and 24 hours. B and D: The results of MSP analysis of p16 gene in human B lymphoblastoid cells (B) and in A549 cells (D) treated with lead chromate at the concentrations of 0, 1.25 $\mu g/cm^2$, 2.5 $\mu g/cm^2$, and 5.0 $\mu g/cm^2$ for 4 hours and 24 hours.

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Cr (VI) Down-regulated mRNA Levels of CDK4 and CDK6

The mRNA expression of CDK4 gene in both cell lines was significantly repressed by 5–15 μM of $K_2Cr_2O_7$ in 24-hour exposure groups ($p<0.05$, $p<0.01$), and no significant expression change was observed in 2-hour exposure groups (Fig. 6-A, C). Particulate chromate didn't change the expression of CDK4 in human B lymphoblastoid cells regardless of the exposure time (Fig. 6-B), but the mRNA expression of CDK4 in A549 cells was significantly ($p<0.01$) repressed by moderate and high concentrations of particulate chromate (Fig. 6-D). The mRNA expression of CDK6 in both cell lines was down-regulated by soluble chromate after 24 hours of exposure ($p<0.01$), but no significant change was found in 2-hour exposure groups (Fig. 7-A, C). Also, the mRNA expression of CDK6 in both cell lines was significantly suppressed by 2.5–5.0 $\mu g/cm^2$ of particulate chromate in 24-hour exposure groups ($p<0.01$), and no significant change was observed in 2-hour exposure groups (Fig. 7-B, D).

The Effects of Cr (VI) on p16 Protein Expression

The expression change of p16 protein in these two cell lines after being exposed to Cr (VI) for 24 hours was detected by west blotting (Fig. 8). Our results showed that significant ($P<0.05$) increase of p16 protein expression levels was only observed in human B lymphoblastoid cells exposed to 15 μM of $K_2Cr_2O_7$ and in A549 cells exposed to 5.0 $\mu g/cm^2$ of $PbCrO_4$.

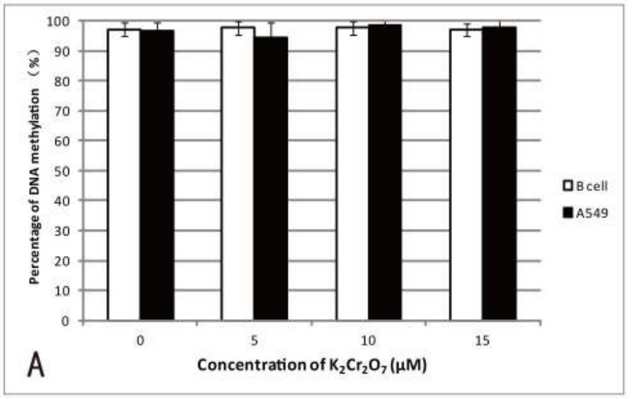

Figure 4. Detection of DNA methylation status at the promoter of p16 gene by pyrosequencing. A: Percentages of methylation at the promoter of p16 gene in human B lymphoblastoid cells and in A549 cells exposed to potassium dichromate at the concentrations of 0, 5 μM, 10 μM, and 15 μM for 24 hours. B: Percentages of methylation at the promoter of p16 gene in human B lymphoblastoid cells and in A549 cells exposed to lead chromate at the concentrations of 0, 1.25 μg/cm^2, 2.5 μg/cm^2, and 5.0 μg/cm^2 for 24 hours.
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Discussion

DNA methylation, one of three main types of epigenetic modifications, plays an important role in the regulation of gene expression. Aberrant DNA methylation is believed to be associated with various diseases and developmental disabilities such as cancer and mental retardation, and global hypomethylation and site-specific hypermethylation are common features of human tumors [17,18,19]. Previous studies have demonstrated that Cr (VI) exposure could induce abnormal DNA methylation in Brassica napus L. plants [8], mammalian cells [7,20,21,22], and exposed populations [9,10,23]. Our results indicated that both soluble ($K_2Cr_2O_7$) and particulate ($PbCrO_4$) chromate could induce global DNA hypomethylation in human B lymphoblastoid cells and A549 cells, and it was consistent with reports by Wang et al. that chronic occupational chromate exposure also could induce global DNA hypomethylation in chromate manufacturing workers [24]. DNA hypomethylation often targets various genomic

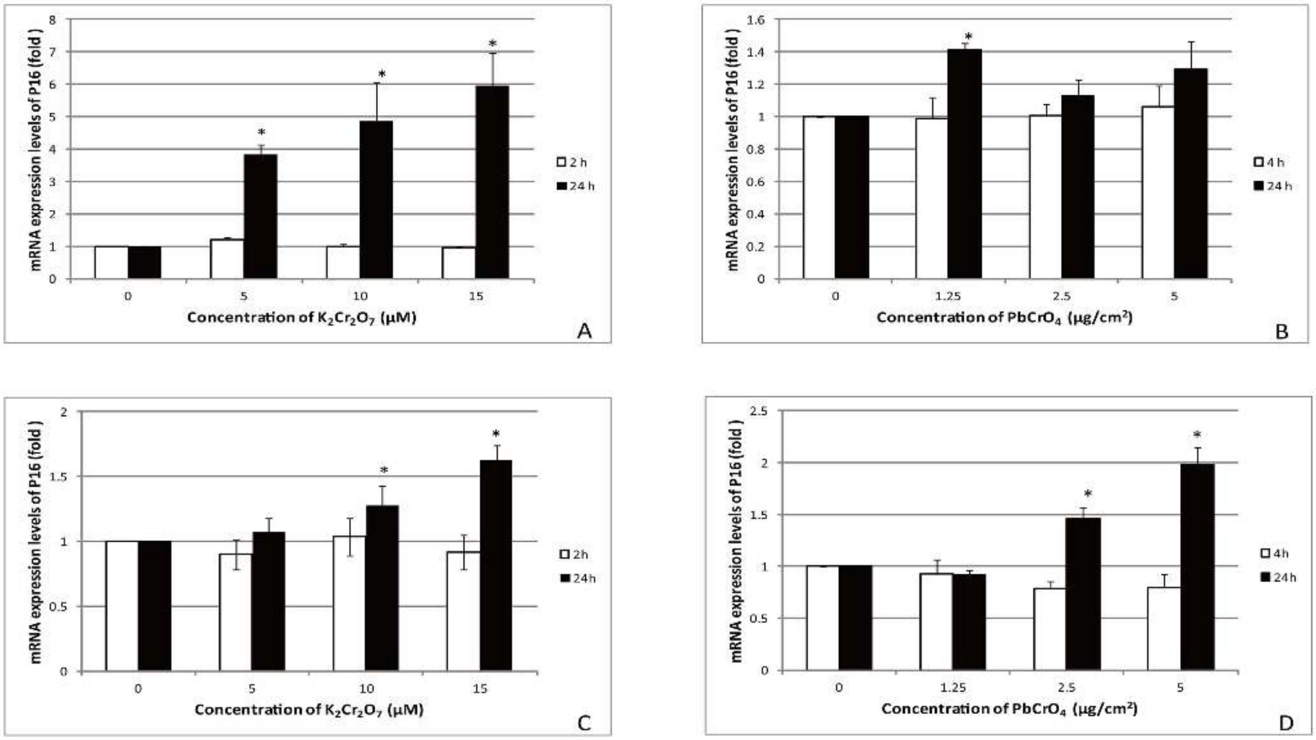

Figure 5. mRNA expression of p16 gene. A and C: mRNA expression levels (fold change) of p16 gene in human B lymphoblastoid cells (A) and in A549 cells (C) cells exposed to potassium dichromate at the concentrations of 0, 5 μM, 10 μM, and 15 μM for 2 hours and 24 hours. B and D: mRNA expression levels (fold change) of p16 gene in human B lymphoblastoid cells (B) and in A549 cells (D) cells exposed to lead chromate at the concentrations of 0, 1.25 μg/cm^2, 2.5 μg/cm^2, and 5.0 μg/cm^2 for 4 hours and 24 hours. Asterisks above the bars indicate that the difference between exposure and control was significant ($P<0.01$).
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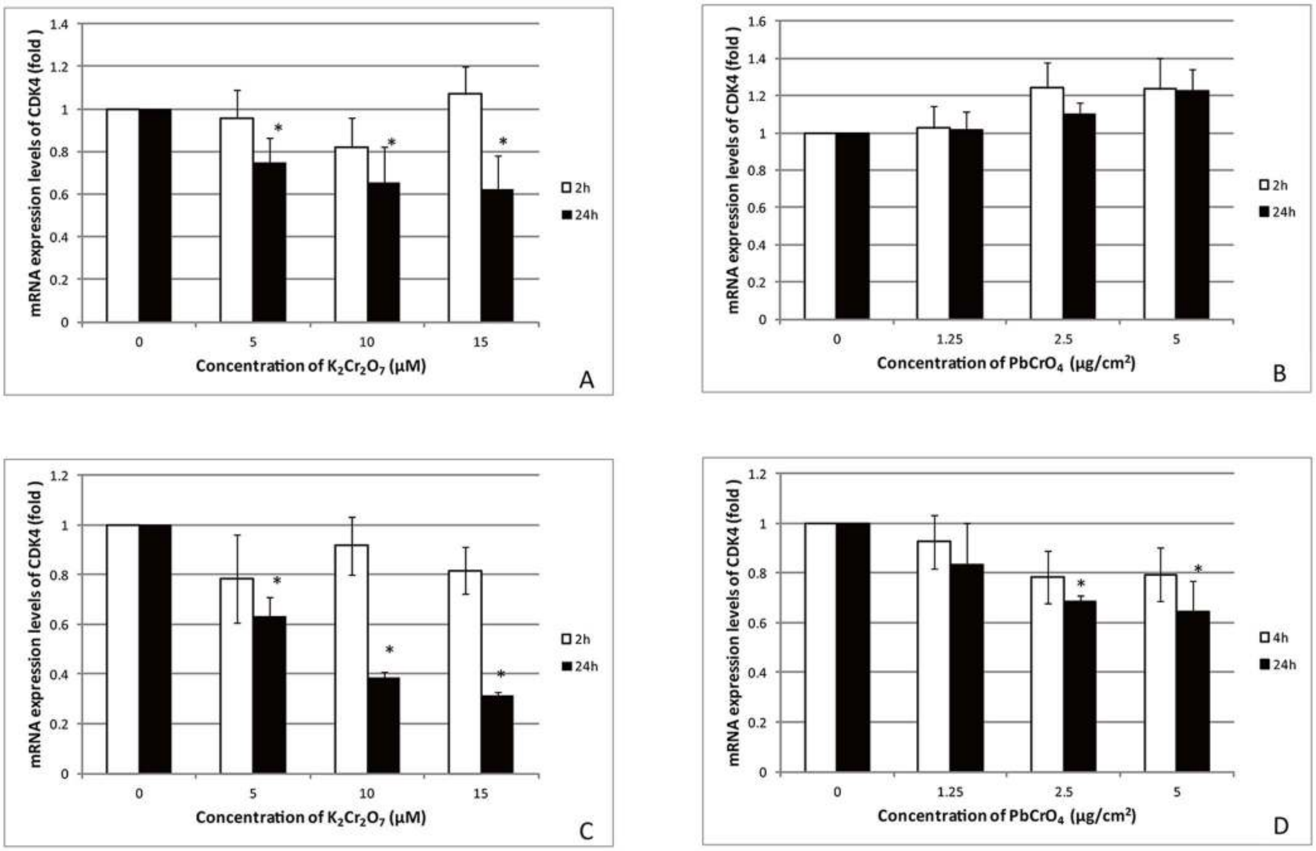

Figure 6. mRNA expression of CDK4 gene. A and C: mRNA expression levels (fold change) of CDK4 gene in human B lymphoblastoid cells (A) and in A549 cells (C) cells exposed to potassium dichromate at the concentrations of 0, 5 μM, 10 μM, and 15 μM for 2 hours and 24 hours. B and D: mRNA expression levels (fold change) of CDK4 gene in human B lymphoblastoid cells (B) and in A549 cells (D) cells exposed to lead chromate at the concentrations of 0, 1.25 μg/cm^2, 2.5 μg/cm^2, and 5.0 μg/cm^2 for 4 hours and 24 hours. Hash keys above the bars: $P<0.05$ as compared with control; asterisks above the bars: $P<0.01$ as compared with control.
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sequences including repeat sequence, retrotransposons, and CPG poor promoters. It may induce genomic instability, gene activation, and can also disrupt genomic instability [18,25]. Genomic instability paradigm is considered as a possible model for Cr (VI)-induced carcinogenesis, but the specific mechanism remains unclear [3]. Our findings may contribute to investigating its mechanism since global DNA hypomethylation can lead to genomic instability. In addition, we found that the decrease of global DNA methylation levels in 24-hour exposure group was not as obvious as that in short-term (2-hour or 4-hour) exposure group, although it was also statistically significant. This may be due to the fact that DNA methylation change is reversible, and the alteration of DNA methylation status may be just a transient event. Klein et al. [7] also found that exposure time might be a factor affecting the effects of Cr (VI) on methylation in a transgenic Chinese Hamster Lung cell line, and they reported that 2-hour exposure to soluble Cr (VI) could result in partial methylation in the *gpt* gene while 24-hour exposure to particulate chromate induced no methylation changes.

Panayiotidis et al. [26] reported that no changes in global DNA methylation status were observed in A549 cells arrested at either the S- or G2/M-phase of the cell cycle. However, we found decreased global DNA methylation in human B lymphoblastoid cells and A549 cells arrested at G1-phase by Cr (VI). The discrepancy may be due to the different kinds of exposure agents used in these two studies. It can also attribute to the different cell cycle phases arrested in these two experiments. Other previous studies also reported that Cr (VI) could result in cell cycle arrest, but different cells were arrested at different cell phases of cell cycle. For example, Wakeman et al. [27] found that cell cycle was arrested at S-phase in HeLa cells after 10 μM of potassium chromate exposure for 4 hours. Wakeman and Xu [28] reported S-phase arrest in 293T cells treated with 40 μM of potassium chromate for 4 hours. Zhang et al. [29] observed G_2/M phase arrest in human lung epithelial A549 cells exposed to 1 μM – 25 μM of potassium dichromate. Hayashi et al. [30] found that 20 μM of CrO_3 could induce G_2 phase arrest in U937 and P53 mutated cells after exposure for 24 hours. Our results were consistent with that reported by Stanley et al. [13], and they found that both granulosa cells and spontaneously immortalized rat granulosa cells were arrested at G_1 phase after being exposed to 10 μM of potassium dichromate for 24 hours. Therefore, the cellular response of cell cycle arrest to Cr (VI) treatment may be dependent on the types of cells.

Cell cycle progression is regulated by cyclin dependent kinases (CDKs), cyclins, and CDK inhibitors. G_1 phase check point is mainly regulated by CDK 4/6, and cyclins D1, D2, and D3, and p16 is a CDK inhibitor targeting CDK 4/6 [31,32]. In the present study, soluble and particulate Cr (VI) inhibited the mRNA expression of CDK 4/6 in both cell lines except that particulate Cr (VI) didn't repress the mRNA expression of CDK 4 in human B lymphoblastoid cells. It was consistent with the results showed by

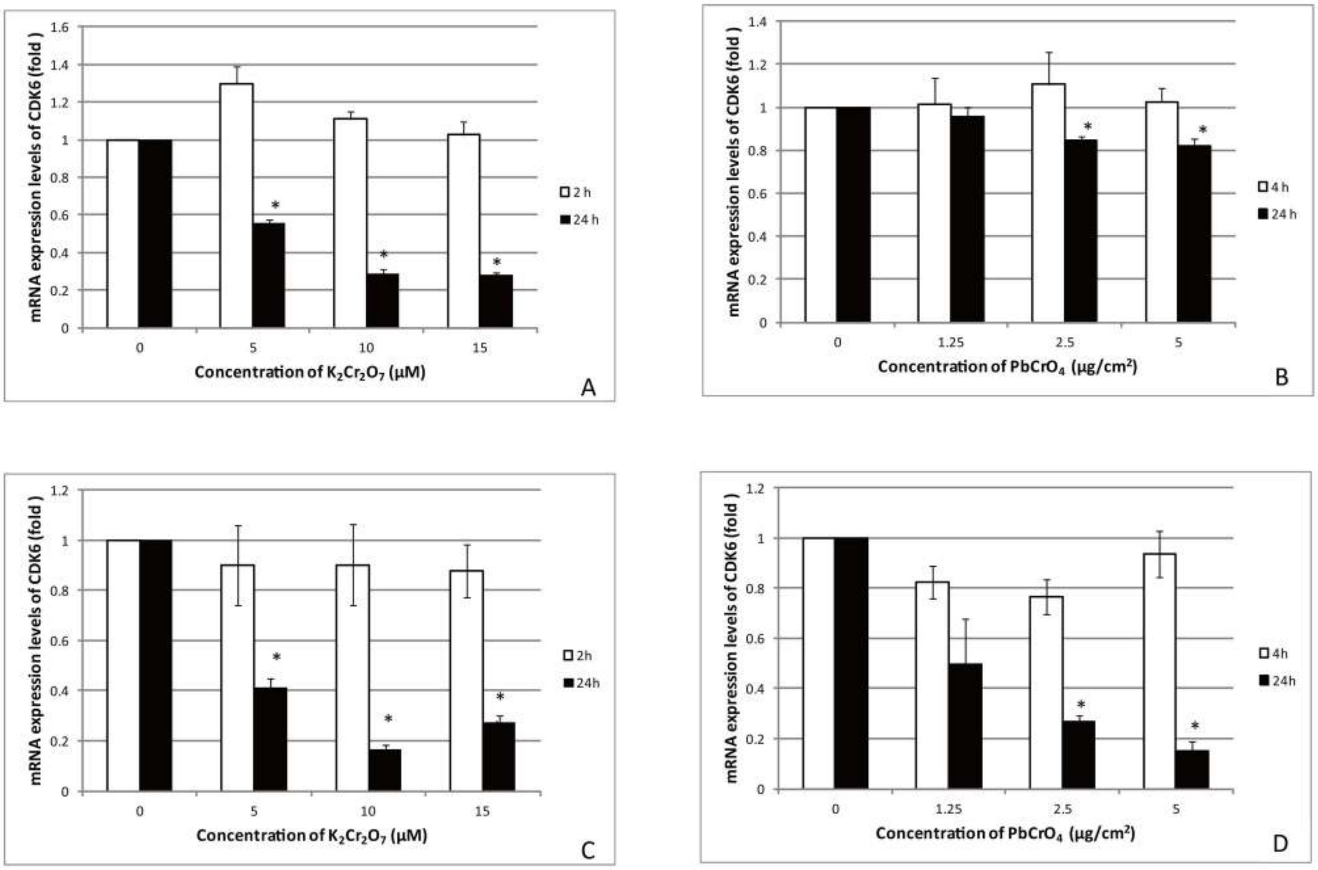

Figure 7. mRNA expression of CDK6 gene. A: mRNA expression levels (fold change) of CDK6 gene in human B lymphoblastoid cells (A) and in A549 cells (C) cells exposed to potassium dichromate at the concentrations of 0, 5 µM, 10 µM, and 15 µM for 2 hours and 24 hours. B and D: mRNA expression levels (fold change) of CDK6 gene in human B lymphoblastoid cells (B) and in A549 cells (D) cells exposed to lead chromate at the concentrations of 0, 1.25 µg/cm^2, 2.5 µg/cm^2, and 5.0 µg/cm^2 for 4 hours and 24 hours. Asterisks above the bars indicate that the difference between exposure and control was significant ($P<0.01$).
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Stanley et al. [13] that potassium dichromate significantly decreased protein levels of G_1-S phase regulators CDK4 and CDK6 in primary and immortalized granulosa cells, but they didn't compare the difference of the effects of Cr (VI) on cell cycle arrest between soluble and particulate chromates. The difference of inhibiting effects on CDK 4/6 expression between soluble and particulate chromate might be due to the fact that the up-regulating effect of particulate chromate on CDKs inhibitor p16 was weaker than that of soluble chromate. Thus, Cr (VI) could inhibit both mRNA and protein expressions of CDK4/6 genes, and it may contribute to arresting cell cycle at G_1 phase.

Furthermore, we measured the effects of Cr (VI) on mRNA expression of CDK inhibitor p16. p16 is known to inhibit the formation of cyclin D-CDK 4/6 complex and thereby contribute to the G_1/S checkpoint response [33]. The results of our study indicated that soluble and particulate chromate could significantly up-regulate mRNA expression of p16, but the up-regulating effect of particulate chromate was weaker than that of soluble chromate in human B lymphoblastoid cells. In addition, slight increase of p16 protein expression was observed in two cell lines after being exposed to the highest concentration of Cr (VI). Elevated expression of p16 is a potent mechanism for inhibiting proliferation, and several distinct stresses, including DNA damage and oncogenic stress, may lead to the enhancement of p16 expression [34]. A number of previous study showed the ability of Cr (VI) to induce DNA damage, and it may be responsible for the elevation of p16 expression. Due to only slight increase of p16 protein was observed in two cell lines after Cr (VI) exposure, p16 might not be physiologically relevant to the growth arrest observed in our study. In addition, we hypothesize that the increased mRNA expression of p16 by Cr (VI) may be associated with changed methylation status at the promoter of this gene. However, our results indicated that p16 gene was completely methylated in both cell lines, and neither soluble nor particulate chromate could change the methylation status of p16 gene, although both of them lowered the global DNA methylation levels of these two cell lines. Therefore, Cr (VI) up-regulated mRNA expression of p16 not through lowering DNA methylation levels at the promoter of this gene, and other mechanisms, such as microRNA and histone modification [5], may be responsible for this up-regulating effect of Cr (VI). Actually, Raynal et al. [35] reported that hypermethylated genes could be reactivated by histone deacetylase inhibitors (HDACi) without any loss in promoter DNA methylation, which showed that DNA methylation did not lock gene expression. Therefore, it is possible that Cr (VI) can up-regulate mRNA expression of p16 through suppressing HDAC expression.

In conclusion, our study suggested that G_1 phase cell cycle arrest induced by Cr (VI) may be associated with global hypomethylation in human B lymphoblastoid cells and A549 cells. Cr (VI) could down-regulate mRNA expression of CDK 4/6 genes and up-

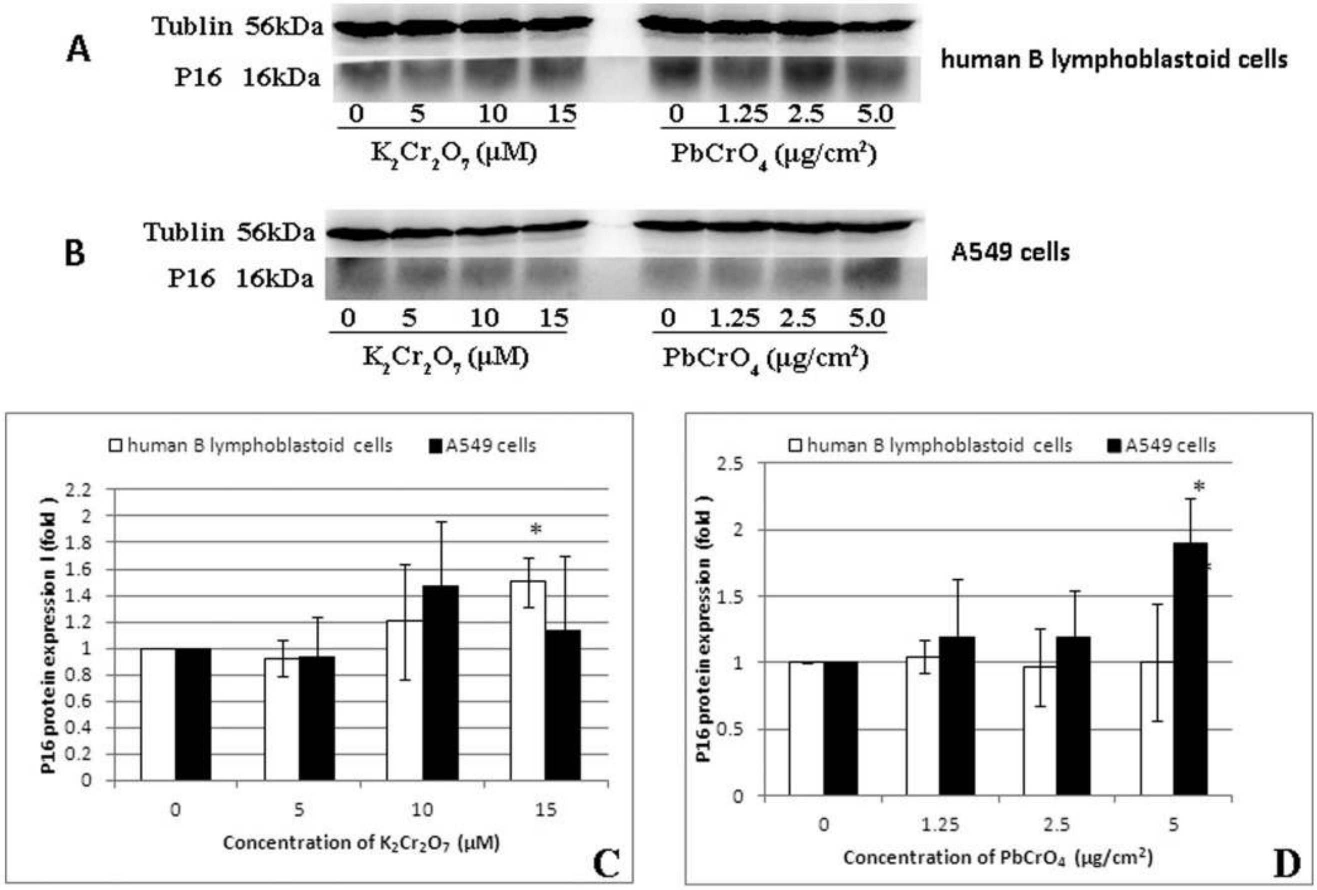

Figure 8. Protein expression of p16 gene. Human B lymphoblastoid cells and A549 cells were exposed to potassium dichromate or lead chromate for 24 hours, and p16 protein expression was analyzed by western blot with 100 μg of protein. A–B: Western blots of p16 and tublin in human B lymphoblastoid cells (A) and A549 cells (B). C–D: Histograms of Integrated Density Value for each protein in human B lymphoblastoid cells (C) and A549 cells (D), normalized to tublin. Asterisks above the bars indicate that the difference between exposure and control was significant ($P<0.05$).

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regulate mRNA expression of p16 gene, but p16 might be not related to growth arrest for little change in protein expression. In addition, other mechanisms rather than methylation change at the promoter of p16 gene may be involved in up-regulating mRNA expression of p16 gene, and suppression of HDAC expression may be one of them.

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Author Contributions

Conceived and designed the experiments: JL XZ. Performed the experiments: JL YW LJ XW PS CY MG KL. Analyzed the data: JL YT NW. Contributed reagents/materials/analysis tools: YX YS. Wrote the paper: JL.

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