

Effect of pure curcumin, demethoxycurcumin, and bisdemethoxycurcumin on *WT1* gene expression in leukemic cell lines

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Abstract

Purpose Leukemias are groups of hematological malignancies with high incidence and mortality rates in patients worldwide. There have been shown in many studies that *Wilms' tumor1* (*WT1*) gene were highly expressed in leukemic blast cells. Curcuminoids, major active components of the spice turmeric, are well known for its anticancer. Curcuminoids consist of pure curcumin, demethoxycurcumin, and bisdemethoxycurcumin. In this study, the effect of each curcuminoids' components on *WT1* gene expression in leukemic cell lines (K562, HL60, U937, and Molt4) was investigated.

Methods The levels of *WT1* mRNA and *WT1* protein in leukemic cell lines were assessed by RT-PCR and Western blot analysis, respectively.

Results It was found that the *WT1* mRNAs were detected in all 4 types of leukemic cell lines. However, the *WT1* protein levels were found only in the cell lines K562 and Molt4. Pure curcumin exhibited a strong inhibitory effect

on *WT1* mRNA and *WT1* protein expression. The treatment of leukemic cell lines with non-cytotoxic doses (5, 10, and 15 μ M) of pure curcumin for 2 days reduced the level of *WT1* mRNA expression and *WT1* protein in a dose-dependent manner. In addition, pure curcumin at 10 μ M significantly decreased the level of *WT1* mRNA and protein in a time-dependent manner.

Conclusion Pure curcumin, an excellent curcuminoid derivative, decreased *WT1* gene expression in both transcriptional and translational levels. Thus, pure curcumin is one of a potential chemotherapeutic agent used for treatment of human leukemia. However, its chemotherapeutic property will need to be studied more in future.

Keywords Pure curcumin · Demethoxycurcumin · Bisdemethoxycurcumin · *WT1* gene · Leukemic cell lines

Introduction

Leukemia is a group of diseases involving the blood-forming organs, and is characterized by uncontrolled increase of white blood cells. Approximately 35,000 new cases of leukemia will be diagnosed in United States in 2006 [1]. The detection of overexpression in specific oncogenes or tumor suppressor genes provides information that is useful in the diagnosis of leukemia and prognosis of the disease. The overexpression of *Wilms' tumor* (*WT1*) protein in leukemia is one example.

The *Wilms' tumor1* (*WT1*) gene is involved in tumorigenesis. It is located on the human chromosome 11p13 [2, 3]. In normal tissue, *WT1* is restricted to kidney, testis, ovary, spleen, hematopoietic precursors, and the mesothelial cell lining of visceral organs [4]. *WT1* transcripts have been detected in adult bone marrow, lymph nodes, and

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peripheral blood. These data suggest that WT1 may play a role in the development of erythroid, myeloid, and lymphoid cells during both the fetal and the adult stages. Previous studies demonstrated that the *WT1* gene is overexpressed in many types of cancer. It has been described as a tumor suppressor gene responsible for Wilms' tumor or nephroblastoma and other cancers [5–8]. However, recent studies have shown that *WT1* acts as an oncogene in many types of malignant tumors, especially leukemia [9]. It plays an important role in the progression of disease and prognosis of human malignancies [10, 11]. Significant levels of *WT1* gene expression have been found in leukemic samples; the average levels are approximately 1,000–100,000 times higher than in normal bone marrow and peripheral blood, respectively [10].

The *WT1* gene product is a 48–52 kDa nuclear protein that has four zinc fingers and acts as a transcriptional activator or repressor, depending on the cellular or chromosomal context [12, 13]. The four major isoforms of WT1 protein identified to date result from two alternative splices in its transcript. WT1 protein plays an important role in the development of normal cells and tissues. It may influence the proliferation and differentiation of blood cells by differential regulation of the genes for *TGF β* , *C-Myc*, *C-Myb*, *Bcl2*, and the retinoic acid receptor [14]. Low levels of WT1 protein expression have been found in normal blood cells. In contrast, the overexpression of WT1 protein has been found in leukemic blood cells. The expression of WT1 in leukemic cells is involved in cell proliferation, differentiation, and apoptosis [14, 15]. Moreover, the expression of the *WT1* gene and its product have been used as biological markers for diagnosis and evaluation of the prognosis of leukemia and minimal residual disease (MRD) [10, 16]. All of these findings support the conclusion that *WT1* gene expression may be involved in leukemogenesis.

To date, chemotherapy has been the most frequently used treatment for leukemia. Chemotherapy works by destroying leukemic cells, hence stopping them from growing or multiplying. However, some normal cells are destroyed as well by this method of treatment. Due to the wide range of biological activities and lack of toxicity in animal models, natural remedies have been used as alternative treatments for leukemia and other malignant tumors.

Turmeric (*Curcuma longa* Linn) is one of the most popular herbs used for medical treatment, due to its wide variety of medicinal properties such as anti-inflammatory, anti bacterial, anti fungal, anti-oxidant, anticarcinogen, antimutagen, and anticancer properties. The active constituents of turmeric are known as curcuminoids, yellow pigmented substances isolated from the rhizome of turmeric. This active extract can be subdivided into three distinct components: pure curcumin, demethoxycurcumin, and bisdemethoxycurcumin. Curcuminoids are a group of diet-derived agents that are being

clinically evaluated as chemopreventive agents for major cancer targets, including the breast, prostate, lung, stomach, duodenal, and colon cancers, as well as leukemias [17, 18]. Curcuminoids, especially pure curcumin, have strong anticancer agent and anti-tumor progression properties [19–21].

The commercial grade curcuminoid mixture is commonly known as “curcumin” due to its main component being, curcumin. Curcumin has been found to induce cell death in two leukemic cell lines: K562 and Jurkat cells [22]. Moreover, the dietary component of pure curcumin induces apoptosis in human leukemia HL60 cells at the very low concentration of 3.5 $\mu\text{g/ml}$ [23]. Recently, all three curcuminoids has been shown to have cytotoxic activity on leukemic cell lines HL60, U937, and K562 [24]. Moreover, the inhibitory effects of curcumin were associated with a decrease in the levels of *WT1* gene expression in patient leukemic cell and K562 cell lines [25, 26].

In this study, the effects of turmeric curcuminoids; curcumin, demethoxycurcumin, bisdemethoxycurcumin, commercial grade curcuminoid mixtures (Sigma-Aldrich), and in-house curcuminoid mixtures, on *WT1* gene expression in four leukemic cell lines: K562, U937, HL60, and Molt4 were investigated and compared.

Materials and methods

Cell culture

Human erythroid leukemia (K562), human promyeloid leukemia (HL60), human monocytic leukemia (U937), and human lymphoblastic leukemia (Molt4) were cultured as described elsewhere [25, 26].

Extraction and isolation of curcuminoids

Curcuminoid extraction and isolation were prepared as described previously [27, 28]. In this study, individual curcuminoids (pure curcumin, demethoxycurcumin, and bisdemethoxycurcumin) has been purified from turmeric powder by column chromatography.

Western blotting

Cell nuclear extracts were prepared by NE-PER® Nuclear and Cytoplasmic Extraction Reagents (PIERCE, USA). The cell nuclear proteins (100 $\mu\text{g/lane}$) were separated by 12% SDS-polyacrylamide gel electrophoresis. WT1 protein detection was performed using primary rabbit polyclonal anti-WT1 clone C-19 (Santa Cruz, USA) at 1:1,000, followed by a treatment with HRP-conjugated goat anti-rabbit IgG (Promega, USA) at a 1:15,000 dilution. Then the same membrane was reprobed for GAPDH protein by Restore™

Western Blot Stripping Buffer (PIERCE, USA). After the stripping procedure, the nitrocellulose membrane was probed again with primary rabbit polyclonal anti-GAPDH clone FL-335 (PIERCE, USA) at a 1:1,000, followed by a treatment with HRP-conjugated goat anti-rabbit IgG (PIERCE, USA) at a 1:15,000 dilution. Proteins were visualized by the SuperSignal® protein detection kit (PIERCE, USA) and quantified by scan densitometer.

RNA extraction and quantitative RT-PCR

RNAs of leukemic cells were isolated by TRIZOL® reagent according to the manufacturer's instructions. RNaseOUT™ (Invitrogen, USA) was added to the RNA extraction products for RNA protection. RT-PCR was performed using SuperScript™ III One-step RT-PCR System with Platinum® *Taq* DNA polymerase reagent (Invitrogen, USA). For WT1, the sense primer was 5'-GGCATCTGAGAC-CAGTGAGAA-3', and the antisense primer was 5'-GAGAGTCAGACTTGAAAGCAGT-3', corresponding to residues 780–800 and residues 1,232–1,253, respectively, of the published cDNA sequence [29]. cDNA was synthesized from 1 µg of total RNA at 60°C for 30 min and denatured at 94°C for 2 min. PCR amplification was performed for 30 cycles of sequential denaturation (94°C, 1 min); annealing (60°C, 1 min); and extension (72°C, 1 min), which yields gave a 474-bp product. For GAPDH, the sense primer (5'-CGAAGTCAACGGATTTGGTCGTAT-3') and the anti-sense primer (5'-AGCCTTCTCGGTGGTG AAGAC-3') were used. These sequences were corresponding to residues 888–911 and residues 1,174–1,194, respectively. The GAPDH cDNA was synthesized from 1 µg of total RNA at the same condition of WT1, which yield a 306-bp product. For the negative control, water was amplified a total of 30 cycles to detect possible contamination. A total 15 µl of each PCR product was analyzed via 1% agarose gel electrophoresis, visualized with ethidium bromide staining (2 mg/ml), and quantified using scan densitometry (BIO-RAD, Richmond, CA, USA).

Statistical analysis

All data were expressed as the mean \pm standard deviation (SD) from triplicate samples of three independent experiments. Statistical differences between the means were tested one-way ANOVA. Probability values $P < 0.05$ were considered to be statistically significant.

Results

WT1 mRNA and WT1 protein were detected in K562, U937, HL60, and Molt 4 cell lines. However, the WT1

protein levels were found only in K562 and Molt4 cells (Fig. 1a, b). To determine the effect of three turmeric curcuminoids, including commercial grade curcuminoid (Sigma-Aldrich) and in-house curcuminoids on WT1 gene expression, all leukemic cell lines were treated with a non-cytotoxic concentration (10 µM) of curcuminoids for 2 days. All curcuminoid derivatives decreased the WT1 mRNA levels and WT1 protein levels in leukemic cell lines. The levels of WT1 mRNA (after normalization to GAPDH expression) in K562 cells were decreased by 59, 29, 39, 54, and 37% (Fig. 2a, e), in U937 cells by 43, 18, 28, 25, and 8% (Fig. 2b, e), in HL60 cells by 37, 14, 15, 16, and 7% (Fig. 2c, e), and in Molt4 cells by 17, 3, 3, 2, and 0.8% (Fig. 2d, e). The levels of WT1 protein in K562 cells were decreased by 48, 13, 42, 40, and 22% (Fig. 3a, c), and in Molt4 cells were 90, 57, 68, 30, and 26% (Fig. 3b, c) in response to treatment with pure curcumin, demethoxycurcumin, bisdemethoxycurcumin, commercial grade curcuminoid mixture (Sigma-Aldrich), and curcuminoid mixture (in-house curcuminoids), respectively, compared with the vehicle control. However, pure curcumin exhibited a strong inhibitory effect on WT1 mRNA and protein levels in K562, U937, HL60, and Molt4.

To verify that pure curcumin could modulate the spontaneous WT1 expression (mRNA) occurring in vitro, as well as WT1 protein expression, Leukemic cells were treated with pure curcumin (5, 10, and 15 µM) for 2 days. Levels of WT1 mRNA expression in K562 cells were decreased by 15, 28 and 50% (Fig. 4a, e), in U937 cells by 10, 17, and 19% (Fig. 4b, e), in HL60 cells by 5, 11, and 18% (Fig. 4c, e) and in Molt 4 cells by 6, 19 and 21% (Fig. 4d, e) in

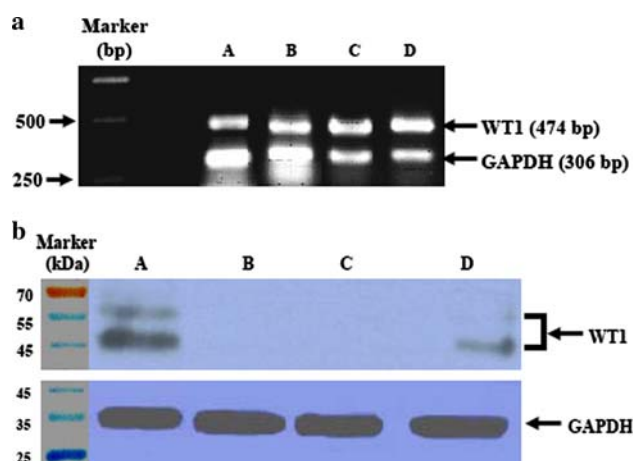


Fig. 1 The WT1 mRNA (a) and protein (b) levels in K562, U937, HL60 and Molt4 cell lines. The WT1 and GAPDH mRNA levels in untreated K562 (A), U937 (B), HL60 (C), and Molt4 (D) cell lines were determined by RT-PCR. Fifteen microlitres of the PCR products (474 bp for WT1 and 306 bp for GAPDH) were run on 1% agarose gel. The WT1 protein level was determined by Western blot analysis using rabbit polyclonal anti-WT1 antibody (WT1; C-19). The level of GAPDH protein was used as an internal control

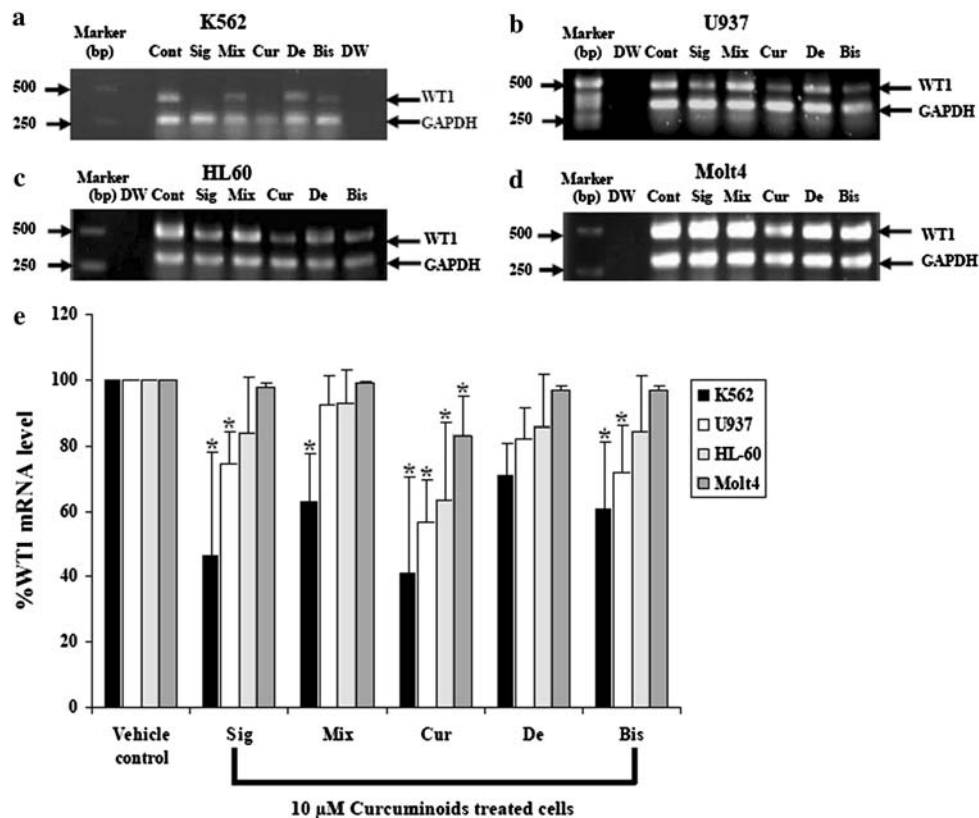


Fig. 2 Analysis of the effect of curcuminoid extracts on WT1 mRNA level in K562, U937, HL60, and Molt4 cell lines. The WT1 and GAPDH mRNA levels following treatment with 0.05% DMSO (Cont; Control) and 10 μ M of commercial grade curcuminoid mixture (Sig; Sigma-Aldrich), curcuminoid mixture (Mix), pure curcumin (Cur), demethoxycurcumin (De), and bisdemethoxycurcumin (Bis) were determined in K562 (a), U937 (b), HL60 (c), and Molt4 (d) cells after 2 days by RT-PCR. Fifteen microlitres of the PCR products (474 bp for

WT1 and 306 bp for GAPDH) were run on 1% agarose gel. The bands were quantified using a scan densitometer (e). WT1 mRNA levels were measured and normalized with GAPDH mRNA level. Distilled water (DW) was used as a negative control. Data are the mean values \pm standard deviation (SD) of three independent experiments. Asterisks (*) denote values that were significantly different from the vehicle control ($P < 0.05$)

response to treatment with 5, 10, and 15 μ M pure curcumin, respectively, compared with the vehicle control. WT1 protein levels in K562 cells were decreased by 17, 37, and 81% (Fig. 5a, c) and in Molt4 cell line by 56, 79, and 94% (Fig. 5b, c) in response to treatment with 5, 10, and 15 μ M pure curcumin, respectively.

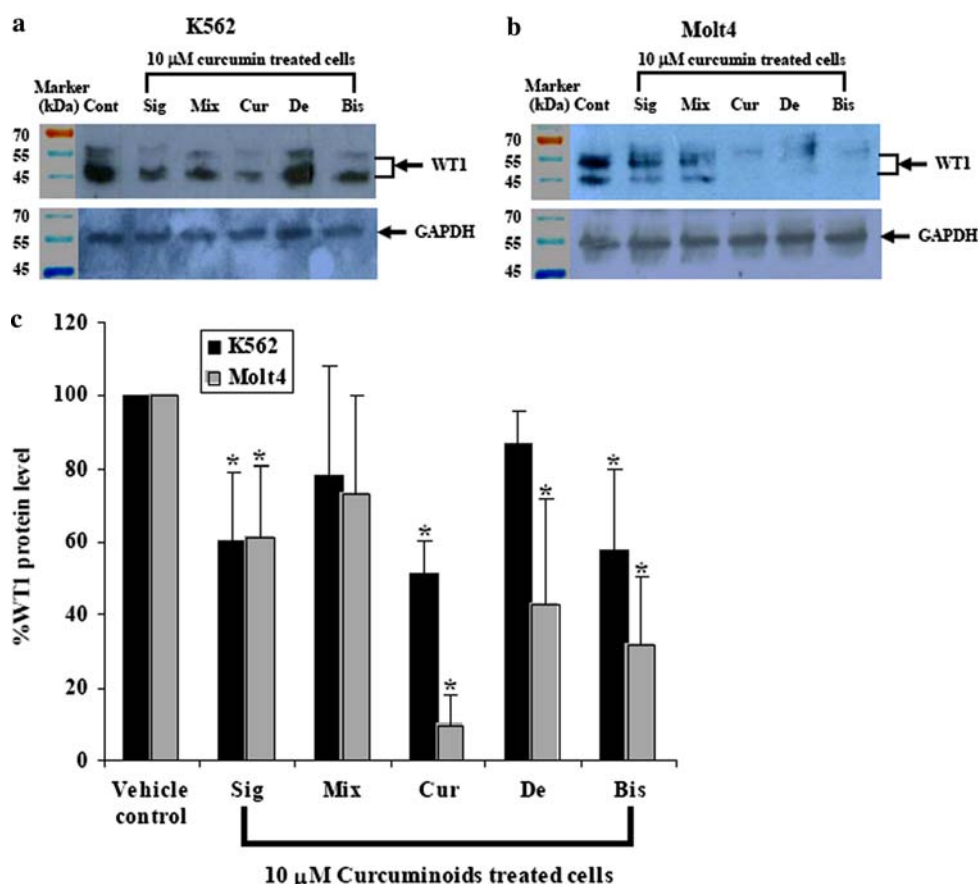
Pure curcumin significantly decreased WT1 expression at the mRNA and protein levels. Therefore, subsequent experiments were designed to observe modulating effects of pure curcumin on WT1 expression at various incubation times. Expression of WT1 mRNA in K562 cells after treatment for 1, 2, and 3 days with pure curcumin was decreased by 37, 48, and 54% (Fig. 6a, e), in U937 cells by 13, 33, and 64% (Fig. 6b, e), in HL60 cells by 4, 8, and 30% (Fig. 6c, e) and in Molt4 cells by 7, 11, and 16% (Fig. 6d, e), respectively, compared with the vehicle control. WT1 protein levels in K562 cells were decreased by 50, 92, and 99% (Fig. 7a, c) and in Molt4 cell line by 53, 84, and 92% (Figs. 7b, 6c) in response to treatment with 10 μ M pure curcumin for 1, 2, and 3 days, respectively. To investigate the

rate of proliferation after incubating leukemic cells with various concentrations of pure curcumin (0, 5, 10, and 15 μ M), the number of leukemic cells was determined at 0, 1, 2, and 3 days after incubation using a trypan blue dye exclusion assay. The proliferation rates of K562 cells were decreased by 25, 30, and 49% (Fig. 8a), the rates of Molt4 cell proliferation were decreased by 13, 32, and 42% (Fig. 8b), the proliferation rates of U937 cells were decreased by 31, 33, and 38% (Fig. 8c) and the proliferation rates of HL60 cells were decreased by 22, 33, and 64% (Fig. 8d) when treated with 5, 10, and 15 μ M pure curcumin, respectively (compared to control without curcumin treatment).

Discussion

Leukemia is a cancerous disorder of the blood-forming tissues, especially bone marrow. It is characterized by excessive production of immature or mature leukocytes and

Fig. 3 Analysis of the effect of curcuminoid extracts on WT1 protein level in K562 and Molt4 cell lines. The WT1 and GAPDH protein levels following treatment with 0.05% DMSO (Cont; Control) and 10 μ M of commercial grade curcuminoid mixture (Sig; Sigma-Aldrich), curcuminoid mixture (Mix), pure curcumin (Cur), demethoxycurcumin (De), and bisdemethoxycurcumin (Bis) were determined in K562 (a) and Molt4 (b) cells after 2 days by Western blot analysis. The bands (48–54 kDa for WT1 and 37 kDa for GAPDH) were quantified using a scan densitometer (c). WT1 protein levels were measured and normalized with GAPDH protein level. Data are the mean value \pm standard deviation (SD) of three independent experiments. Asterisks (*) denote values that were significantly different from the vehicle control ($P < 0.05$)



consequently a crowding-out of red blood cells and platelets. *Wilms' tumor1* (WT1) gene is involved in leukemogenesis. Previous studies have shown that the wild-type WT1 gene is strongly expressed in leukemic blast cells with an increase in its expression levels at relapse and inverse correlation between its expression levels and prognosis [10, 30–32]. In addition, WT1 gene has been shown to be overexpressed in leukemic cells [33]. These findings suggest that WT1 plays an important role in leukemogenesis and may have an oncogenic function rather than a tumor-suppressive function in hematopoietic progenitor cells and leukemic blast cells.

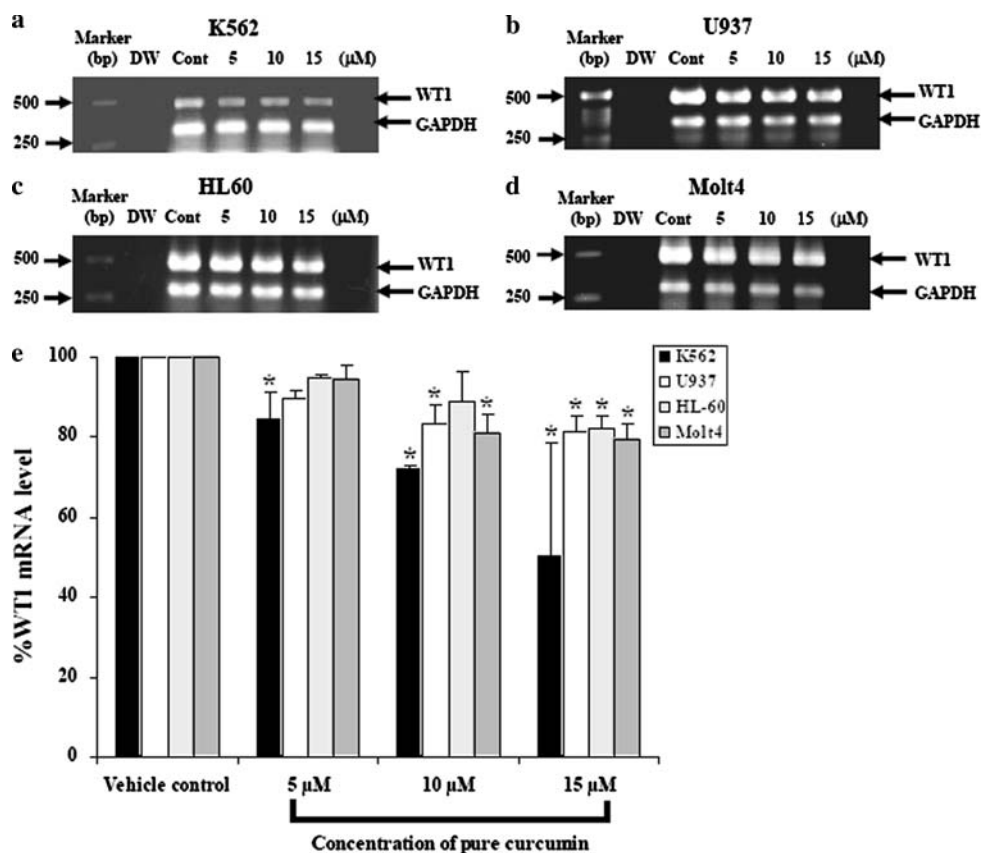
In anticancer drug research, dietary and/or medicinal plants, such as turmeric, ginger, garlic, chili, and pepper are becoming popular as chemotherapeutic drugs. Turmeric is a spice grown in tropical regions of Asia. Curcuminoids have been identified as the major active yellow pigment in turmeric and consist of three major active ingredients; pure curcumin, demethoxycurcumin, and bisdemethoxycurcumin. These three curcuminoid compounds are always mixed together in turmeric powder as found in commercial grade curcuminoids. Curcuminoids have a wide range of biological and pharmacological activities, including antioxidant and anti-inflammatory effects, as well as anti-mutagen and anticancer properties [19–21, 34]. The expression of

STAT5 mRNA and protein in K562 cells was inhibited by curcumin, as well as K562 cell proliferation [35]. Moreover, the expression of several oncogenes such as *c-jun* and *NF κ B* are suppressed by curcumin [36, 37]. Recently, commercial grade curcuminoids (Sigma-Aldrich) have shown suppressive effects on the expression of WT1 mRNA and WT protein levels in human leukemic cells [25, 26]. However, there has been to date no indication of which component of turmeric has the strongest suppressive effect on WT1 gene and protein expression in leukemic cell lines.

The WT1 mRNA was detected in four types of leukemic cell lines. The WT1 gene was overexpressed in all types of leukemic cells. This supports the conclusions from previous studies, that the WT1 gene plays a role in leukemogenesis and may have an oncogenic function rather than a tumor-suppressor gene function in leukemic cells [9, 14, 38]. Conversely, high levels of WT1 protein were detected in K562 and Molt4 cell lines. Possibly the WT1 protein levels in U937 and HL60 are too low to be detected by our methods.

After being treated with 10 μ M curcuminoids (non-cytotoxic dose), the morphology and viability of the leukemic cells did not change when compared to those of the vehicle control (data not shown). This suggests that curcuminoid extracts at a concentration of 10 μ M do not alter the morphology and viability of leukemic cell lines. In addition,

Fig. 4 The WT1 mRNA levels in K562, U937, HL60, and Molt4 cell lines cultured in 5, 10, and 15 μM of pure curcumin for 2 days. The WT1 and GAPDH mRNA levels following treatment with 0.05% DMSO (Cont; Control) and pure curcumin at a concentration 5, 10, and 15 μM were determined in K562 (a), U937 (b), HL60 (c), and Molt4 (d) cells after 2 days by RT-PCR. Fifteen microlitres of the PCR products were electrophoresed on 1% agarose gel. The bands were quantified using a scan densitometer (e). WT1 mRNA level was measured and normalized with GAPDH mRNA level. Distilled water (DW) was used as a negative control. Data are the mean value \pm SD of three independent experiments. Asterisks (*) denote values that were significantly different from the vehicle control ($P < 0.05$)



WT1 mRNA and WT1 protein levels in leukemic cell lines were decreased by all curcuminoid derivatives, including commercial grade curcuminoids, in-house curcuminoid mixture, pure curcumin, demethoxycurcumin, and bisdemethoxycurcumin after normalization. Moreover, the results clearly show that pure curcumin, the major component of curcuminoid powder, is the most effective component in decreasing WT1 mRNA and WT1 protein levels, followed in decreasing order by bisdemethoxycurcumin, and demethoxycurcumin. This result is similar to that of Nagabhushan [19]. Pure curcumin affected cell proliferation rates of four leukemic cell lines due to the suppression of *WT1* gene expression.

The vanillyl (4-hydroxy-3-methoxyphenyl) moiety and a ketone functional group in the structure of [6]-Gingerol and [6]-paradol, which share common structural features found in curcuminoid, induce HL60 cell death via cell apoptosis [39]. Moreover, the diketone system of curcuminoids appears to be the part of the molecule involved in the anti-proliferative effect of curcuminoids [40]. Both phenolic hydroxyl groups, phenolic methoxyl groups, and the diketone moiety could be responsible for the inhibitory effect on *WT1* gene expression. The present study suggests that hydroxyl groups on the benzene rings are not essential for this activity, because various curcuminoid derivatives have the same number of hydroxyl groups but show different

levels of inhibitory effect. The present results are consistent with the hypothesis that the functional groups, which play a role in the inhibitory effect on *WT1* gene expression are phenolic methoxyl groups of each curcuminoid derivative. Pure curcumin, which possesses two methoxyl groups, exhibited the maximum inhibitory effect, while demethoxycurcumin and bisdemethoxycurcumin, which possess one and no methoxyl group, respectively, were less inhibitory. In addition, an imbalance between the methoxyl groups on the structure of demethoxycurcumin may influence this activity. This study suggests that the diketone groups and the imbalance of the phenolic methoxyl groups of curcuminoids may contribute to the inhibitory effect of curcuminoids on *WT1* gene expression.

The effect of pure curcumin on *WT1* gene expression in leukemic cell lines was evaluated. It was found that pure curcumin significantly decreased the WT1 mRNA and WT1 protein levels in dose and time-dependent manners. A decrease in *WT1* gene expression with increasing pure curcumin concentrations (5–15 μM), demonstrated that pure curcumin inhibited the level of immunoreactive WT1 protein observed in K562 and Molt4 cells and also reduced the level of WT1 mRNA under the same conditions in four types of leukemic cell lines used in this study. Furthermore, the experiments also showed that treatment of cells with pure curcumin at 10 μM for 1–3 days inhibited the *WT1*

Fig. 5 The WT1 protein level in K562 and Molt4 cell lines cultured in 5, 10, and 15 μM of pure curcumin for 2 days. The WT1 and GAPDH protein levels following treatment with 0.05% DMSO (Cont; Control) and pure curcumin at concentrations of 5, 10, and 15 μM were determined in K562 (a) and Molt4 (b) cells after 2 days by Western blot analysis. The bands (48–54 kDa for WT1 and 37 kDa for GAPDH) were quantified using a scan densitometer (c). WT1 protein levels were measured and normalized with GAPDH protein level. Data are the mean value \pm standard deviation (SD) of three independent experiments. Asterisks (*) denote values that were significantly different from the vehicle control ($P < 0.05$)

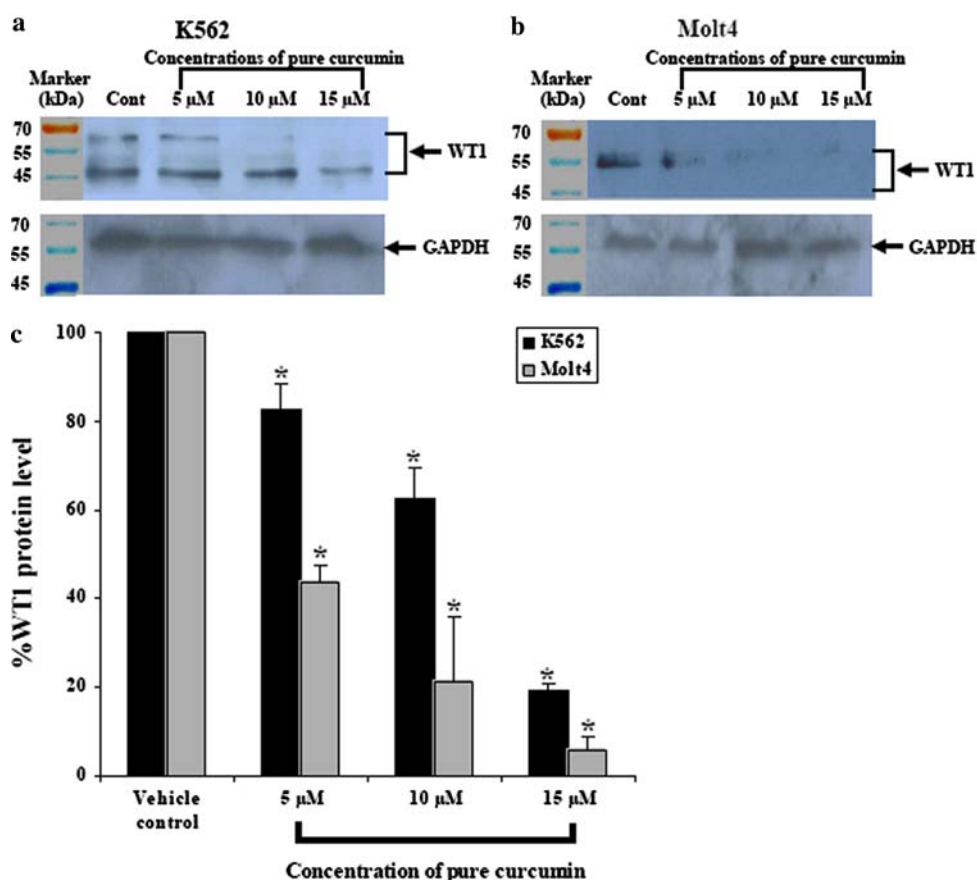


Fig. 6 The WT1 mRNA levels in K562, U937, HL60, and Molt4 cell lines cultured in 10 μM of pure curcumin for 1, 2, and 3 days. The WT1 and GAPDH mRNA levels following treatment with 0.05% DMSO (Cont; Control) for 3 days and 10 μM pure curcumin for 1, 2, and 3 days were determined in K562 (a), U937 (b), HL60 (c), and Molt4 (d) by RT-PCR. Fifteen microliters of the PCR products were electrophoresed on 1% agarose gel. The bands were quantified using a scan densitometer (e). WT1 mRNA level was measured and normalized with GAPDH mRNA level. Distilled water (DW) was used as a negative control. Data are the mean value \pm SD of three independent experiments. Asterisks (*) denote values that were significantly different from the vehicle control ($P < 0.05$)

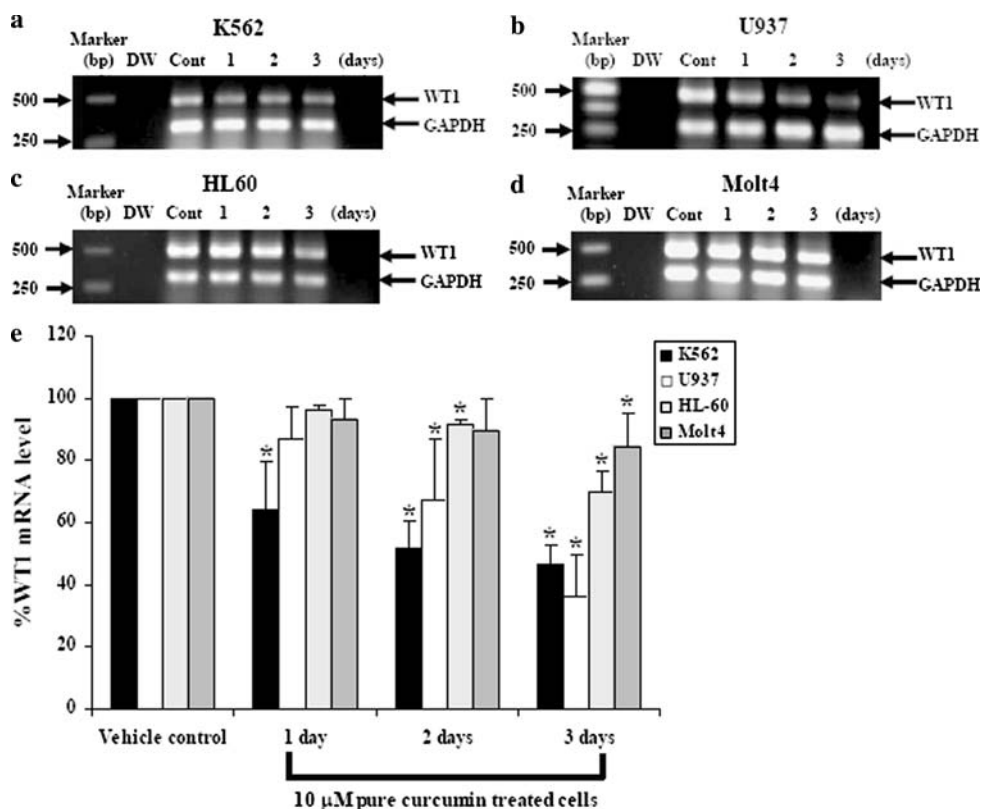


Fig. 7 The WT1 protein level in K562 and Molt4 cell lines cultured in 10 μ M of pure curcumin for 1, 2, and 3 days. The WT1 and GAPDH protein levels following treatment with 0.05% DMSO (Cont; Control) and 10 μ M of pure curcumin for 1, 2, and 3 days were determined in K562 (a) and Molt4 (b) cells by Western blot analysis. The bands (48–54 kDa for WT1 and 37 kDa for GAPDH) were quantified using a scan densitometer (c). WT1 protein levels were measured and normalized with GAPDH protein level. Data are the mean value \pm standard deviation (SD) of three independent experiments. Asterisks (*) denote values that were significantly different from the vehicle control ($P < 0.05$)

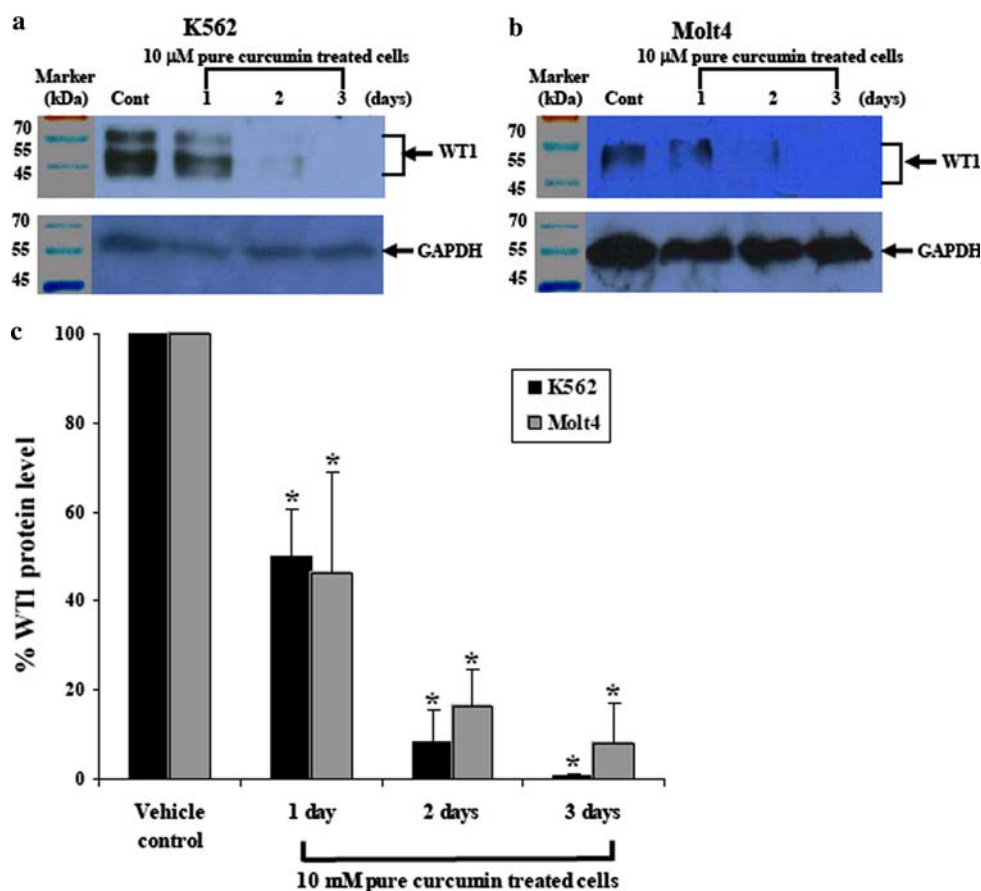
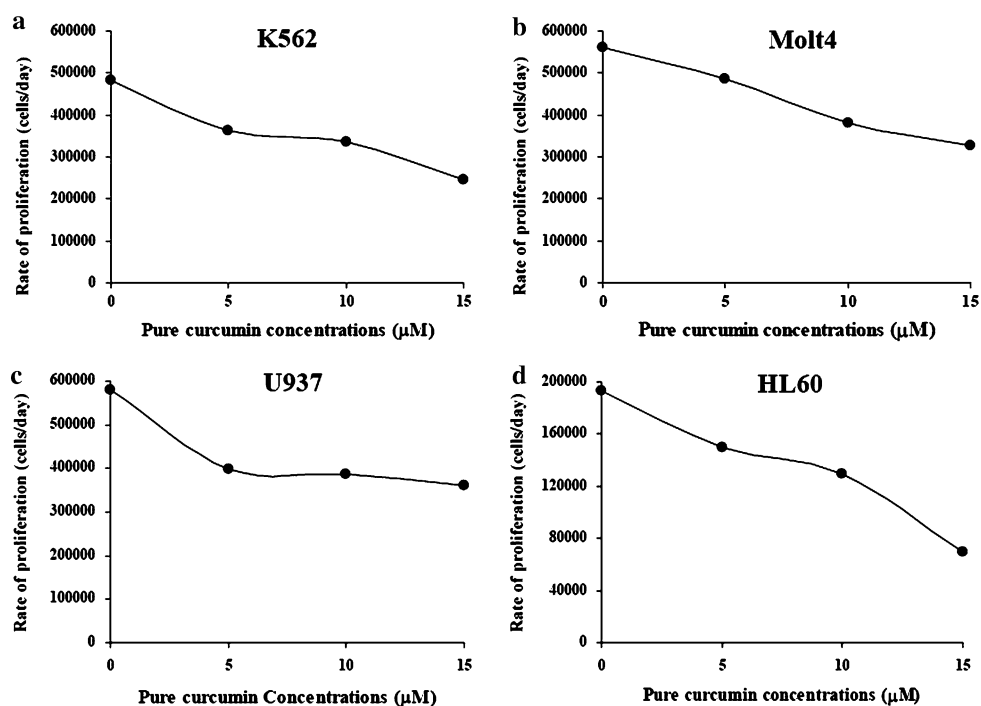


Fig. 8 The proliferation rate of K562 (a), Molt4 (b), U937 (c), and HL60 (d) cell lines cultured in 5, 10, and 15 μ M of pure curcumin for 1, 2, and 3 days. After incubating cells with various concentrations of pure curcumin (0, 5, 10 and 15 μ M), the numbers of leukemic cells were determined after 0, 1, 2, and 3 days via a trypan blue dye exclusion assay. The slope or cell growth rate at each predetermined pure curcumin concentration was determined from the plot of incubating time and cell number. Consequently, the rates of cell growth at different pure curcumin concentrations were compared with the normal growth rate, which was obtained from the control wells (no pure curcumin)



gene expression in a time-dependent manner. The changes in WT1 protein levels of Molt4 cells were more prominent compared to the mRNA levels. This could be explained in

two ways: (a) via the effect of pure curcumin on mRNA stability and (b) by the effect of pure curcumin on post-transcription processing. Previous studies have suggested that

compounds with antioxidant or anti-inflammatory activities also inhibit tumor promotion and cell proliferation. Pure curcumin is one of the compounds with remarkable antioxidant and free radical-scavenging activities [41–44]. Thus, pure curcumin also has an inhibitory effect on tumor promotion and cell proliferation. In a previous study pure curcumin was found to be the most effective in the DNA cleavage reaction and reduction of Cu (II) [45]. The presence of the diketone moiety in the pure curcumin molecule seems to be essential for the inhibitory activity [40].

Taken as a whole, the results indicate that treatment of human leukemic cell lines with non-cytotoxic concentrations (low doses; cell survival is higher than 80%) of pure curcumin inhibited *WT1* gene expression, whereas pure curcumin, at high dose, induced cell cytotoxicity (IC₅₀ = 44 µM). In an additional study, the three curcuminoid compounds also showed cytotoxicity to K562, U937, and HL60 cell lines [25]. The current results suggest that pure curcumin can potentially be used as a chemotherapeutic agent in human leukemic cancer. This research may lead to clinical trials in the future.

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