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## Histone deacetylase inhibitors, valproic acid and trichostatin-A induce apoptosis and affect acetylation status of p53 in ERG-positive prostate cancer cells

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### Abstract

An ETS family member, ETS Related Gene (ERG) is involved in the Ewing family of tumors as well as leukemias. Rearrangement of the ERG gene with the TMPRSS2 gene has been identified in the majority of prostate cancer patients. Additionally, overexpression of ERG is associated with un-favorable prognosis in prostate cancer patients similar to leukemia patients. Histone acetyltransferases (HATs) and histone deacetylases (HDACs) regulate transcription as well as epigenetic status of genes through acetylation of both histones and transcription factors. Deregulation of HATs and HDACs is frequently seen in various cancers, including prostate cancer. Many cellular oncogenes as well as tumor viral proteins are known to target either or both HATs and HDACs. Several studies have demonstrated that there are alterations of HDAC activity in prostate cancer cells. Recently, we found that ERG binds and inhibits HATs, which suggests that ERG is involved in deregulation of protein acetylation. Additionally, it has been shown that ERG is associated with a higher expression of HDACs. In this study, we tested the effect of the HDAC inhibitors valproic acid (VPA) and trichostatin-A (TSA) on ERG-positive prostate cancer cells (VCaP). We found that VPA and TSA induce apoptosis, upregulate p21/Waf1/CIP1, repress TMPRSS2-ERG expression and affect acetylation status of p53 in VCaP cells. These results suggest that HDAC inhibitors might restore HAT activity through two different ways: by inhibiting HDAC activity and by repressing HAT targeting oncoproteins such as ERG.

### Keywords

valproic acid; trichostatin A; histone deacetylase; histone acetyltransferase; CBP/p300; p53; ETS related gene; prostate cancer

### Introduction

ERG (Ets Related Gene) belongs to the ETS family of transcriptional factors, which shares a homologous 84 amino acids DNA binding domain (1,2). ERG gene codes for sequence specific DNA binding proteins that function as transcriptional activators (3,4). ERG gene is rearranged in Ewing family of tumors and also in leukemias (5–9). ERG gene and its fusion genes (EWS-ERG and TLS/FUS-ERG) code for sequence specific transcriptional activators

(7,8). It appears that fusion of RNA binding proteins (EWS and TLS/FUS) with DNA binding proteins (ERG and Fli-1) leads to human cancers (7,8,10,11). These fusion proteins were shown to inhibit apoptosis, which may be one of the reasons for the activation of the ERG gene in leukemias and human solid tumors (12).

Rearrangement of ERG is also observed in prostate cancer (13). Among genetic alterations associated with prostate cancer, the rearrangement between the androgen responsive transmembrane protease serine 2 (TMPRSS2) and transcriptional factor ERG has been detected in approximately 50% of patients (13). This rearrangement results in overexpression of ERG (14–17). TMPRSS2 also fuses with other ETS genes, namely ETV1 (ER81), ETV4 (PEA3) and ETV5; however, they are less common in prostate cancers (15,18,19). ERG is involved in numerous roles in the developmental processes of neural crest, angiogenesis/vasculogenesis, hematogenesis, and chondrogenesis (20–24). Overexpression of normal or aberrant ERG is associated with transformation, antiapoptotic property, and invasiveness (12,25–28). In prostate cancer, the majority of TMPRSS2-ERG rearrangements produce truncated ERG proteins (29,30). The expression of the chimeric protein, TMPRSS2-ERG, in which the first five amino acids of TMPRSS2 are fused to truncated ERG is associated with early PSA recurrences and seminal vesicle invasion. Additionally, chimeric TMPRSS2-ERG mRNA which translates into full length ERG proteins, is associated with aggressive phenotypes (29). Several studies suggest that an overexpression of ERG alone is responsible for inducing epithelial hyperplasia and prostatic intraepithelial neoplasia (PIN) in mouse; however, it requires PTEN loss or forced expression of activated Akt for full carcinoma progression (31–34). Thus, it is possible that ERG is a potential therapeutic target in prostate cancer.

Covalent modification of amino-terminal tails of core histones (H2A, H2B, H3, and H4) plays an important role in transcriptional regulation and epigenetic control. Acetylation/deacetylation of core histones represent just one of the complex modulations on nucleosome (35). In general, acetylation of histone H3 and H4 following recruitment of histone acetyltransferases (HATs), are attributed to transcriptional activation. On the other hand, recruitment of histone deacetylases (HDACs) represses transcription by reversing acetylation. The substrates of HATs as well as HDACs are not limited to histones, but expanded to transcriptional factors such as p53, E2F, and NF- $\kappa$ B (36).

Several lines of evidence suggest that disruption of acetylation/deacetylation activity contributes to tumorigenesis. The individuals diagnosed with Rubinstein-Tybi syndrome exhibit hemizygoty at CBP locus show higher incidence of cancer of neural crest origin (37). Chromosomal translocation of CBP/p300 with MOZ, MORF, and MLL has been documented in several hematological malignancies (28–40). Viral onco-proteins such as E1A of adenovirus, E6 of human Papilloma virus, Tax of HTLV-1, and large T of SV40 are known to target CBP/p300 and repress its cofactor activity (41–44). Cellular chimeric fusion proteins AML1-ETO and E2A-PbX-1 also target p300/CBP (45,46). We have shown that EWS-ATF-1 from malignant melanoma of soft parts repress p53 transcriptional activation through binding to CBP (47). Additionally, we and others found that EWS-Fli-1 in Ewing's sarcoma and normal Fli-1, which is the closest member of ERG in ETS family, also targets CBP/p300 and repress its HAT activity of transcriptional cofactor (48,49). Recently, we also found that truncated ERG specific to prostate cancer can bind to CBP and repress its cofactor activity for a nuclear receptor, which requires CBP/p300 (unpublished data). These studies suggest that alteration of HAT activity is a contributing factor for pathogenesis of these malignancies. In terms of HDAC, AML1-ETO recruits a co-repressor complex that contains HDAC1 activity (50,51). Administration of HDAC inhibitors subvert ETO-mediated repression and induce differentiation. PML-RAR $\alpha$  in acute promyelocytic leukemia (APL) associates N-CoR/Sin3/HDAC1 complex with higher affinity than normal

RAR $\alpha$  and its dissociation requires a pharmacological dose of all-trans retinoic acid (52). These studies suggest that modulating HAT/HDAC activity by oncoproteins plays an important role in tumorigenesis.

Recently HDAC inhibitors have begun emerging as a new class of chemotherapeutic agents for various cancers including prostate cancer. Histone deacetylase (HDAC) family including 18 members are subdivided into four classes based on homology of the catalytic domain, organization of the domain, and requirement for cofactor (53). Class I and class II HDAC subfamilies are yeast Rpd3 and Hda1 homologues, respectively. Class III is comprised of NAD-dependent deacetylases (sirtuins) and shares homology with yeast Sir2. Class IV contains only HDAC11 and its characterization remains for further study. There are several lines of evidence suggesting upregulation of HDACs in prostate cancer. Higher expression of class I HDAC (HDAC1, 2, 3) was observed in aggressive prostate cancer (54,55). High HDAC2 expression correlates with shorter survival time (55). Nuclear localization of class II HDAC4, which is shuttling between nucleus and cytoplasm in normal cells, was detected in hormone refractory prostate cancer (56).

Valproic acid (2-propylpentanoic acid) (VPA) is a short-chain fatty acid class of histone deacetylase inhibitor (HDACI). VPA is a well-tolerated, established drug for epilepsy and bi-polar disorder (57). VPA inhibits class I and class II HDACs except HDAC6 or HDAC10 (58). It is suggested that VPA inhibits HDAC activity by binding to the HDAC catalytic site (59). Both Valproic acid and Trichostatin-A serve as a basis for newly-developing HDACI inhibitors. Because VPA is one of the least toxic among HDAC inhibitors, it is now subjected to late clinical trials; however, little is known as to how it affects gene network in prostate cancer.

In this report, we show that VPA and TSA induce apoptosis, upregulate p21/Waf1/CIP1 expression, repress TMPRSS2-ERG expression, and affect acetylation status of p53 in ERG-positive prostate cancer cells.

## Materials and methods

### Tissue culture and cell viability assay

The human VCaP prostate cancer cell line was obtained from the American Type Culture Collection. VCaP cells were maintained in Dulbecco's Modified Eagle Medium (DMEM) supplemented with 15% fetal bovine serum and 1% penicillin/streptomycin at 37°C with 5% CO<sub>2</sub> atmosphere. Valproic acid (VPA) and trichostatin-A (TSA) were purchased from Sigma-Aldrich. For viability assay, cells were seeded at 15,000 cells/well in opaque-walled 96-well plates for 24 h before the administration of drugs. TSA, VPA, or vehicle control was added to the cells at the indicated concentrations. Cells were allowed to incubate at 37°C for 24, 48, or 72 h. The cell viability was measured using CellTiter-Glo reagent according to the manufacturer's instructions (Promega). The luminescent signal was measured using Fluoroskan Ascent FL and data were analyzed with Ascent software version 2.6 (Thermo Electron Corp.). IC<sub>50</sub> was calculated using the Hill-Slope model.

### In situ cell death detection (TUNEL) assay

Cells were seeded at 200,000 cells per chamber on glass slides and incubated overnight. Medium was replaced with fresh medium containing TSA or VPA for 24 h. Cells were washed with PBS, then allowed to air dry. Cells were fixed using freshly prepared 4% formaldehyde in PBS and incubated at room temperature for 1 h. Cells were washed with PBS and then incubated with permeabilization solution (0.1% Triton X-100 in 0.1% sodium citrate) for 2 min on ice. Cell death was detected using *In Situ* Cell Death Detection kit, Fluorescein (Roche) according to the manufacturer's instructions. Subsequently cells were

stained using DAPI (Santa Cruz). Micrographs were taken using Olympus IX-71 fluorescence microscope.

### Caspase 3/7 activity assay

Cells were seeded at 15,000 cells/well in 96-well plates 24 h before the addition of TSA or VPA. Cells were treated with TSA (5–1000 nM) or VPA (0.05–20 mM) or control (DMSO) for 12 or 24 h. Caspase 3/7 activity was measured using Caspase-Glo 3/7 assay reagent (Promega) according to manufacturer's protocol. The luminescent signals were measured using Fluoroskan Ascent FL (Thermo Electron Corp.).

### Western blot analysis

VCaP cells were seeded at 10 millions per 100 mm plate overnight. The next day TSA or VPA was added to cells at the indicated concentrations for 12 or 24 h. Total cell lysate was prepared using the lysis buffer (50 mM Tris-HCl (pH 7.4), 1% NP-40, 0.125 % sodium deoxycholate, 150 mM NaCl, 1 mM EDTA, 1 mM PMSF, 100  $\mu$ M NaF, protease inhibitor tablet (Roche). Protein concentration was determined using Bradford method (Bio-Rad). Cells were then lysed and protein complexes were separated on 4–20% gradient SDS-PAGE gel. Membrane was incubated with ERG (C-20, Santa Cruz), p21 (12D1, Cell Signaling), acetylated p53 (Lys373, Upstate), total p53 (Ab-1, Calbiochem) and  $\beta$ -actin (C-4, Santa Cruz) primary antibodies. Proteins were detected using ECL detection kit (GE Healthcare).

### Quantitative RT-PCR studies

Total RNA was isolated from VCaP cells treated with 1  $\mu$ M TSA or 10 mM valproic acid for 24 h using RNAspin Mini kit (GE Healthcare) and immediately treated with RNase inhibitor (Roche). First strand cDNA was synthesized with 1  $\mu$ g of total RNA using Advantage RT-for-PCR kit (Clontech). SYBR Green (Qiagen) was used to detect PCR products using Bio-Rad Mini Opticon real-time PCR system and data were analyzed with Opticon Monitor 3 software (Bio-Rad). GAPDH was used to normalize samples. The primers used were as follows: ERG (forward: 5'-CGCCTACAAGTTCG ACTTCC-3', reverse: 5'-CCCAGTTGGTGAATTCCAGT-3'), p21 (forward: 5'-CCTCATCCCGTGTCTCCTTT-3', reverse: 5'-GTACCACCCAGCGGACAAGT-3'), and GAPDH (forward: 5'-AAGGTGAAGGTCGGAGTCAA-3', reverse: 5'-AATGAA GGGGTCATTGATGG-3').

### Statistical analysis

One way analysis of variance was performed to detect overall difference among the samples. Then the Student-Newman-Keuls (SNK) test was applied to determine the significant values among the samples. Also student's t-test was used wherever applicable.

## Results

### Induction of apoptosis by TSA and VPA in ERG-positive prostate cancer cells

VCaP cell line was established from a vertebral metastasis of hormone refractory prostate cancer (60). VCaP cells have an androgen-responsive, AR-positive and PSA-positive phenotype. Recently, the expression of fusion genes by rearrangements of TMPRSS2 and ERG on chromosome 21 was found in VCaP cells. In consequence of this rearrangement, amino-terminal 39 amino acids of ERG are deleted and the open reading frame starts from the first in-frame ATG of ERG resulting in shorter 423 aa protein. We confirmed the expression of truncated ERG proteins in VCaP cells by Western blot analysis as a major band shown in Fig. 1. There also exists minor lower bands possibly reflecting alternative splicing variants in VCaP cells suggested in other studies (29).

Previous studies suggest that Valproic acid is effective on ERG-negative prostate cancer cell lines, therefore we examined the effect on TMPRSS2-ERG positive VCaP cells (61). First we tested whether VPA or TSA would have any effect on VCaP cell growth. Cell viability assays were performed using VPA or TSA at various concentrations and time intervals. Our results indicate that VPA and TSA inhibit cell growth in a dose- and time- dependent manner (Fig. 2). More than 80% decrease in viability was observed at the concentration of 10 mM VPA after 72 h incubation, or 100 nM TSA after 72 h incubation, respectively. The IC<sub>50</sub> (95% CI) values after 72 h treatment were 1.3 mM (1.0 mM–1.5 mM) for VPA and 10 nM (6.4 nM–14 nM) for TSA, respectively. These declines of viability are comparable to other TMPRSS2-ERG-negative prostate cancer cell lines (61). We observed that morphological changes characteristics to apoptosis such as membrane blebbing and nuclear condensation appeared within 24 h with either 100 nM TSA or 10 mM VPA (data not shown). These observations were confirmed by terminal deoxynucleotidyl transferase-mediated dUTP nick end labeling (TUNEL) assay. As shown in Fig. 3, the number of apoptotic cells labeled with fluorescein-dUTP increased in dose-dependent manner in both VPA (Fig. 3A) and TSA (Fig. 3B) while vehicle treated control cells showed no significant sign apoptosis. The induction of apoptosis was further confirmed by caspase activities. As shown in Fig. 4A and B, caspase 3/7 activity was dramatically increased over 5 mM VPA or 100 nM TSA after 24 h incubation. Taken together these data suggest that these drugs induce apoptosis in VCaP cells. The effect of VPA for apoptosis was consistent with VPA effect on ERG- negative prostate cancer cell lines (61).

### The effect of TSA and VPA on TMPRSS2-ERG and tumor suppressor genes

Next we tested the effect of TSA and VPA on p21Waf1/CIP1 (CDKN1A) expression. Western blot assay revealed that p21 was induced at 100 nM TSA at 12 h (Fig. 5A and B). Similar induction was observed at 10 mM VPA for 12 h, however, a strong induction occurred after 24 h incubation (Fig. 5B). The induction of p21 was further confirmed with quantitative RT-PCR. Fourteen-fold induction of p21 mRNA at 10 mM VPA (Fig. 5C) and 25-fold induction at 1  $\mu$ M TSA (Fig. 5D) were observed after 24 h treatment, suggesting that both VPA and TSA activate p21 transcription. These results are consistent with the induction of p21 by HDAC inhibitors in various cancer cells including prostate cancer (62–64).

Previous studies have shown that HDAC inhibitors repress ERG expression (64,65). Therefore, we investigated the effect of TSA and VPA on TMPRSS2-ERG expression. Western blot analysis showed that expression of TMPRSS2-ERG decreased at 1  $\mu$ M TSA treatment or 10 mM VPA treatment at as early as 12 h of incubation (Fig. 6). Similar reduction was observed after 24 h of incubation (Fig. 6). These results were confirmed with quantitative RT-PCR. VCaP cells were treated with either TSA or VPA and the relative expression level of mRNA was measured. As shown in Fig. 6C, the mRNA levels were significantly decreased after 24 h incubation with 10 mM VPA. Similar repression was observed in 1  $\mu$ M of TSA (Fig. 6D). These results suggest that VPA and TSA may interfere with TMPRSS2-ERG expression in prostate cancer.

Histone acetyltransferase CBP/p300 acetylates p53 at Lys-373/Lys382 which affects DNA binding activity, and transcriptional activation of target genes such as p21 and Bax (66). Viral oncoproteins are known to inhibit this acetylation by targeting CBP/p300 (41–44). We found that both normal and truncated ERG also bind to CBP and repress its activity (unpublished data). Since VPA and TSA repress ERG expression in VCaP cells, we postulated that the downregulation of expression of ERG by HDAC inhibitor leads to the restoration of CBP/p300 histone acetylase activity subsequently allowing HATs to acetylate its target transcriptional factors, such as p53. As shown in Fig. 7, acetylation of p53 at Lys-373 was greatly enhanced at 10 mM VPA and 1  $\mu$ M TSA after 24 h incubation. These

treatments do not appear to have any effect on total p53 protein levels. These results suggest that VPA and TSA affect acetylation status of p53 in prostate cancer.

## Discussion

In this study, we found that VPA induces apoptosis in ERG rearranged prostate cancer cells, affects status of tumor suppressor genes, and represses expression of TMPRSS2-ERG. TMPRSS2-ERG expression is one of the most frequent genetic alterations known to occur in prostate cancer patients (13). The majority of TMPRSS2-ERG transcripts seen in patients skip Exon 3, which contain native ATG and result in a truncated ERG protein (29). Also, several studies indicate that ERG expression in prostate cancer contributes to the oncogenic properties of cell proliferation, invasion, metastasis, and cell motility (28,31,67). The higher expression of ERG in prostate cancer correlates with unfavorable prognosis (14). Therefore, targeting ERG expression by HDAC inhibitor may have an impact on developing new therapeutic strategy.

Deregulation of HDAC activities are observed in a variety of cancers. Administration of HDAC inhibitors to prostate cancer cells demonstrate suppression of growth, differentiation, and induce apoptosis, which suggests that HDAC activity is essential for maintaining tumor status (61,64,68). However how these HDAC inhibitors affect transcriptional network that sustain tumor properties is poorly understood. HDAC inhibitors are thought to modulate selectively the expression of fraction of genes. Among these genes, p21/Waf1/CIP1 has emerged as a common target of HDAC inhibitors for upregulation (62–64). It appears that the repression of negatively regulating factor is required for upregulation of p21. For example, p21 is repressed by c-Myc through the interaction of Sp1/Sp3 or Miz-1 (69). Sp1/Sp2 on p21 promoter has an important role in both activation and repression of HDAC1 (63). EWS-Fli-1, which is closely related to ERG at DNA-binding domain binds to p21 promoter and downregulates p21 expression through inhibition of p300 acetyltransferase activity. This repression of EWS-Fli-1 was relieved by either overexpression of p300 or by the administration of sodium-butylate (48). Downregulation of EWS-Fli-1 by antisense dramatically increased p21 expression (70). We and others showed that EWS-Fli-1 and normal ERG share the same target sequences (3,4,7,10). Therefore, it might be possible that TMPRSS2-ERG is involved in p21 repression through binding to its promoter. The association between ERG and HDAC has been demonstrated in several studies. ERG recruits HDAC and represses collagen promoter activity and TSA relieves this repression (71). ESET, which was cloned as interacting protein with ERG, recruits HDAC1/mSin3 (72). One might think administration of VPA and TSA could reduce this inhibition at least in part by repressing TMPRSS2-ERG expression.

Acetylation of p53 by CBP/p300 increases DNA binding and transcriptional activity on p21 promoter (66,73). Viral oncoproteins frequently target histone acetylase CBP/p300 and repress its activity (41–44). Recently, we found that truncated ERG binds and interferes with CBP mediated transcriptional activation of a nuclear receptor. Since VPA and TSA repress TMPRSS2-ERG expression, it could be possible that these HDAC inhibitors rescue CBP/p300 by subverting the inhibitory effect of ERG that restore p53 acetylation under certain situations where the HDACs are inactivated by VPA or TSA. In this regard, acetylation of p53 is not evident until 24 h after administration of TSA or VPA while the repression of TMPRSS2-ERG precedes acetylation by at least 12 h. The acetylation also requires the amount of 1  $\mu$ M TSA and 10 mM VPA that is enough to repress TMPRSS2-ERG. The reason that the effective concentration of VPA to affect p53 is relatively high in this study might reside in its ineffectiveness to repression of TMPRSS2-ERG even at higher concentration or HDAC selectivity of VPA (59). It might be possible that the release of CBP/p300 from blockade of TMPRSS2-ERG following the repression of TMPRSS2-ERG

expression restores acetylation of p53 in the absence of the activity of HDACs. The TMPRSS2-ERG fusion gene was associated with upregulation of HDAC1 (74). Recently, we found that ectopic expression of truncated-ERG increases SIRT1 activity (data not shown). Given that the re-arrangement of ERG is supposedly an early event of tumorigenesis, it is hypothesized that TMPRSS2-ERG insulates p53 from acetylation through both interference with CBP/p300 HAT activity and inducing HDAC expression and therefore maintains p53 inactive (Fig. 8). In this model, HDAC inhibitors reactivate tumor suppressor genes not only by repressing HDAC activities, but also by repressing the expression of HAT targeting oncogenes such as ERG.

We showed the dual role of HDAC inhibitors in repressing TMPRSS2-ERG expression and affecting p53 acetylation status, therefore, valproic acid and other HDAC inhibitors may be useful to prevent further advance of early stage prostate cancer. In this regard, a combination of different HDAC inhibitors might help in order to retain the therapeutic dose of each inhibitor in the moderate range and to inhibit all of the HDACs involved in repressing major tumor suppressor genes.

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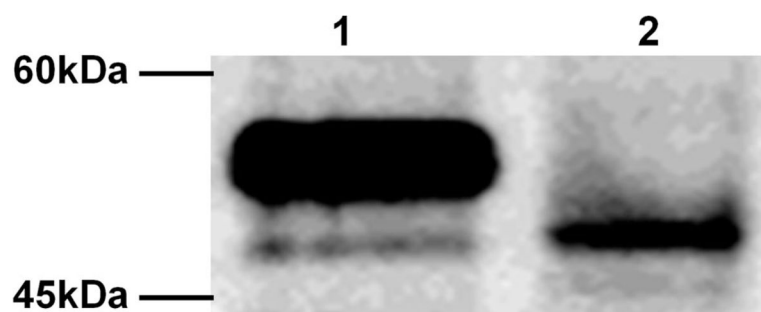
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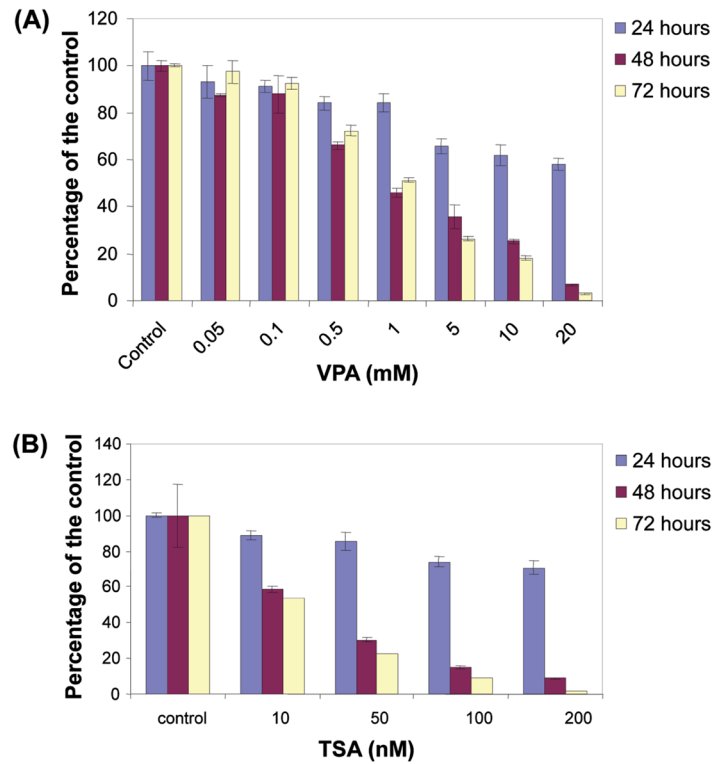
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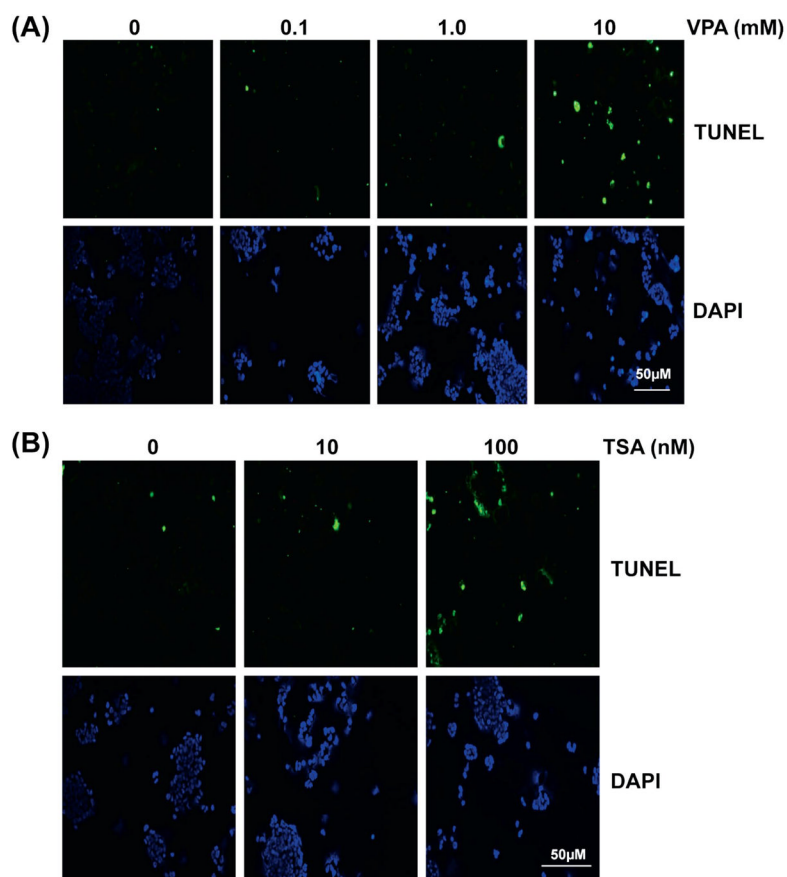
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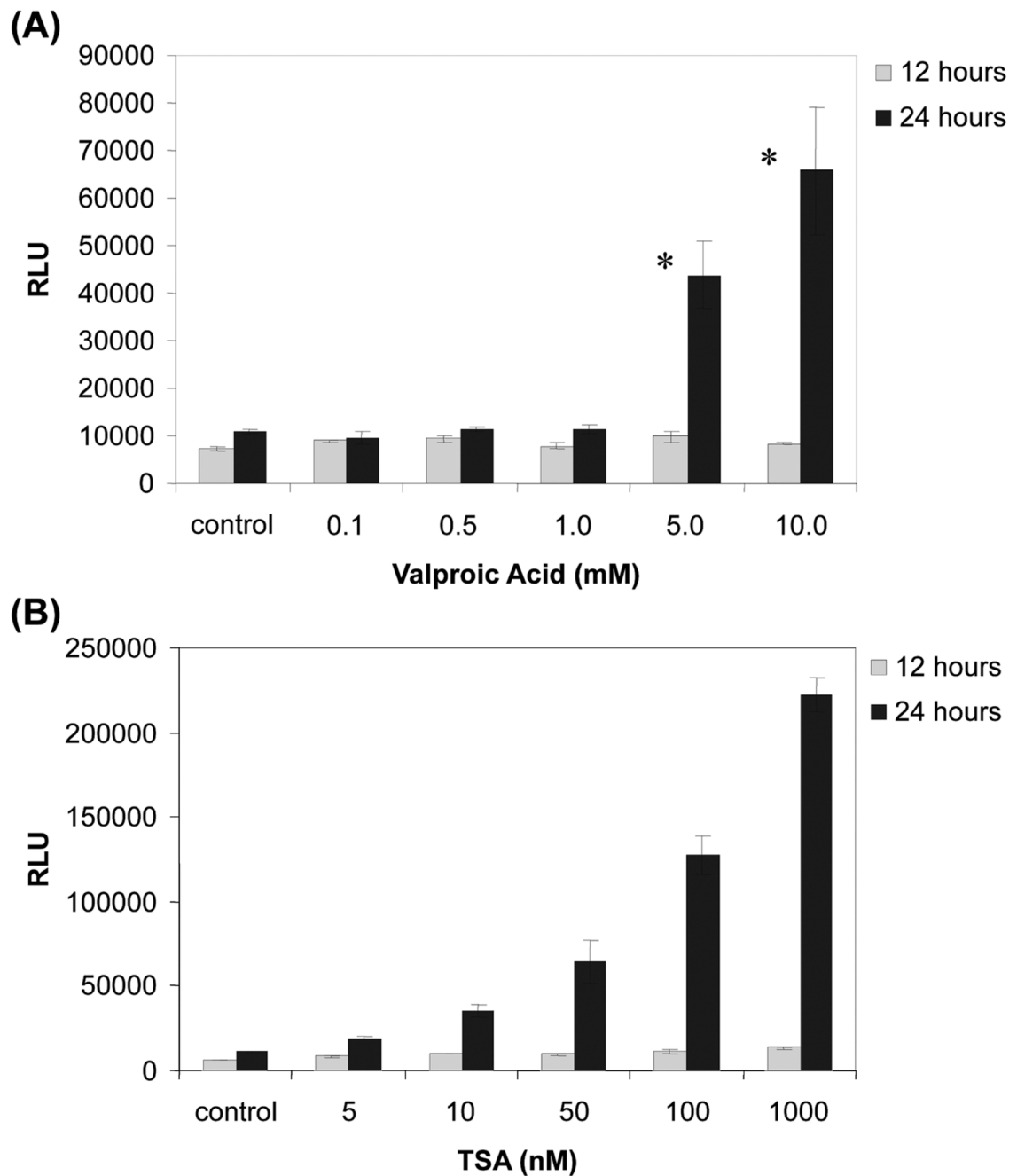
**Figure 1.** Truncated-ERG is expressed in a prostate cancer cell line. Western blot analysis was performed with either COS-1 transfected with full-length ERG-2 expression vector (lane 1) or VCaP cell lysate (lane 2).



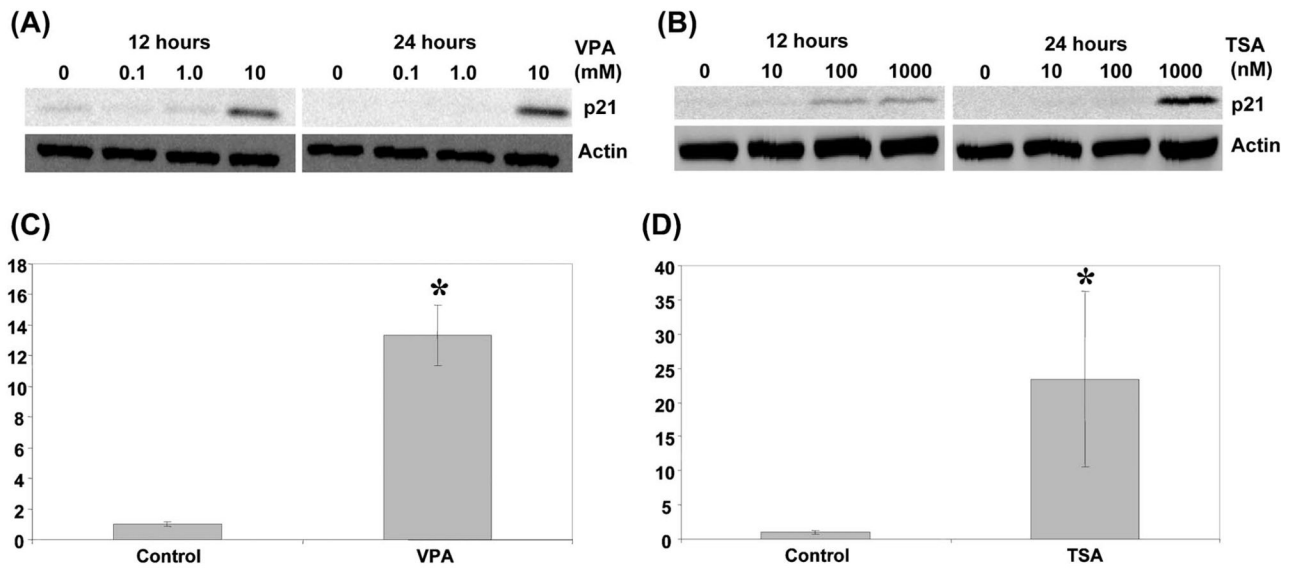
**Figure 2.** Both TSA and valproic acid impair cell viability of VCaP cells. (A) Cells were treated with variable amount of valproic acid (0.05–20 mM) or vehicle control for 24, 48, or 72 h. (B) Cells were treated with variable amount of trichostatin-A (10–200 nM) or vehicle control for 24, 48, or 72 h. Results are shown as the mean of percentage of control of three independent experiments with standard deviations.



**Figure 3.** Both TSA and valproic acid induce apoptosis in VCaP cells. Apoptosis of VCaP cells were analyzed using TUNEL reaction. (A) Cells were treated with variable amount of valproic acid (0.1–10 mM) or vehicle control for 24 h. (B) Cells were treated with variable amount of TSA (10–100 nM) or vehicle control for 24 h. Fluorescent signals after labeling with fluorescein-dUTP are shown in the top panels. Bottom panels show DAPI staining for nucleus. Scale bar, 50  $\mu$ m.

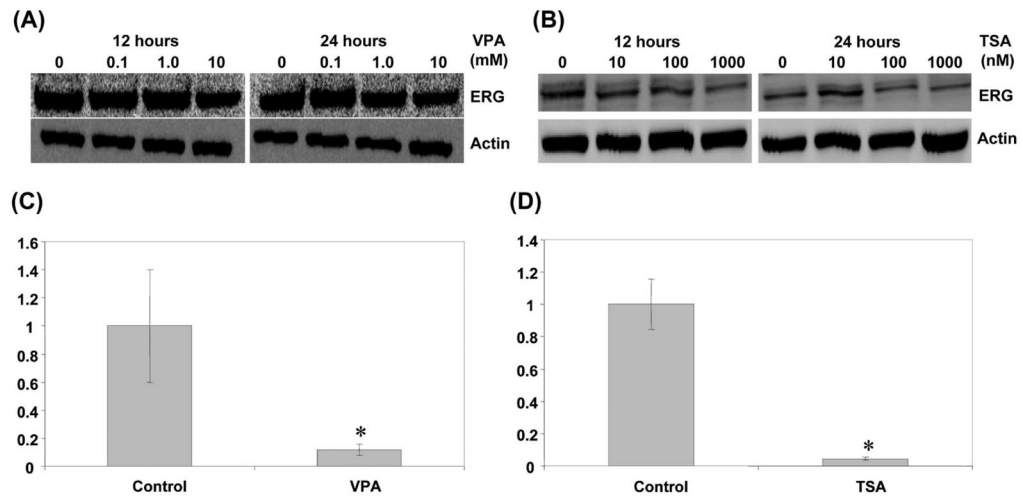


**Figure 4.** Both valproic acid and TSA increase caspase 3/7 activity. (A) Cells were treated with valproic Acid (0.1–10 mM) or vehicle control for 12 or 24 h before the measurement of caspase 3/7 activity. (B) Cells were treated with TSA (5–1000 nM) or vehicle control (DMSO) for 12 or 24 h before the measurement of caspase 3/7 activity. Caspase 3/7 activity was determined using Caspase-Glo 3/7 assay reagent (Promega) according to manufacturer’s protocol. Values represent the mean of luminescence signals of three independent experiments with standard deviations. \*P<0.01



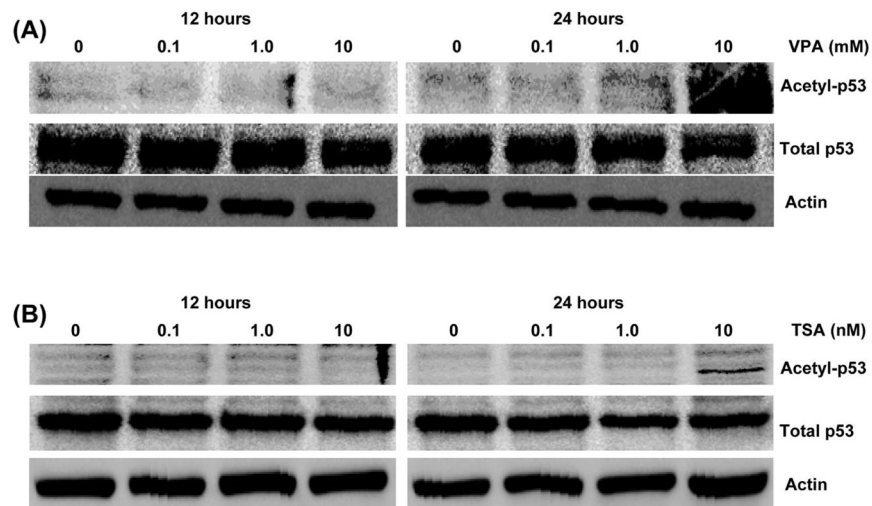
**Figure 5.** Effect of TSA and valproic acid on p21 expression. (A) Western blot assay was performed after 12 or 24 h valproic acid treatments at the indicated concentrations. The blot with anti-p21 antibody is shown at the top.  $\beta$ -actin used as a loading control is shown at the bottom. (B) Western blot assay was performed after 12 or 24 h TSA treatments at the indicated concentrations. The blot with anti-p21 antibody is shown at the top.  $\beta$ -actin used as a loading control is shown at the bottom. (C) The relative expression level of p21 mRNA was determined with quantitative RT-PCR after 24 h treatment with 10 mM valproic acid. (D) The relative expression level of p21 mRNA was determined with quantitative RT-PCR after 24 h treatment with 1  $\mu$ M TSA. In both cases, GAPDH was used to normalize samples. The results represent fold activation over control of three independent experiments with standard deviations. \* $P < 0.05$





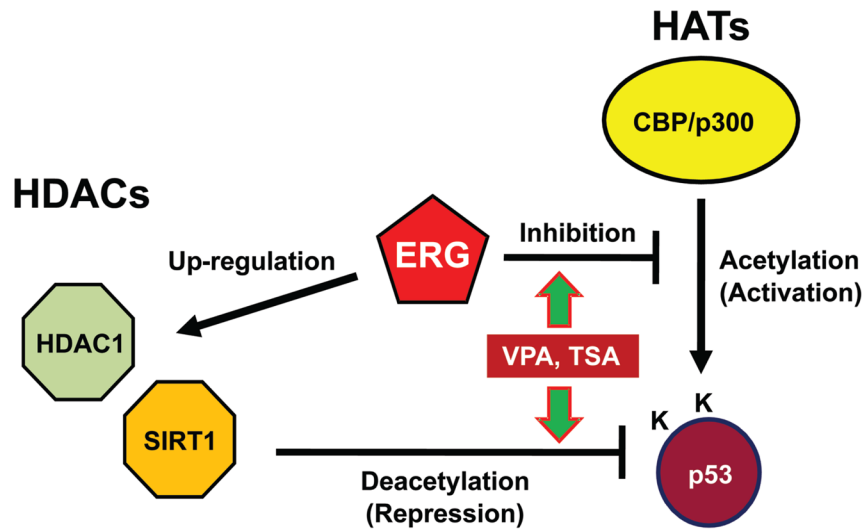
**Figure 6.**

Effect of TSA and valproic acid on TMPRSS2-ERG expression. (A) Western blot assay was performed after 12 or 24 h valproic acid treatments at the indicated concentrations. The blot with anti-ERG antibody is shown at the top.  $\beta$ -actin used as a loading control is shown at the bottom. (B) Western blot assay was performed after 12 or 24 h TSA treatments at the indicated concentrations. The blot with anti-ERG antibody is shown at the top.  $\beta$ -actin used as a loading control is shown at the bottom. (C) The relative expression level of TMPRSS2-ERG mRNA was determined with quantitative RT-PCR after 24 h treatment with 10 mM valproic acid. (D) The relative expression level of TMPRSS2-ERG mRNA was determined with quantitative RT-PCR after 24 h treatment with 1  $\mu$ M TSA. In both cases, GAPDH was used to normalize samples. The results represent relative values against control (arbitrarily set to 1) of three independent experiments with standard deviations. \*  $P < 0.05$



**Figure 7.**

Both TSA and valproic acid induce acetylation of p53 in VCaP cells. (A) Western blot assays were performed on VCaP cells incubated for 12 or 24 h at the indicated concentrations of valproic acid. Blot with anti-acetylated p53-Lys 373 (top), anti-p53 (middle), or anti- $\beta$ -actin (bottom) are shown. (B) Western blots were performed on VCaP cells incubated for 12 or 24 h at the indicated concentrations of TSA. Blot with anti-acetylated p53-Lys 373 (top), anti-p53 (middle), or anti- $\beta$ -actin (bottom) are shown.



**Figure 8.** ERG interferes with acetylation of p53 in two ways. ERG binds CBP/p300 histone acetyltransferase and inhibits its activity of acetylation on p53. ERG also induces expression of HDACs which deacetylate p53.