

# Role of cofilin-1 in arsenic trioxide-induced apoptosis of NB4-R1 cells

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**Abstract.** All-trans retinoic acid (ATRA) and arsenic trioxide ( $As_2O_3$ ) are currently first-line treatments for acute promyelocytic leukemia (APL). However, a number of patients with APL are resistant to ATRA but still sensitive to  $As_2O_3$ , and the underlying mechanisms of this remain unclear. In the present study, two-dimensional gel electrophoresis, mass spectrometry and other proteomic methods were applied to screen and identify the differentially expressed proteins between the retinoic acid-sensitive cell lines and drug-resistant cell lines. The results demonstrated that in retinoic acid-resistant NB4-R1 cells, the protein expression of cofilin-1 was markedly increased compared with that in the drug-sensitive NB4 cells. Subsequently, the effects of cofilin-1 on  $As_2O_3$ -induced apoptosis in NB4-R1 cells were further investigated. The results revealed that cell viability was markedly suppressed and apoptosis was increased in the  $As_2O_3$ -treated NB4-R1 cells, with increased expression levels of cleaved-poly (ADP-ribose) polymerase and cleaved-caspase 12. Cofilin-1 expression was significantly decreased at both the mRNA and protein levels in the  $As_2O_3$ -treated group compared with the control. Western blotting further revealed that  $As_2O_3$  treatment decreased the cytoplasmic cofilin-1 level but increased its expression in the mitochondrion. However, the opposite effects of  $As_2O_3$  on the cytochrome C distribution were found in NB4-R1 cells. This suggested that  $As_2O_3$  can induce the transfer of cofilin-1 from the cytoplasm to mitochondria and trigger the release of mitochondrial cytochrome C in NB4-R1 cells. Moreover, cofilin-1 knockdown by its specific short hairpin RNA significantly suppressed  $As_2O_3$ -induced NB4-R1 cell apoptosis and inhibited the release of mitochondrial cytochrome C. Whereas, overexpression of cofilin-1 using a plasmid vector carrying cofilin-1 increased the release of cytochrome C into the

cytoplasm from the mitochondria in  $As_2O_3$ -treated NB4-R1 cells. In conclusion, cofilin-1 played a role in  $As_2O_3$ -induced NB4-R1 cell apoptosis and it might be a novel target for APL treatment.

## Introduction

Acute promyelocytic leukemia (APL) accounts for 10-12% of all cases of acute myeloid leukemia worldwide, with a characteristic chromosomal abnormality t(15;17)(q22;q23) and a specific promyelocytic leukemia protein (PML)/retinoic acid receptor  $\alpha$  (RAR $\alpha$ ) fusion protein (1,2). APL results from a blockade of granulocyte differentiation at the promyelocytic stage and is associated with a high incidence of coagulopathy, including disseminated intravascular coagulation, fibrinolysis and proteolysis (3). In APL, there is a tendency to bleed, disproportionate to thrombocytopenia (4). APL blasts in the bone marrow can lead to megakaryocyte inhibition. Besides, the promyelocytes of APL are able to activate the coagulation cascade and increase procoagulant activity in endothelial cells (3). The coagulopathy would also induce thrombocytopenia. Currently, combined all-trans retinoic acid (ATRA) and arsenic trioxide ( $As_2O_3$ ) treatment is recommended as the first-line treatment for low-risk APL worldwide (5), with a complete remission rate of 94-100%, a 2-year overall survival rate of 97% and a 4-year survival rate of 93% (6,7). It has been reported that arsenic agent can bind to the PML portion of PML/RAR $\alpha$  protein and activate the ubiquitin-proteasome system, leading to the degradation of PML/RAR $\alpha$  protein (8) and the apoptosis of APL cells. When ATRA combines with RARs or retinoid X receptors of PML/RAR $\alpha$  protein, RAR $\alpha$  can further induce APL cell differentiation, and promote myeloid and granulocyte maturation (9). However, the key pathways and proteins involved in the degradation of PML/RAR $\alpha$  protein and apoptosis remain unclear; and certain patients relapse with resistance to ATRA or  $As_2O_3$ . Therefore, there have been numerous studies on the APL apoptosis pathway and the mechanism of resistance to ATRA and  $As_2O_3$ . Several studies have found mutations in the PML gene that contribute to resistance to arsenic. Goto *et al* (10) reported A216V and L218P mutations of the PML protein in two arsenic-resistant cases. In 2014, a previous study found a PML gene mutation through gene sequencing and proposed a 'mutation hotspot' (c202-s220) of PML in the case of arsenic resistance (11).

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Patients with PML mutations have a high fatality rate when arsenic resistance occurs. A French study successfully established a mouse model of the A216V mutation, which presented resistance to arsenic treatment (12). ATRA resistance has a more complex mechanism. Prolonged oral administration of ATRA can lead to increased cytochrome P450 oxidase activity, which results in decreased blood ATRA concentration (13). Elevation of cellular retinoic acid-binding protein contributes to a decrease in free ATRA, and a decreased ATRA concentration in the nucleus also results in reduced efficacy (14,15). In the present study, using proteomics research methods, a total of 21 differentially expressed proteins between retinoic-resistant cell lines and non-resistant cell lines were screened and identified, among which the expression of cofilin-1 was upregulated.

Cofilin is a 21-kD actin-binding protein that is universally present in eukaryotes and is crucially involved in regulating the reorganization of the cytoskeleton and muscle development (16). In humans, there are two cofilin gene subtypes, cofilin-1 and cofilin-2, which encode different proteins. The former is expressed in a variety of tissues except for muscle, whereas the latter is mainly expressed in muscle. Cofilin can bind to F-actin, accelerate the dissociation of actin monomers from the filament, and lead to the depolymerization of F-actin (17). Besides the basic function of regulating the actin cytoskeleton, cofilin plays a role in the metastasis, infiltration and apoptosis of tumor cells (18,19). It was previously reported that at the early stage of apoptosis, cofilin transferred from the cytoplasm to the mitochondria and altered the permeability of mitochondrial membranes, leading to the release of cytochrome C and triggering cell apoptosis via the mitochondrial apoptosis pathway (20).

In the present study, a significant increase of cofilin-1 expression was found in retinoic acid-resistant NB4-R1 cells. Following which, the effects of cofilin-1 in As<sub>2</sub>O<sub>3</sub>-induced apoptosis in NB4-R1 cells were evaluated, and the possible underlying mechanisms were explored. The present study could provide novel strategies for APL treatment.

## Materials and methods

**Reagents and antibodies.** As<sub>2</sub>O<sub>3</sub> was purchased from Sigma-Aldrich (Merck KGaA) and dissolved at a concentration of 5  $\mu$ M in DMSO. Primary antibodies against poly (ADP-ribose) polymerase (PARP; cat. no. 9532), cleaved PARP (cat. no. 5625), caspase 12/cleaved caspase 12 (cat. no. 2202), cofilin (cat. no. 5175), cytochrome C (cat. no. 11940), cytochrome c oxidase subunit 4 isoform 1 mitochondrial (COX IV; cat. no. 4850) and GAPDH (cat. no. 5174) were purchased from Cell Signaling Technology, Inc. The annexin V-FITC Apoptosis kit was purchased from BD Biosciences.

**Cell culture.** Human APL cell lines, NB4-R1 and NB4 cells were obtained from the Institute of Hematology, Shanghai Ruijin Hospital (Shanghai, China). The NB4 cell line was derived from a patient with APL who underwent relapse and was established by Dr Lanotte (Saint Louis Hospital, France) in 1991, with characteristic chromosome translocation t(15;17) and positive PML-RAR $\alpha$  (L type) gene. The NB4-R1 cell line is an APL subclone resistant to ATRA and is derived from NB4 cells. The NB4-R1 and NB4 cells were maintained in

RPMI-1640 medium (Cytiva) supplemented with 10% fetal bovine serum (Gibco; Thermo Fisher Scientific, Inc.) and 1% penicillin-streptomycin in a humidified atmosphere of 5% CO<sub>2</sub> at 37°C. The culture medium was replaced every 3 days.

**Two-dimensional gel electrophoresis (2-DE) and image analysis.** Cells were collected and solubilized in lysis buffer containing 7 mol/l urea, 2 mol/l thiourea, 4% (w/v) 3-[(3-Cholamidopropyl)-dimethylammonio]-1-propane sulfonate (CHAPS), 1% (w/v) dithiothreitol (DTT), 1% protease inhibitor cocktail (v/v), and 2% (v/v) IPG buffer at 11,000 IU/min on ice. The agents used were purchased from Promega Corporation. Suspensions were then placed at 4°C for 1 h followed by centrifugation at 10,000  $\times$  g for 30 min at 4°C. Supernatants were obtained and protein concentrations were measured using the Bradford method. Each protein sample (90  $\mu$ g) was loaded on 24-cm immobilized pH gradient (IPG) strips (pH 3-10; non-linear; Cytiva). Following the rehydration of the IPG-strips and isoelectric focusing, the strips were equilibrated. Subsequently, 2-DE was performed in an Ettan-Dalt twelve electrophoresis system (Cytiva). Following silver-staining, as previously described (21), all the gels were scanned using ImageScanner™ (Cytiva) and the resulting images were used for detection, quantification, matching and analysis using ImageMaster™ 2D Platinum software (version 5.0; Cytiva). Each sample was run three times to minimize the variation and an average gel was made to represent the medium protein expression level of each group. The protein spots that changed in all three gels were compared between each conditioned group. The differentially expressed proteins were further identified by matrix-assisted laser desorption/ionization (MALDI) time-of-flight (TOF) mass spectrometry (MS).

**Protein identification by MS.** The selected protein spots were excised from silver-stained gels, cut into small pieces, and dehydrated in 50  $\mu$ l acetonitrile (ACN) for 5 min at room temperature. The gel pieces were dried following removal of the acetonitrile and incubated in 50  $\mu$ l 10 mM DTT at 56°C for 1 h, followed by an alkylating incubation in 50  $\mu$ l 55 mM iodoacetamide in the dark. Subsequently, the spots were dehydrated with 50  $\mu$ l ACN, rehydrated in 5  $\mu$ l trypsin for 30 min, and then 10  $\mu$ l 25 mM ammonium bicarbonate was added. Proteolysis continued overnight at 37°C and was then stopped by adding 10  $\mu$ l 2% formic acid and desalted using C18 ZipTips (EMD Millipore). The resulting peptides were concentrated, mixed with  $\alpha$ -cyano-4-hydroxycinnamic acid ( $\alpha$ -HCCA), deposited on a 384-well MALDI target and air-dried. All samples were analyzed in the positive-ion, reflectron mode on a TOF Ultraflex II mass spectrometer (Bruker Corporation). The accelerating potential was 20 kV with eight shots per second. Trypsin autodigestion peaks were used for internal calibration.

**Database searching using MS/MS data.** All peptide mass fingerprinting (PMF) and MS/MS data were used for protein identification using the MASCOT search program (<http://www.matrixscience.com>) based on the Uniprot protein database (<http://www.uniprot.org>). Up to one missed trypsin cleavage per peptide was allowed, although most matches did not contain any missed cleavages. A mass tolerance of 100 ppm was the window of error allowed for matching the peptide

mass values. Proteins with a score >56 identified by MASCOT were considered significant and were verified manually for spectral quality.

**Lentiviral vector infection.** Three short hairpin RNAs (shRNAs) targeting the human cofilin-1 gene (GenBank no. NM\_005507) for RNA interference were designed using siRNA Wizard™ software version 3.1 (<https://www.invivogen.com/sirnazard/design.php>). The efficacy of the sequence for cofilin-1 knockdown was evaluated using western blotting (data not shown) and the most effective one was screened as follows: 5'-GACAGGGATCAAGCATGAA-3'. The scrambled sequence (5'-AAUCGCAUAGCGUAUGCCGUU-3') was used as a negative control. Following heating and annealing, the sequence was ligated into the *Age*I and *Eco*RI sites of pGCSIL-GFP (containing human U6 promoter; Shanghai GeneChem Co., Ltd.) to generate a pGCSIL-GFP-cofilin vector, which was then transformed into *E. coli*. Positive recombinant clones were selected by DNA sequencing. The new recombinant viral vector was generated by co-transfecting 293T cells (American Type Culture Collection) with the lentivirus expression plasmid and packaging plasmids (pHelper 1.0 and pHelper 2.0) using Lipofectamine® 2000 (Invitrogen; Thermo Fisher Scientific, Inc.) according to the manufacturer's protocol. A total of 48 h after transfection, the recombinant lentiviral vector was harvested for the subsequent viral infection.

NB4-R1 cells were divided into two groups: i) Sc, infected with negative control lentiviral vector; and ii) shCofilin, infected with the pGCSIL-GFP-cofilin lentiviral vector. Cells were cultured at a density of  $6 \times 10^5$ /well in 6-well plates with addition of 8  $\mu$ g/ml polybrene (Sigma-Aldrich; Merck KGaA) and infected with specific or negative control lentiviral vectors (viral titer range,  $2 \times 10^8$ - $2 \times 10^9$  TU/ml). Following incubation for 48 h, cells were observed under a fluorescence microscope (magnification, x200 or x400). The knockdown efficiency of transfection was analyzed by reverse transcription-quantitative PCR (RT-qPCR) and western blotting. For the subsequent experiments, 48 h after infection, cells were divided to four groups, sc, sc+As<sub>2</sub>O<sub>3</sub>, shCofilin and shCofilin+As<sub>2</sub>O<sub>3</sub>. Cells in the sc+As<sub>2</sub>O<sub>3</sub> or shCofilin+As<sub>2</sub>O<sub>3</sub> groups were then treated with 2.5  $\mu$ M of As<sub>2</sub>O<sub>3</sub>, while the other two groups were treated with an equal volume of culture medium. One day later, cells were collected for the subsequent experiments.

**Overexpression plasmid.** Cofilin-1 overexpression plasmid (pcDNA3.1-cofilin) and a control vector were designed and constructed by Shanghai GeneChem Co., Ltd. For transfection, NB4-R1 cells at a density of  $5 \times 10^5$ /ml in 6-well plates were transfected with 3  $\mu$ g expression plasmid in each group using Lipofectamine 2000 reagent (Invitrogen; Thermo Fisher Scientific, Inc.) according to the manufacturer's protocol. After 48 h of transfection, cells were divided into three groups, control, As<sub>2</sub>O<sub>3</sub> and As<sub>2</sub>O<sub>3</sub> + oeCofilin groups. The cells were then treated with 2.5  $\mu$ M of As<sub>2</sub>O<sub>3</sub> (or an equal volume of culture medium for the control). One day later, cells were collected for subsequent experiments. The present study aimed to investigate the effects of As<sub>2</sub>O<sub>3</sub> on drug-resistant cell NB4-R1, so NB4 cells were not used for the overexpression experiments.

**3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay.** Cell viability was determined using the MTT method. The NB4-R1 cells were inoculated in 96-well plates at  $5 \times 10^3$  cells/well and then treated with As<sub>2</sub>O<sub>3</sub> of different concentrations (0, 0.625, 1.25, 2.50, 5.0, 7.5 and 10 mmol/l). After 24 h, 20  $\mu$ l MTT reagent (cat. no. ab211091; Abcam) was added into each well and incubated for 4 h, then 150  $\mu$ l DMSO was added and the plates were oscillated until the crystalline matter was fully dissolved. The absorbance at 490 nm was measured using a spectrophotometric plate reader.

**Isolation of mitochondria.** The cytoplasm and mitochondria extraction was conducted using a Mitochondria Isolation kit (cat. no. MITOISO2; Sigma-Aldrich; Merck KGaA) in accordance with the manufacturer's protocols. Briefly, cells from each group were collected, washed with ice-cold PBS, and subsequently were subjected to a 5 min 600 x g centrifugation step at 4°C. The supernatant was discarded and cells were incubated and homogenized with Extraction Buffer A on ice for 10 min. Then, the homogenate was pelleted for 10 min at 700 x g at 4°C. The post-nuclear supernatant was subjected to a 25 min, 10,000 x g centrifugation step at 4°C to pellet the mitochondrial fraction. The post-mitochondrial supernatant was collected and regarded as the remaining cellular cytoplasm for further analysis. The pellet was suspended with Fractionation Buffer Mix as the mitochondrial fraction. To confirm the protein origin, GAPDH was applied as the internal reference for cytoplasm, while COX IV, a membrane protein in the inner mitochondrial membrane, was the internal reference for mitochondria.

**Western blot analysis.** NB4-R1 cells were cultured in 6-well plates and following the different treatments, proteins were collected and lysed with RIPA buffer (Thermo Fisher Scientific, Inc.) containing a protease and phosphatase inhibitor cocktail (Sigma-Aldrich; Merck KGaA) for western blotting. Protein concentration was determined using the BCA method (Pierce; Thermo Fisher Scientific, Inc.) and lysates (20-40  $\mu$ g/sample) were subjected to 12% SDS-PAGE and transferred onto PVDF membranes. Membranes were blocked at room temperature for 1 h in 5% non-fat dry milk in Tris-HCl buffer followed by incubation with primary antibodies overnight at 4°C. Primary antibodies (1:1,000 dilution) against COX IV and GAPDH served as loading controls, GAPDH for cytoplasm (22) and COX IV for mitochondria (23). Membranes were then incubated with HRP-conjugated anti-rabbit IgG secondary antibody (1:1,000; cat. no. 7074; Cell Signaling Technology, Inc.) for 1 h at room temperature. Following a thorough rinse, immunoreactive bands were detected using an enhanced chemiluminescent substrate (Pierce; Thermo Fisher Scientific, Inc.) and were visualized by the charge-coupled device imaging system (Bio-Rad Laboratories, Inc.). The protein expression was quantified using ImageJ 3.5 software (National Institutes of Health). The values were normalized to the GAPDH band.

**RT-qPCR.** NB4-R1 cells were cultured in 6-well plates and treated with different concentrations (0.625, 1.25, 2.5, 5, 7.5 and 10  $\mu$ mol/l) of As<sub>2</sub>O<sub>3</sub> for 24 h. Total RNA was extracted from cultured cells using TRIzol® reagent (Thermo Fisher Scientific, Inc.). RT was performed using the RevertAid First

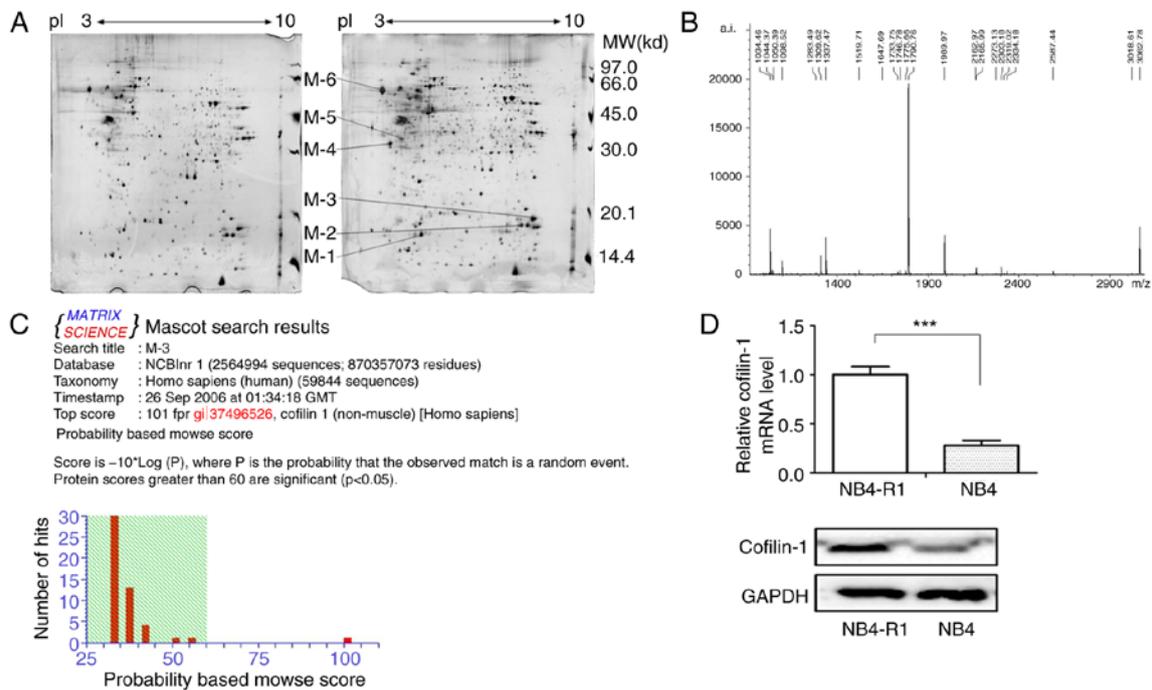


Figure 1. Analysis of differentially expressed proteins between NB4-R1 and NB4 cells. (A) Detection of protein spots by 2-dimensional electrophoresis in NB4-R1 and NB4 cells. (B) Matrix-assisted laser desorption ionization-time-of-flight-mass spectrometry analysis of the M3 spot. (C) Identification of the M3 spot by the MASCOT search program. (D) Cofilin-1 expression in NB4-R1 and NB4 cells, as indicated by reverse transcription-quantitative PCR and western blotting. \*\*\* $P < 0.001$ .

Strand cDNA Synthesis kit (Thermo Fisher Scientific, Inc.) and the reaction was carried out in a thermocycler at 25°C for 5 min, 42°C for 60 min, and 70°C for 5 min. The relative abundance of mRNA in each sample was determined by qPCR using the SYBR Premix Ex Taq™ II kit (Takara Biotechnology Co., Ltd.) on an iQ™ Multicolor Real-time PCR Detection System (Bio-Rad Laboratories, Inc.). The corresponding primers were designed and synthesized by Takara Biotechnology Co., Ltd., as follows: Cofilin-1 forward, 5'-CACCTTTGT CAAGATGCT-3' and reverse, 5'-GGAGCTGGCATAAAT CAT-3'; GAPDH forward, 5'-GTCATCCCAGAGCTGAAC-3' and reverse, 5'-TCAGTGTAGCCCAAGATG-3'. The PCR cycles were performed under the following conditions: 95°C for 30 sec, 40 cycles at 95°C for 5 sec and 60°C for 30 sec. Data were analyzed using the  $2^{-\Delta\Delta C_q}$  method (24) and GAPDH served as the internal control. The results are presented as the mean  $\pm$  standard deviation (SD) of triplicate reactions from three separate experiments.

**Flow cytometry analysis.** NB4-R1 cells with or without cofilin-1 shRNA treatment were routinely cultured in the 6-well plates, and cell density was adjusted to  $4.0 \times 10^5$ /well. Subsequently, cells were treated with  $As_2O_3$  or an equal amount of solvent for 24 h according to the grouping. The cells were then collected, washed with cold PBS, stained with Annexin V-fluorescein isothiocyanate (FITC) and propidium iodide (PI) using an Annexin V-FITC Apoptosis Detection kit (Merck KGaA) according to the manufacturer's instructions, and then analyzed by a FACSCalibur (BD Biosciences) accompanied with CellQuest™ software (version 5.1; BD Biosciences). Each experiment was performed in triplicate wells and repeated three times.

**Fluorescence.** NB4-R1 cells were cultured at a density of  $1 \times 10^5$ /well in 6-well plates, following the different treatments. After fixation in 4% formaldehyde in PBS (pH 7.2) at room temperature for 15 min, cells were stained with 20  $\mu$ M DAPI in antifade solution (Qbiogene, Inc.) at room temperature for 5 min. The stained cells were visualized using a BX51 fluorescent microscope (magnification, x200 or x400) equipped with a DP70 digital camera (Olympus Corporation).

**Statistical analysis.** All the data are reported as the mean  $\pm$  SD from at least three independent *in vitro* experiments. Shapiro-Wilk test was used to test normality of data. Differences among groups were analyzed using one-way analysis of variance, followed by Tukey's post hoc test. All statistical analyses were performed using the SPSS statistical software (version 19.0; IBM Corp.).  $P < 0.05$  was considered to indicate a statistically significant difference.

## Results

**Protein expression profiles of NB4-R1 and NB4 cells.** In the present study, 2-DE and silver staining were used to analyze the proteomic profile of NB4-R1 and NB4 cells from three independent biological replicates. The representative gel images are shown in Fig. 1, which indicates the total differential spots. In total,  $>1,000$  protein spots per gel ( $1,068 \pm 33$  for NB4-R1 cells and  $1,160 \pm 51$  for NB4 cells) were detected using ImageMaster™ 2D Platinum software. One 2-DE gel of the NB4 cells was randomly selected as the reference gel, and other gels were matched with it for analysis. The results showed that the matching rate of protein spots was 81% in NB4 cells and 78% in NB4-R1 cells. The matching rate between NB4-R1

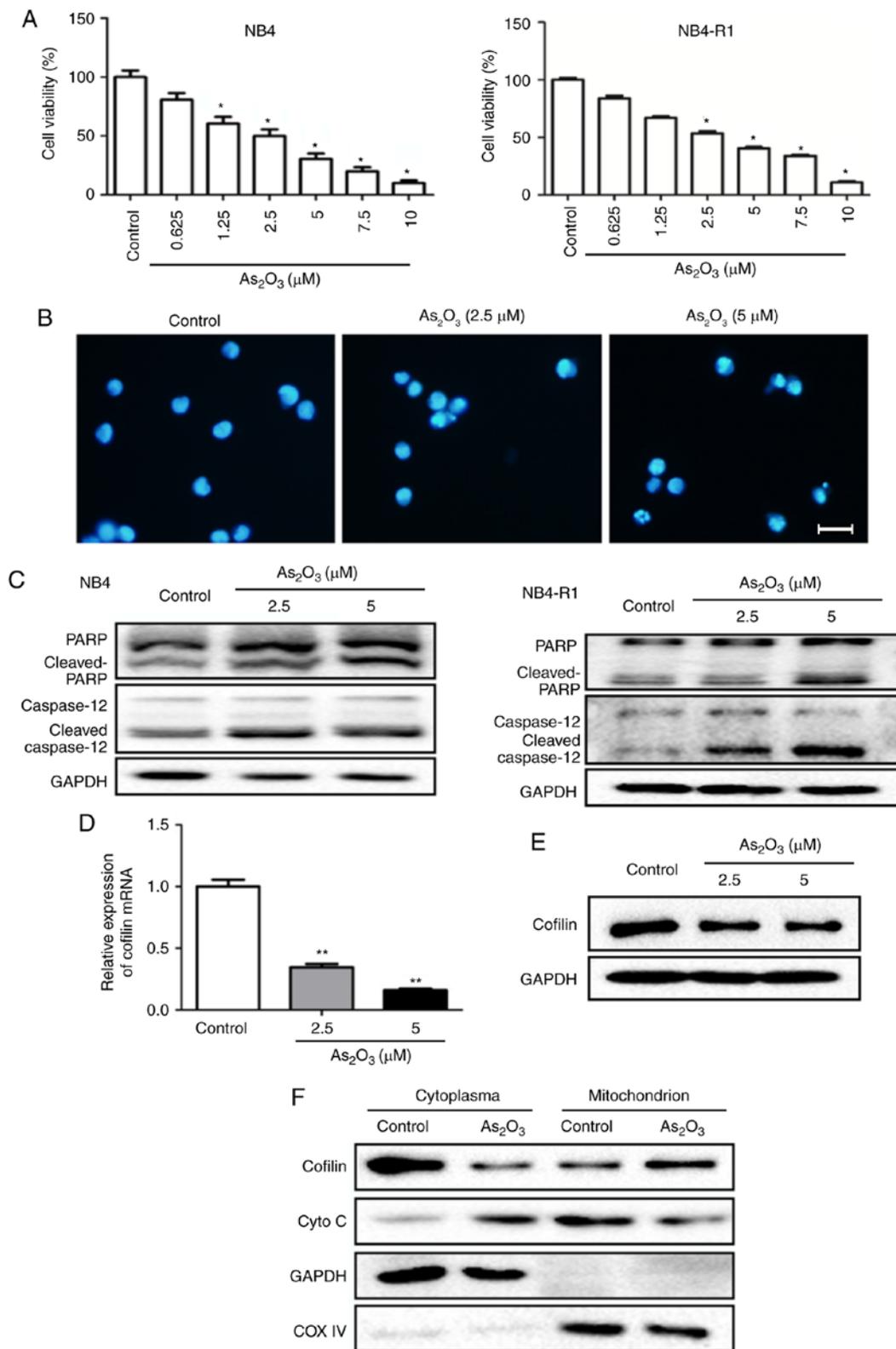


Figure 2. Effects of As<sub>2</sub>O<sub>3</sub> in NB4-R1 or NB4 cells. (A) As<sub>2</sub>O<sub>3</sub> treatment with a concentration  $\geq 2.5 \mu\text{mol/l}$  significantly inhibited cell viability of NB4 and NB4-R1 cells. (B) As<sub>2</sub>O<sub>3</sub> inhibited NB4-R1 cell growth, as indicated by immunofluorescence (scale bar,  $50 \mu\text{m}$ ). (C) As<sub>2</sub>O<sub>3</sub> treatment at concentrations of 2.5 and  $5 \mu\text{mol/l}$  notably increased cleaved-PARP and cleaved-caspase 12 expression in NB4 and NB4-R1 cells, as indicated by western blotting. As<sub>2</sub>O<sub>3</sub> decreased cofilin expression at the (D) mRNA and (E) protein levels in NB4-R1 cells. (F) As<sub>2</sub>O<sub>3</sub> notably reduced cytoplasmic cofilin expression, whereas it markedly increased the mitochondrial content, as indicated by western blotting. The opposite result was found for the cytoplasmic and mitochondrial levels of cytochrome C. \* $P < 0.05$ , \*\* $P < 0.01$  vs. control group. As<sub>2</sub>O<sub>3</sub>, arsenic trioxide; PARP, poly (ADP-ribose) polymerase; COX IV, cytochrome c oxidase subunit 4 isoform 1 mitochondrial.

and NB4 cells was 67%. Moreover, there were 21 protein spots found to be significantly up- or downregulated,  $\geq 2$  or  $\leq 0.5$ -fold,

respectively, in NB4-R1 cells (data not shown). Among these, six proteins were upregulated, M1-M6 shown in Fig. 1A.

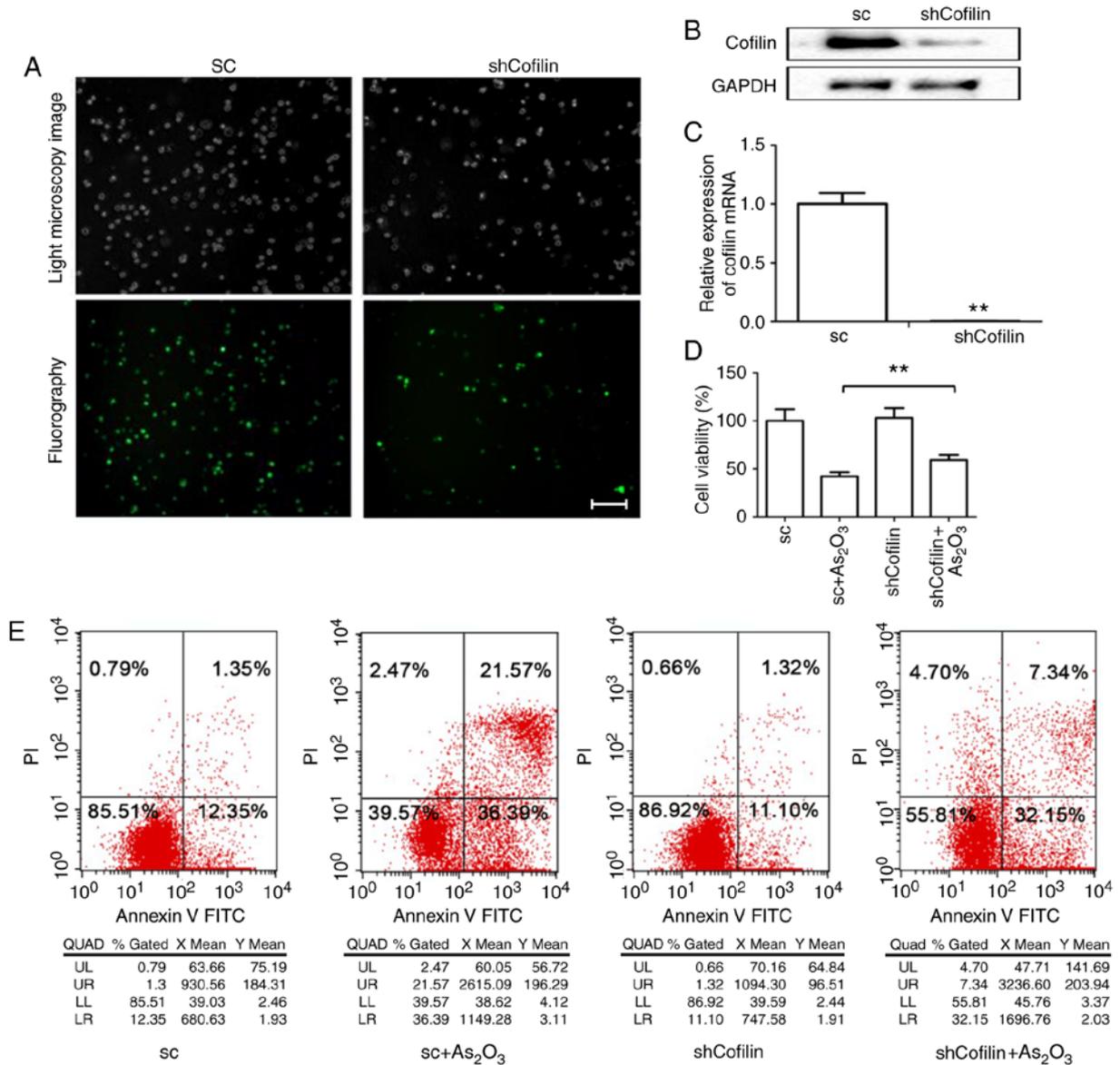


Figure 3. Cofilin knockdown suppresses the effects of As<sub>2</sub>O<sub>3</sub> on cell viability and apoptosis in NB4-R1 cells. (A) Immunofluorescence staining showed that the recombinant viral vectors containing shRNA were successfully transfected into the NB4-R1 cells (scale bar, 100  $\mu$ m). The expression of cofilin was markedly decreased by shRNA at the (B) mRNA and (C) protein levels. (D) Cofilin knockdown increased cell viability in As<sub>2</sub>O<sub>3</sub>-treated NB4-R1 cells. (E) Cofilin knockdown inhibited apoptosis in As<sub>2</sub>O<sub>3</sub>-treated NB4-R1 cells. \*\*P<0.01 vs. sc or sc + As<sub>2</sub>O<sub>3</sub> group. As<sub>2</sub>O<sub>3</sub>, arsenic trioxide; shRNA, short hairpin RNA; sc, negative control.

The M3 spot was further studied using PMF and MALDI-TOF-MS analysis (Fig. 1B) and the data were analyzed using the MASCOT search program (<http://www.matrixscience.com>) (25,26). The results revealed that M3 corresponded to cofilin-1 (Fig. 1C). The RT-qPCR and western blotting results further confirmed the significantly increased expression of cofilin-1 at the mRNA and protein levels in NB4-R1 cells, compared with that in the NB4 cells (Fig. 1D).

*As<sub>2</sub>O<sub>3</sub> suppresses cell viability and promotes apoptosis in NB4-R1 or NB4 cells.* NB4 and NB4-R1 cells were treated with different concentrations (0.625, 1.25, 2.5, 5, 7.5 and 10  $\mu$ mol/l) of As<sub>2</sub>O<sub>3</sub> for 24 h, and the results showed that cell viability was significantly inhibited by As<sub>2</sub>O<sub>3</sub> at a concentration  $\geq 2.5$   $\mu$ mol/l in both cell types (Fig. 2A). Immunofluorescence staining further indicated the inhibitory effect of As<sub>2</sub>O<sub>3</sub> on NB4-R1 cell growth (Fig. 2B). A similar result that As<sub>2</sub>O<sub>3</sub> suppressed

the proliferation was also seen in NB4 cells (data not shown). Besides, western blotting demonstrated that both cleaved-PARP and cleaved-caspase 12 were notably increased following As<sub>2</sub>O<sub>3</sub> treatment at a concentration of 2.5 and 5  $\mu$ mol/l in NB4-R1 cells. Similar results were found in NB4 cells (Fig. 2C).

*Effects of As<sub>2</sub>O<sub>3</sub> on cofilin-1 expression and transfer in NB4-R1 cells.* Cytoplasmic and mitochondrial cofilin levels in NB4-R1 cells were detected using RT-qPCR and western blotting, with or without As<sub>2</sub>O<sub>3</sub> treatment. The results showed that following As<sub>2</sub>O<sub>3</sub> treatment at 5  $\mu$ mol/l for 24 h, both the mRNA level and cytoplasmic protein content of cofilin-1 were significantly decreased, whereas the protein level of cofilin-1 in mitochondria was markedly increased (Fig. 2D-F). This indicated that As<sub>2</sub>O<sub>3</sub> could decrease the production of cofilin-1, as well as induce cofilin-1 transfer to the mitochondria from the cytoplasm in NB4-R1 cells. Besides, experiments were

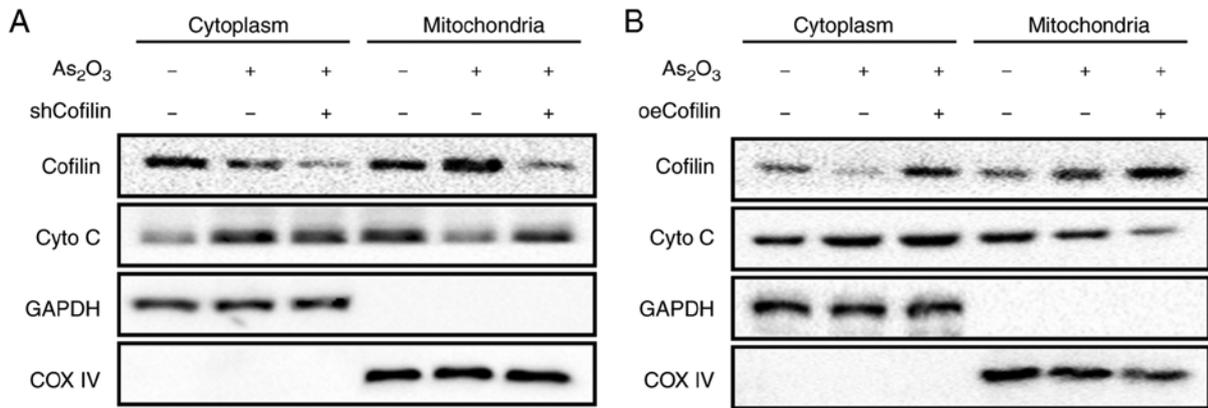


Figure 4. Role of cofilin-1 in mitochondrial cytochrome C release. (A) Knockdown of cofilin-1 increased the mitochondrial expression of cytochrome C, whereas it decreased the cytoplasmic content of cytochrome C in  $As_2O_3$ -treated NB4-R1 cells. (B) Overexpression of cofilin-1 markedly decreased the mitochondrial expression of cytochrome C, whereas it increased its cytoplasmic content in  $As_2O_3$ -treated NB4-R1 cells.  $As_2O_3$ , arsenic trioxide; shRNA, short hairpin RNA; oe, overexpression vector; COX IV, cytochrome c oxidase subunit 4 isoform 1 mitochondrial.

conducted to study the effects of  $As_2O_3$  on cofilin-1 translocation in NB4 cells. The results showed that  $As_2O_3$  treatment could also induce cofilin-1 transfer to the mitochondria from the cytoplasm in NB4 cells (data not shown).

**Effects of  $As_2O_3$  on the production and transfer of cytochrome C in NB4-R1 cells.** In NB4-R1 cells, mitochondrial expression of cytochrome C was notably decreased, whereas the cytoplasmic level was markedly increased after  $As_2O_3$  treatment, compared with the control group (Fig. 2F). Combined with the result of increased cleaved-caspase 12 following  $As_2O_3$  treatment (Fig. 2C), the data suggested that cytochrome C was released to the cytoplasm, which activated the mitochondrial apoptosis pathway at the early stage of cell apoptosis.

**Role of cofilin-1 in  $As_2O_3$ -induced apoptosis of NB4-R1 cells.** A stable shCofilin cell line was obtained with a down-regulated expression of the cofilin gene (target gene sequence: GACAGGGATCAAGCATGAA) by transfection of NB4-R1 cells with shRNA. Immunofluorescence staining demonstrated that the recombinant viral vectors containing shRNA were successfully transfected into the NB4-R1 cells, and RT-qPCR and western blotting indicated that cofilin expression was significantly decreased by shRNA (Fig. 3A-C). No significant alterations in viability and apoptosis were found between the shRNA control and shCofilin groups. Compared with the sc +  $As_2O_3$  group, cell viability was increased (Fig. 3D) and apoptosis was significantly decreased in the shCofilin +  $As_2O_3$  group (Fig. 3E).

**Association between cofilin-1 expression and mitochondrial cytochrome C release.** The cytoplasmic and mitochondrial levels of cytochrome C in the shCofilin and oeCofilin groups with or without  $As_2O_3$  treatment were detected using western blotting. The results showed that in the absence of  $As_2O_3$  treatment, the cytoplasmic and mitochondrial levels of cytochrome C were hardly affected by either shCofilin or oeCofilin (data not shown).  $As_2O_3$  treatment markedly increased cofilin expression and decreased cytochrome C expression in the mitochondria, whereas cytoplasmic cytochrome C expression was remarkably increased (Fig. 4A and B). This result was consistent with the

finding in Fig. 2F. However, in the shCofilin +  $As_2O_3$  group, mitochondrial cytochrome C levels were notably increased while its cytoplasmic level was markedly reduced, compared with the  $As_2O_3$  group (Fig. 4A). Opposite results were found in the oeCofilin +  $As_2O_3$  group; the mitochondrial level of cytochrome C was notably decreased and the cytoplasmic level of cytochrome C was marginally increased, compared with the  $As_2O_3$  group (Fig. 4B). It revealed that alterations in cofilin-1 levels had little influence on the release of cytochrome C from the mitochondria, whereas  $As_2O_3$ -induced cofilin-1 translocation was the primary factor triggering cytochrome C release.

## Discussion

Differential proteomics has been widely used in hematological tumors. In the study, comparative proteomics were applied to screen and identify the differentially expressed proteins between retinoic acid-sensitive cell lines and drug-resistant cell lines. Key proteins that may be related to apoptosis and drug resistance were identified and the effects of cofilin-1 on  $As_2O_3$ -induced apoptosis in NB4-R1 cells were further investigated. The results of the primary study indicated that cofilin-1 serves a role in the mitochondrial apoptosis pathway in  $As_2O_3$ -treated NB4-R1 cells.

The combined treatment of ATRA and  $As_2O_3$  has achieved favorable clinical efficacy in APL, which can be mainly attributed to the targeted mechanism of inducing cell differentiation and apoptosis (27). However, these results are not seen in patients with other types of acute leukemia as there are no specific targeted drugs. Therefore, further studies are required to illustrate the molecular mechanisms in APL and identify novel factors that regulate differentiation and apoptosis. NB4-R1 cells are naturally resistant to ATRA but sensitive to  $As_2O_3$ , thus this cell line is a useful model for the study of drug resistance and apoptosis (28,29). Through protein spectrum analysis, the present study identified that the expression of a number of proteins was significantly increased in NB4-R1 cells, a retinoid-resistant cell line, compared with that in NB4 cells, a retinoid-sensitive cell line. Particularly, the expression of M3 protein was increased by 2.3-fold. Following the PMF and database retrieval, cofilin-1 was identified for

M3. Increased expression of cofilin-1 in non-small cell lung cancer has been reported, suggesting cisplatin resistance and poor prognosis (30). Liao *et al* (31) found that cofilin-1 expression was markedly increased in drug-resistant liver cancer cell lines and an inhibitor of cofilin-1 could abolish drug resistance and induce tumor cell apoptosis. Nevertheless, little is known about the role of cofilin-1 in APL. Cofilin-1 may be involved in the resistance of NB4-R1 cells to retinoic acid, but hardly affect the pro-apoptotic potency of As<sub>2</sub>O<sub>3</sub> in NB4-R1. Thus, the present study further investigated the role of cofilin-1 in the As<sub>2</sub>O<sub>3</sub>-induced apoptosis of NB4-R1 cells.

The main pathways of apoptosis include extracellular signal-triggered caspase activation and intracellular apoptotic enzyme release from mitochondria, which activates caspase (32). At the early stage of apoptosis, cytochrome C is released by mitochondria and binds to apoptotic protease-activating factor 1, ATP/dATP and pro-caspase-9 in the cytoplasm, forming an apoptotic complex. Then, the complex activates caspase-9 and leads to apoptosis (20,33,34). Increasing evidence has suggested that mitochondrial translocation of cofilin seems to be necessary in regulating apoptosis. It was reported that in the pathogenesis of Alzheimer's disease activated cofilin could form a complex with p53 and promote its mitochondrial localization, resulting in promotion of apoptosis (35,36). Moreover, Li *et al* (37) demonstrated that allyl isothiocyanate (AITC) could induce dephosphorylation of cofilin, which then translocated to mitochondria, leading to the release of cytochrome C and apoptosis. Furthermore, it was revealed that the underlying mechanisms of cofilin activation by AITC might involve the ROCK1/PTEN/PI3K signaling pathway (37). In the present study, the results indicated that As<sub>2</sub>O<sub>3</sub> treatment significantly decreased the expression of cytoplasmic cofilin-1 and increased the mitochondrial expression of cofilin-1 in NB4-R1 cells. Downregulation of cofilin-1 expression using specific shRNAs did not have much of an effect on the proliferation and apoptosis of NB4-R1 cells. This suggested that alterations in the location of cofilin-1 rather than its expression level were the primary cause of As<sub>2</sub>O<sub>3</sub>-induced apoptosis in NB4-R1 cells, which was consistent with the aforementioned studies (35-37). Besides, Xing *et al* (38) demonstrated that isoalantolactone inhibits IKK $\beta$  kinase activity and promotes apoptosis of glioblastoma cells by inducing translocation of cofilin-1 to the mitochondria and the release of mitochondrial cytochrome C to the cytoplasm, which activates caspase-3/9. In human leukemia cells, cofilin-1 translocation to the mitochondria could induce mitochondrial injury and cell apoptosis (39). Xiao *et al* (40) revealed that docetaxel induced apoptosis of prostate cancer cells by inhibiting cofilin-1 and paxillin signaling pathways. These results were consistent with the data of the present study. However, others found that genetic ablation of cofilin does not affect apoptosis in mouse embryonic fibroblasts (MEF), suggesting that cofilin activity is not generally required for inducing apoptosis (17). The observation that cytochrome C release from mitochondria proceeds normally in the absence of cofilin in MEF suggests that cell-type-specific functions for cofilin in apoptosis might exist. Further studies are needed to explore the underlying mechanisms.

The current results confirmed for the first time that the downregulation of cofilin-1 expression suppressed As<sub>2</sub>O<sub>3</sub>-induced apoptosis in NB4-R1 cells. The underlying mechanism may involve the reduction of cytochrome C release from mitochondria following cofilin-1 translocation to the mitochondria. These results suggested that the change of cofilin-1 location occurs earlier than the release of cytochrome C in the mitochondrial apoptosis pathway. Cofilin-1 serves as a key regulatory point in apoptosis, and it may be a novel potential drug target for APL treatment. Both NB4 and NB4-R1 cells are sensitive to As<sub>2</sub>O<sub>3</sub> (41,42). Dual induction therapy is effective in certain patients with APL and arsenic-resistant APL. Besides, the effectiveness of combination therapy is higher compared with that of single drug use (43), which is consistent with the real-world conclusions. Further studies are needed to investigate mechanisms by which cofilin-1 regulates apoptosis in APL cells.

In conclusion, the present study demonstrated that during the process of As<sub>2</sub>O<sub>3</sub>-induced apoptosis in NB4-R1 cells, cofilin-1 is transferred to mitochondria from the cytoplasm, which promotes the release of cytochrome C from mitochondria and further activates the mitochondrial apoptosis pathway. Cofilin-1 may play a key role in the mitochondrial apoptosis pathway and has the potential to be used as a drug target in APL treatment.

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#### Availability of data and materials

The datasets used and/or analyzed during the present study are available from the corresponding author on reasonable request.

#### Authors' contributions

HZ and PH were involved in developing the concept and design of the study, and are guarantors of the integrity of the study. HZ and XZ performed the experiments, and prepared and revised the manuscript. HF and WW performed the experiments. ML and JZ were responsible for the literature review and assisted with data analysis. XW and HW performed the data analysis and revised the manuscript. All authors read and approved the final version of the manuscript.

#### Ethics approval and consent to participate

Not applicable.

#### Patient consent for publication

Not applicable.

## Competing interests

The authors declare that they have no competing interests.

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