

Original Article

Hydroxycamptothecin-induced apoptotic gene expression profiling by PCR array in human Tenon's capsule fibroblasts

Wei Tang*, Yinong Zhang*, Qing Zhang, Qinghua Wang, Zhifeng Wu

Department of Ophthalmology, Wuxi No. 2 People's Hospital Affiliated Nanjing Medical University, Wuxi 214002, China. *Equal contributors.

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Abstract: Studies have indicated that hydroxycamptothecin (HCPT) induces apoptosis of fibroblasts. In this study, we investigated the apoptotic gene expression profiling in HCPT-treated human Tenon's capsule fibroblasts (HTCFs) and identify the most implicated gene in apoptotic signaling of HTCFs by HCPT. Method HTCFs were incubated with HCPT at 0, 0.25 and 4 mg/L for 24, 48 and 72 h, respectively. Anti-proliferative effects were measured by MTT assay. Apoptosis was determined using the Annexin V-FITC/PI apoptosis detection kit and apoptotic cells were identified by flow cytometry. A PCR array was employed to analyze the most implicated apoptotic genes during HCPT-induced apoptosis in HTCFs. Results from our studies showed that HCPT induced apoptosis in HTCFs in a concentration- and time-dependent manner. The apoptotic HTCFs was increased by 9.38% with a multiplicity at 4 mg/L HCPT. PCR array demonstrated remarkable changes in 88 apoptotic genes, including 9 up-regulated genes and 36 down-regulated genes. HCPT treatment induced the upregulation of CHOP and downregulation of XIAP in HTCFs. To conclude, our results support HCPT induced the apoptosis of HTCFs, involving the activation of mitochondrial and endoplasmic reticulum stresses as well as the downregulation expression of XIAP.

Keywords: HCPT, signal pathway, XIAP, HTCFs

Introduction

Glaucoma is a leading cause of bilateral blindness in the world. The glaucoma patients was 60.5 million in 2010, and the estimated number will be increased to 79.6 million by 2020 [1]. Control of intraocular pressure (IOP) is established as the most effective treatment for glaucoma nowadays. Trabeculectomy is widely used to decrease the IOP in cases of glaucoma, although not ideal, the failure rate of trabeculectomy was about 40% after 4 years [2]. The main reason for surgical failure is the proliferation of human Tenon's capsule fibroblasts (HTCFs), which causes scarring in the surgical area. In order to decrease the risk of postoperative scarring, anti-proliferative agents such as mitomycin C or 5-fluorouracil are usually applied to prevent fibroblast growth and scar formation [3, 4]. However, many side effects were accompanied after the administration of anti-proliferative agents, such as chronic hypotony, late-

onset bleb leaks, macular degeneration and endophthalmitis [5-7].

Camptothecin (CPT) is a plant alkaloid isolated from the acuminata in southern China. More recently, eukaryotic Topo I has been identified as the cellular target of CPT, which can prevent DNA religation and therefore causes irreversible DNA break during ongoing DNA and RNA synthesis [8, 9]. Hydroxycamptothecin is one of CPT analogues with fewer side effects and is widely used as chemotherapeutic agents for colon cancer, bladder cancer and retinoblastoma [10-12]. Accumulating data have shown that HCPT can induce apoptosis in HTCFs via activating caspase-3 and caspase-9 [13]. However, the underlying mechanisms of HCPT-induced HTCFs apoptosis are still not clear.

The aims of this study are twofold: (1) to investigate the HCPT-induced changes of apoptotic genes of in HTCFs; and (2) to explore the under-

Apoptotic gene induced by hydroxycamptothecin in fibroblasts

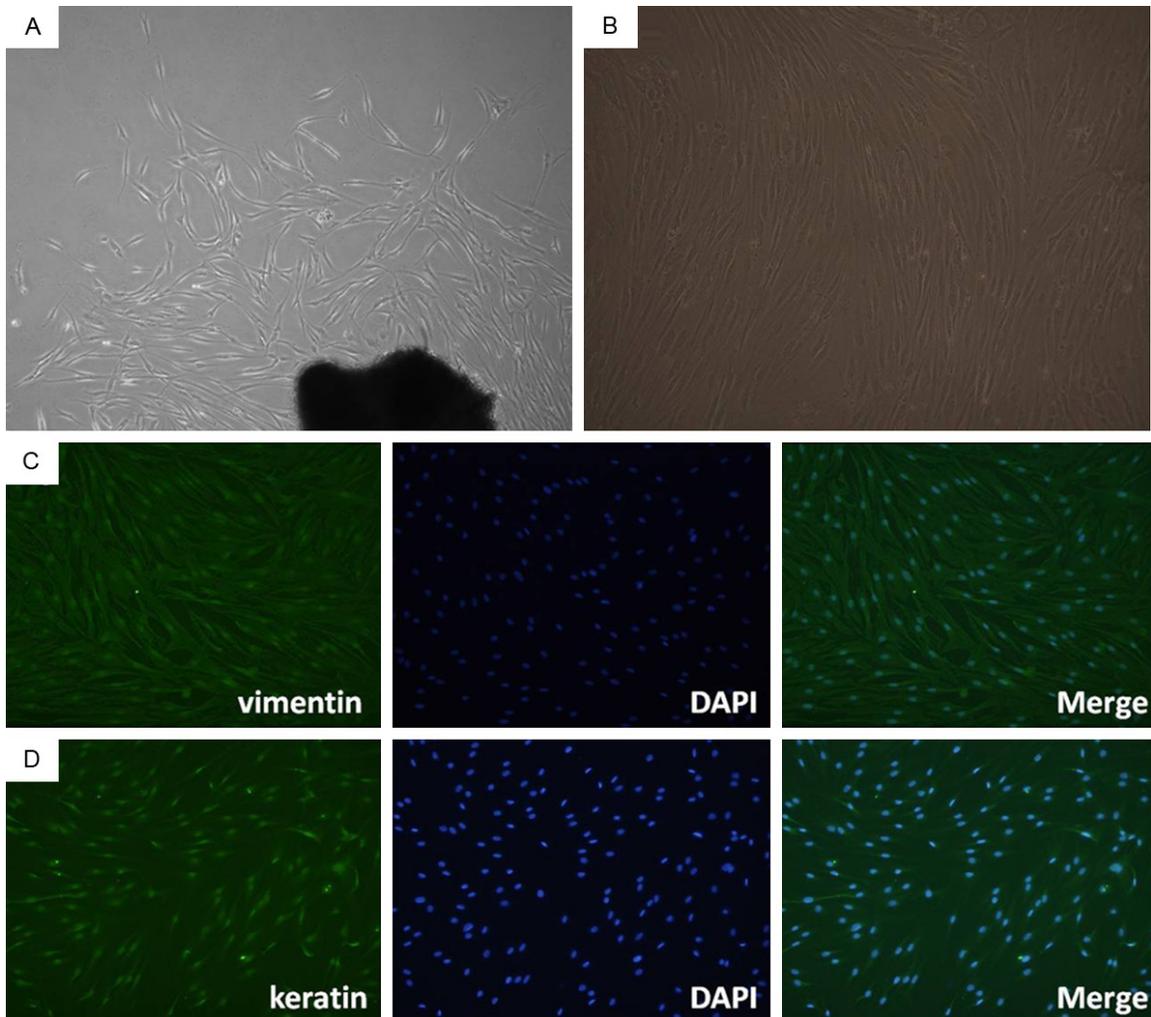


Figure 1. Culture and identification of HTFCs. A. some irregular cells migrated from the initial tissue (100 ×); B. cells showed irregular forms with more abundant cytoplasm and large nuclei after 5-7 d (100 ×); C. immunofluorescence with vimentin-positive staining in green and nuclei (blue) labeled with DAPI (200 ×); D. immunofluorescence with keratin-negative staining and nuclei (blue) labeled with DAPI (200 ×).

lying mechanisms by employing PCR array, a reliable tool for analyzing the expression of focused panel of genes [14].

Materials and methods

Cell culture

HTFCs were isolated from fresh eyes donated to the eye bank of Wuxi No. 2 People's Hospital affiliated Nanjing Medical University. The study conformed to the Declaration of Helsinki, and oral informed consent was obtained from the participants. Cells were maintained in Dulbecco's modified Eagle's medium (DMEM, Gibco, NY) cultured with 10% fetal bovine serum (FBS, Gibco, NY), 0.1 U/L of penicillin and 50 µg/mL streptomycin at 37°C in 5% CO₂

after incubating with HCPT at 0.25 and 4 mg/L, and control (0.9% NaCl only).

Cell proliferation and viability assays

The effects of HCPT on HTFCs proliferation were evaluated by standard MTT assay as previously described [15]. HTFCs were seeded into 96-well plates at an initial density of 6×10^3 cells/well and serum starved overnight. Cells were then incubated in DMEM containing HCPT (0, 0.25 and 0.4 mg/L) for 24, 48 and 72 h, respectively. At the predetermined time point, cultures were washed and incubated in DMEM containing 1 mg/mL MTT. Formazan crystals that formed at 4 h were dissolved in dimethylsulfoxide. Relative concentrations of formazan (as indicators of cell number) were determined

Apoptotic gene induced by hydroxycamptothecin in fibroblasts

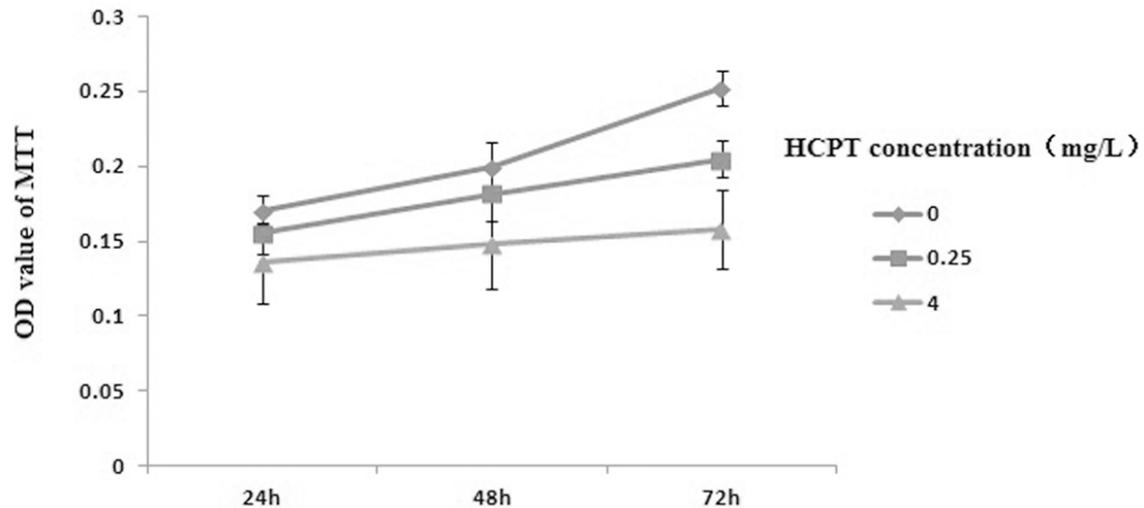


Figure 2. Cell viability of HTCFs measured by MTT. HCPT at the dosage of 0.25 and 4 mg/L caused a significant inhibition of proliferation in HTCFs (Δ means dose-dependent). Differences were significant among 24, 48 and 72 h HCPT groups (* means time-dependent). All experiments were performed at least three times. (* $P < 0.05$; ** $P < 0.01$).

by quantifying optical absorbance at 490 nm against a control wavelength of 590 nm in an automatic plate reader (Bio-Tek, Elx800, USA). All data were performed in triplicate.

Apoptosis analysis by flow cytometry

Apoptosis assessment was performed by flow cytometry analysis using annexin-V FITC and PI double staining assay as previously described [16]. When HTCFs reached up to 90% confluence, cells were starved for 24 h and treated with 0-4 mg/L HCPT for 24 h. HTCFs were digested with 0.25% trypsin (Gibco, USA), and transferred to 6-well plates. HCPT-treated cells were collected and resuspended at density of 2×10^6 cells/mL in binding buffer containing AnnexinV-FITC and PI, and the mixture were incubated for 10 min in the dark at room temperature. Analysis was immediately performed using Flow Cytometry System (Beckman Coulter, Fullerton, CA).

Real-time PCR array analysis of gene expression profile

Total RNA was isolated using Trizol reagent (Invitrogen, Carlsbad, CA), according to the manufacturer's recommendations RNA of 1 μ g was used for reverse transcription using RT kit (CT Bioscience, Cat# CTB101, Changzhou, China) in a 20 μ L volume. After reverse transcription, RT products were diluted to 1000 μ L

using ddH₂O. Mixed the diluted RT products with 1 mL $2 \times$ SYBR Green MasterMix (CT Bioscience, Cat# CTB103, Changzhou, China). Aliquote 20 μ L of the mixture to each well of the 96 well PCR array. Load the sealed PCR plate onto Roche LightCycler 480 II. The cycling condition is as follows: 95°C for 5 min in order to activation of hotstart Taq, 95°C for 15 sec, 60°C for 15 sec, 72°C for 20 sec, 45 cycles. Melting curve analysis condition is as follows: 95°C for 5 sec, 65°C for 1 min, 95°C for 0 sec. The house keeping genes: B2M, ACTB, GAPDH, RPL27, HPRT1 and OAZ1 were used to normalize to the amount of RNA. Fold change values were calculated using the formula of $2^{-\Delta\Delta Ct}$.

PCR array data analysis

The $\Delta\Delta Ct$ method was used to perform the relative quantification analysis. $\Delta\Delta Ct$ is used to calculate expression fold change. The formula is as follows: $2^{-\Delta\Delta Ct} = \text{Target gene expression level of experiment sample} / \text{Target gene expression level of control sample}$.

Statistical analysis

Statistical analysis was carried out using SPSS 13.0 software. Student's t-test was used to analyze differences between groups. For comparisons between multiple groups, one-way ANOVA was followed by SNK tests. Statistical significance was considered at $P < 0.05$.

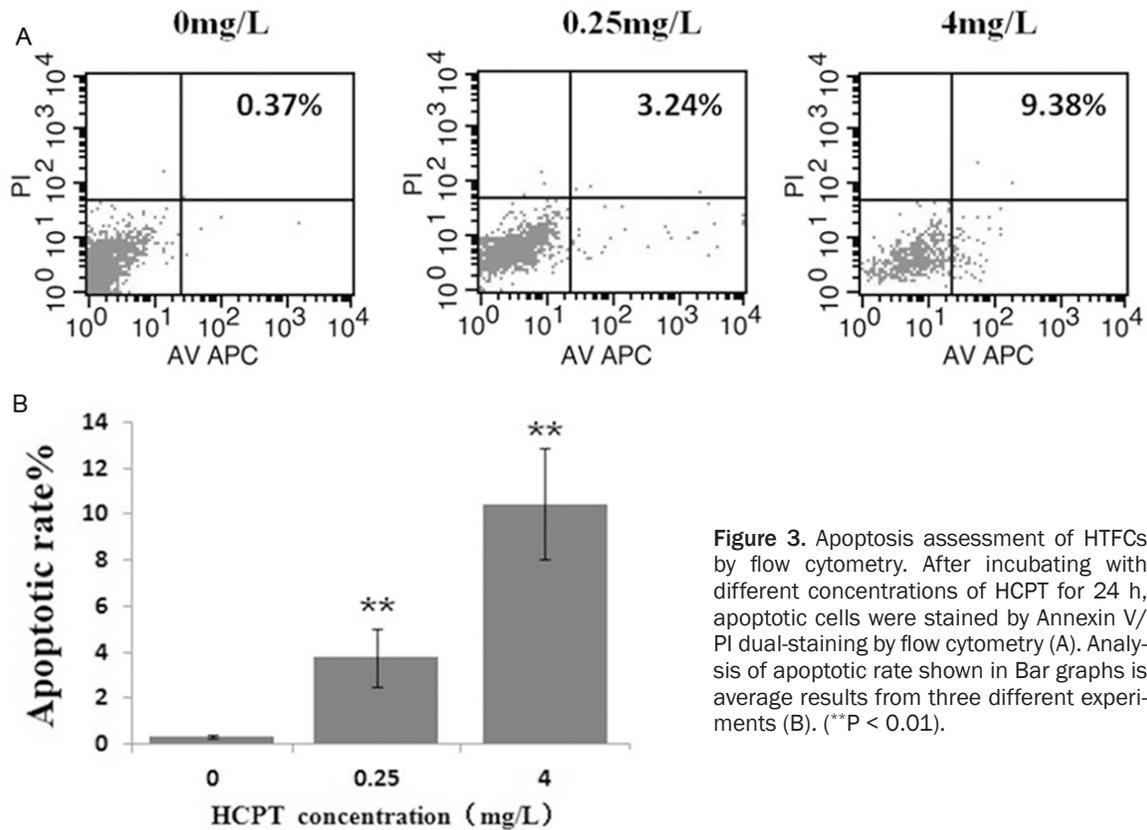


Figure 3. Apoptosis assessment of HTFCs by flow cytometry. After incubating with different concentrations of HCPT for 24 h, apoptotic cells were stained by Annexin V/PI dual-staining by flow cytometry (A). Analysis of apoptotic rate shown in Bar graphs is average results from three different experiments (B). (**P < 0.01).

Results

Culture and identification of HTFCs

The cultured HTFCs were identified as previously describe [13]. After HTFCs adhered to the bottom of the flask, cells gradually migrated from the initial tissue explants (Figure 1A). Cells reached up to 90% confluence after 5-7 d (Figure 1B). The identification of HTFCs was carried out by immunofluorescence with vimentin and keratin. As shown in Figure 1C and 1D, positive vimentin staining and negative keratin staining indicated that the cultured cells were the HTFCs.

Cell viability assessment by MTT

After incubating with HCPT at the concentration of 0, 0.25 and 4 mg/L for 24, 48 and 72 h, we found an obvious increase in OD values between the 0.25 mg/L HCPT and control groups, while higher concentrations of HCPT inhibited HCTFs proliferation in a dose-dependent manner. Differences were also significant among 24, 48 and 72 h HCPT groups, reflecting a time-dependence manner (P < 0.05). Figure 2 showed that HCPT exhibited cytotoxic effects

on HTCFs, and inhibited cell proliferation of HTCFs in time-and dose-dependent manners.

Apoptosis gene expression

Incubation with HCPT at concentrations of 0, 0.25 and 4 mg/L for 24 h led to apoptotic rates of 0.37%, 3.24% and 9.38% of the cells, respectively (Figure 3A). Figure 3B showed that the apoptotic rate gradually increased with increasing concentrations of HCPT.

PCR array of 88 apoptotic genes in HTCFs

Among the 88 apoptotic genes, the expression levels of 9 genes [P53, Bax, cytochrome c, caspase-3, caspase-9, IL1A, IL1B, c-fos and C/EBP homologous protein (CHOP)] were up-regulated when compared with the control. Particularly, CHOP was significantly up-regulated. Among 36 down-regulated genes, BCL-2, AKT and XIAP were the most significant (Table 1).

HCPT activation of mitochondrial, endoplasmic reticulum and downregulation expression of XIAP in HTCFs

When HTCFs were incubated with HCPT at 4 mg/L for 24 h, the expression levels of Bax,

Apoptotic gene induced by hydroxycamptothecin in fibroblasts

Table 1. Apoptotic gene expressions with PCR array at 0 and 4 Mg/L HCPT for 24 h

SyMbols	Full naMe (SynonyMs)	HCPT/control (fold changes)
ATF1	Activating transcription factor 1 (EWS-ATF1 FUS/ATF-1 TREB36)	-1.07
ATF2	Activating transcription factor 2 (CRE-BP1 CREB2 HB16 TREB7)	1.37
AIFM1	Apoptosis-inducing factor, Mitochondrion-associated, 1 (AIF CMTX4)	-2.44
AIFM2	Apoptosis-inducing factor, Mitochondrion-associated, 2 (AMID PRG3)	-1.28
AKT1	V-akt Murine thyMoMa viral oncogene hoMolog 1 (AKT CWS6 PKB)	1.32
AKT2	V-akt Murine thyMoMa viral oncogene hoMolog 2 (PKBB PKBBETA)	-4.65
AKT3	V-akt Murine thyMoMa viral oncogene hoMolog 3 (protein kinase B) (MPPH PKB-GAMMA PKBG PRKBG RAC-PK-gaMMa STK-2)	-8.91
APAF1	Apoptotic peptidase activating factor 1 (APAF-1 CED4)	1.01
BID	BH3 interacting doMain death agonist (FP497)	1.07
BCL-2	B-cell CLL/lyMphoMa 2 (Bcl-2 PPP1R50)	-64.71
BCL2L1	BCL2-like 1 (BCL-XL/S BCL2L BCLX bcl-xL bcl-xS)	-1.17
BAX	BCL2-associated X protein (BCL2L4)	2.63
CASP2	Caspase 2, apoptosis-related cysteine peptidase	-2.21
CASP3	Caspase 3, apoptosis-related cysteine peptidase	7.86
CASP4	Caspase 4, apoptosis-related cysteine peptidase	-1.54
CASP5	Caspase 5, apoptosis-related cysteine peptidase	-1.55
CASP6	Caspase 6, apoptosis-related cysteine peptidase	-1.64
CASP7	Caspase 7, apoptosis-related cysteine peptidase	-1.53
CASP8	Caspase 8, apoptosis-related cysteine peptidase	-3.00
CASP9	Caspase 9, apoptosis-related cysteine peptidase	2.05
CASP10	Caspase 10, apoptosis-related cysteine peptidase	-3.80
CD266	CD226 Molecule (DNAM-1 DNAM1 PTA1 TLISA1)	-1.72
CD24	CD24 Molecule	-1.34
CD27	CD27 Molecule (S152 T14 TNFRSF7 Tp55)	1.61
CD40LG	CD40 ligand	-1.53
CD5	CD5 Molecule	-2.26
CD70	CD70 Molecule	2.29
CDC2	cyclin-dependent kinase 1	-3.62
DDIT3	DNA-daMage-inducible transcript 3 (CHOP CHOP-10 CHOP10)	2.01
CYCS	CytochroMe c, soMatic (CYC HCS THC4)	7.43
DAPK 1	Death-associated protein kinase 1	-8.20
DAPK 2	Death-associated protein kinase 2	-1.61
FOS	FBJ Murine osteosarcoMa viral oncogene hoMolog (AP-1 C-FOS p55)	3.93
JUN	Jun proto-oncogene (AP-1 AP1 c-Jun)	1.32
E2F1	E2F transcription factor 1 (E2F-1 RBAP1 RBBP3 RBP3)	-1.24

Apoptotic gene induced by hydroxycamptothecin in fibroblasts

E2F2	E2F transcription factor 2	-2.15
EGFR	EpiderMal growth factor receptor	-10.97
ENDOG	Endonuclease G	1.18
FADD	Activating transcription factor 2	-1.90
FASLG	Fas ligand (TNF superfamily, Member 6)(ALPS1B APT1LG1 FASL)	-2.28
IFNA2	Interferon, alpha 2	-2.29
IFNB1	Interferon, beta 1, fibroblast	-6.30
IGF1	Insulin-like growth factor 1 (somatomedin C)	-12.52
IGF1R	Insulin-like growth factor 1 receptor	-4.22
IKKB	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta (IKK-beta IKK2 IKKB NFKB1KB)	-1.64
IKBK	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma (AMCBX1 FIP-3 FIP3 Fip3p IKK-gamma IP IP1 IP2 IPD2 NEMO)	-2.36
IL10	Interleukin 10	1.12
IL1A	Interleukin 1, alpha	3.37
IL1B	Interleukin 1, beta	3.85
IL2	Interleukin 2	-1.97
IL4	Interleukin 4	-3.42
IL6R	Interleukin 6 receptor	1.41
IL7	Interleukin 7	-2.44
IRAK1	Interleukin-1 receptor-associated kinase 1	1.07
JAK2	Janus kinase 2	-5.41
MADD	MAP-kinase activating death domain	-1.86
MAP3K1	Mitogen-activated protein kinase 1, E3 ubiquitin protein ligase (MAPKKK1 MEKK MEKK 1 MEKK1 SRXY6)	-3.80
MAP3K5	Mitogen-activated protein kinase 5 (ASK1 MAPKKK5 MEKK5)	-8.55
MAP3K6	Mitogen-activated protein kinase 6 (ASK2 MAPKKK6 MEKK6)	1.25
MAP3K10	Mitogen-activated protein kinase 10 (MEKK10 MLK2 MST)	-2.29
MAP3K11	Mitogen-activated protein kinase 11 (MEKK11 MLK3 PTK1)	-1.71
MAP3K14	Mitogen-activated protein kinase 14	-2.06
MAPK1	Mitogen-activated protein kinase 1 (ERK ERK2 MAPK2 p38 p40 p41)	-1.89
MAPK3	Mitogen-activated protein kinase 3 (ERK-1 ERK1 ERT2)	-1.53
MAPK8	Mitogen-activated protein kinase 8 (JNK JNK-46 JNK1 JNK1A2)	-2.60
MAPK9	Mitogen-activated protein kinase 9 (JNK-55 JNK2)	-2.34
MAPK14	Mitogen-activated protein kinase 14 (CSBP EXIP Mxi2 SAPK2A p38)	-2.84
MYD88	Myeloid differentiation primary response 88	-1.05
NFKB1	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NF-kB1 NF-kappa-B NF-kappaB p105 p50)	1.42
NFKBIA	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (IKBA MAD-3 NFKBI)	-1.62
NR2C2	Nuclear receptor subfamily 2, group C, Member 2	-2.72
NTRK1	Neurotrophic tyrosine kinase, receptor, type 1	-3.11
PDCD1	Programmed cell death 1	-2.84

Apoptotic gene induced by hydroxycamptothecin in fibroblasts

PDCD4	PrograMMed cell death 4 (neoplastic transforMation inhibitor)	-5.72
PDCD7	PrograMMed cell death 7	-1.50
PIK3CA	Phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha	-2.26
PIK3CG	Phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit gaMMa	-2.86
PIK3R2	Phosphoinositide-3-kinase, regulatory subunit 2 (beta)(MPPH P85B p85)	-1.43
PPP3CC	Protein phosphatase 3, catalytic subunit, gaMMa isozyMe	-2.31
PPP3R1	Protein phosphatase 3, regulatory subunit B, alpha	-1.24
RELA	V-rel reticuloendotheliosis viral oncogene hoMolog A (avian) (NFKB3 p65)	1.42
RIPK1	Receptor (TNFRSF)-interacting serine-threonine kinase 1	-1.63
RPS6KA4	RibosoMal protein S6 kinase, 90kDa, polypeptide 4 (MSK2 RSK-B)	-2.44
RPS6KA5	RibosoMal protein S6 kinase, 90kDa, polypeptide 5 (MSK2 RSK-B)	-2.34
TGFB1	TransforMing growth factor, beta 1 (CED DPD1 LAP TGFB TGFbeta)	-1.13
TNF	TuMor necrosis factor (DIF TNF-alpha TNFA TNFSF2)	1.10
TP53	TuMor protein p53 (BCC7 LFS1 P53 TRP53)	2.23
XIAP	X-linked inhibitor of apoptosis (API3 BIRC4 IAP-3 ILP1 MIHA XLP2)	-4.98

Negative folds mean down-graduated genes.

Apoptotic gene induced by hydroxycamptothecin in fibroblasts

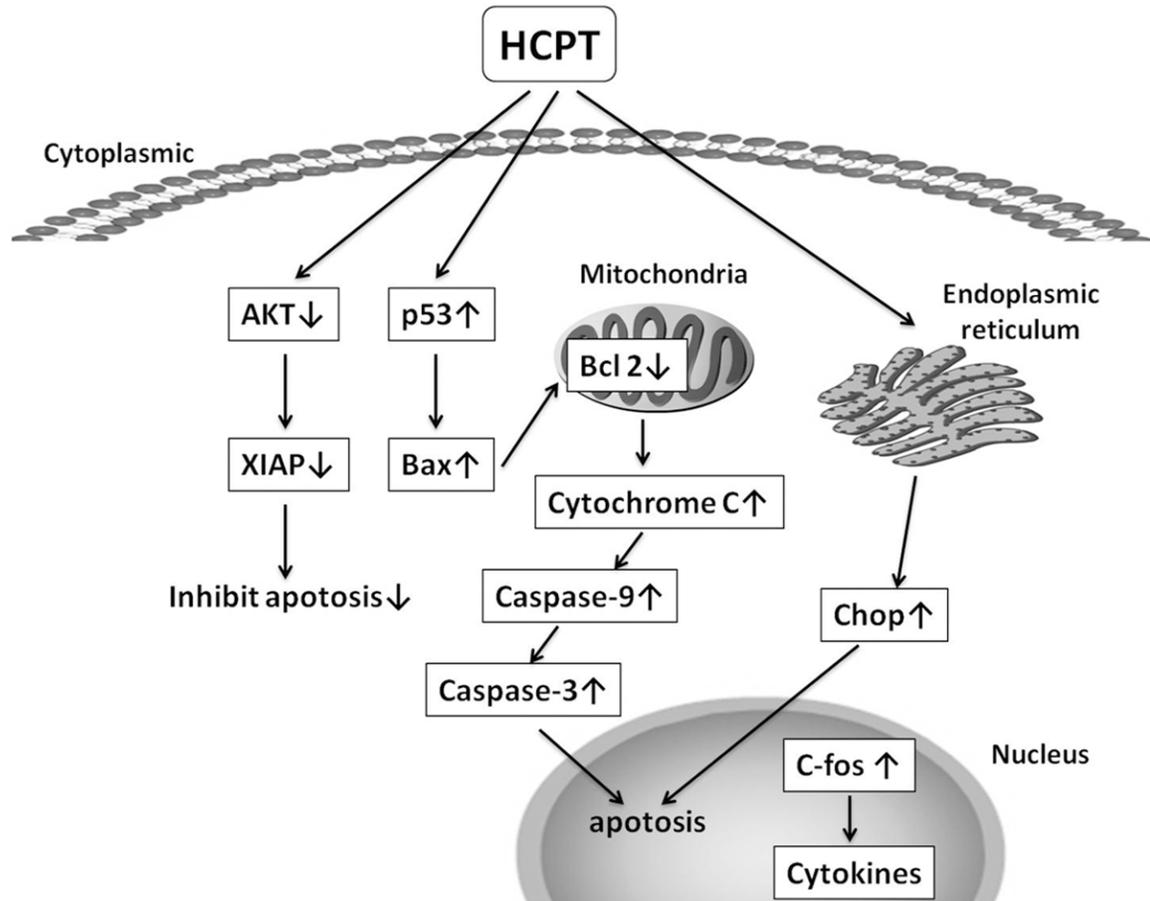


Figure 4. Possible apoptotic signal pathways in HCPT-treated HTFCs. Mitochondrial and endoplasmic reticulum stressed as well as the downregulation expression of XIAP in HTFCs may be involved in the HCPT-induced apoptosis of HTFCs.

P53, cytochrome c, caspase-9, and caspase-3 were promoted by 2.63, 2.23, 7.43, 2.05 and 7.86 fold, respectively. We speculate that HCPT may firstly activate P53 and Bax, and then release cytochrome c to initiate caspase-9, leading to a caspase cascade and apoptosis. We also found that expressions of IL1A, IL1B CHOP and c-fos were increased by 3.37, 3.85, 2.01 and 3.93 fold, respectively, and BCL-2, AKT3 and XIAP were decreased by 64.71, 8.91 and 4.98 fold, respectively. Based on these results and our previous study [13], a possible signal pathway for HCPT induced HTFCs apoptosis was predicted in **Figure 4**.

Discussion

In the current study, we found that different concentrations of HCPT could induce HTFCs apoptosis and inhibit HTFCs proliferation in time- and dose-dependent manners. Nine up-regulated apoptotic genes in HTFCs after HCPT

treatment included cytochrome c, IL1A, IL1B, caspase-3, caspase-9, Bax, Chop, c-fos and P53. Thirty-six apoptotic genes were down-regulated, mainly including BCL-2, AKT and XIAP. Our study indicates that the possible apoptotic signal pathways in HCPT-induced HTFCs may be the down-regulation expression of XIAP and activation of mitochondrial and endoplasmic reticulum (ER) stresses.

Apoptosis is a multiple and important biologic process in our lives, which can be divided into intrinsic (mitochondrial) and extrinsic (death receptor) pathways using caspase and caspase-independent pathways [17-19]. The malfunction of mitochondrial can alter the ratio of Bax/Bcl-2 and release of cytochrome c, which will activate the caspase cascade and apoptosis [20, 21]. As we known, Bcl-2 families (anti-apoptotic proteins such as Bcl-2; pro-apoptotic proteins such as Bax) play critical roles in mitochondria apoptosis pathway [22]. In our study,

following the pretreatment of HCPT, the expression levels of Bax, P53, cytochrome c, caspase-9, and caspase-3 in HTCFCs were promoted and BCL-2, AKT3 and XIAP were down-regulated. A similar finding was found in the study of Yin who proved that HCPT treatment in HTCFCs decreased the expression Bcl-2 and increased expressions of Bax and cytochrome c [23]. The HCPT-induced apoptosis via the mitochondrial-dependent pathway was also found in Sf21 and I OZCAS-Spex-II cell lines [24]. In addition, our previous study confirmed that the protein levels of cleavage caspase -3 (17KD), caspase-3 and caspase-9 were up-regulated in HTCFCs after treatment with HCPT [13]. All these above-mentioned findings suggested mitochondria may play an important role in regulating HCPT-induced apoptosis in HTCFCs.

ER stress is also one of apoptotic pathways in cells, which can be triggered by many physiological and pathophysiological conditions [25, 26]. The transcription factor CHOP can mediate apoptosis by triggering the ER stress [27, 28]. Our findings showed that HCPT promoted the expression levels of CHOP and Bax, and decreased the expression of Bcl-2, which implied that HCPT-induced apoptosis of HTCFCs may be via ER in HTCFCs. The activation of caspases is considered to be irreversible, but this activation process can be blocked by some proteins such as the Inhibitor of Apoptosis Proteins (IAPs). The expression of IAPs has been confirmed in many species and XIAP is the best characterized member in IAP proteins [29]. Some researchers found that XIAP was the only IAP that could directly bind and inhibit caspases by preventing caspase-9 monomers and interfering with dimerization-based caspase-9 activation [30-32]. It has been reported that HCPT induced apoptosis and inhibited tumor growth in colon cancer by down-regulating the expression of XIAP [10]. In this study, we found HCPT down-regulated expressions of XIAP and AKT3, activated caspase-9 and caspase-3, and finally induced apoptosis of HTCFCs, which may be related to the apoptosis inhibition of HTCFCs. Our results provide the theoretical evidence that HCPT-induced degradation of XIAP and AKT may be an important contributor to HCPT-induced apoptosis.

Proliferation of HTCFCs after trabeculectomy has always been a burning question and the inhibition of HTCFCs proliferation is regarded as the

key step to reduce the surgical failure rate HCPT, as a new anti-proliferative agent, not only brings hope to improve the surgical success rate in trabeculectomy but also proposes more possibilities in decreasing the risks of proliferative vitreoretinopathy in retinal disease and recurrent pterygium, and inducing apoptosis of lens epithelial cells in posterior capsular opacification and human retinoblastoma cells in retinoblastoma [12].

In conclusion, our current study demonstrates that HCPT induced cell apoptosis and inhibited cell growth in HTCFCs via down-regulating the expression of XIAP and activating the mitochondrial and endoplasmic reticulum stress. The exact mechanism of intracellular signal transduction remains to be determined, but our current study indicates that HCPT as a new anti-proliferative agent may be applied to prevent fibroblast growth and scar formation during trabeculectomy.

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Disclosure of conflict of interest

None.

Address correspondence to: Dr. Zhifeng Wu, Wuxi Second People's Hospital Affiliated with Nanjing Medical University, Wuxi 214002, China. Tel: 86 510 66681222; Fax: 86 510 82754933; E-mail: zhifeng-wu@hotmail.com

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Apoptotic gene induced by hydroxycamptothecin in fibroblasts

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