

Yiqi Chutan Tang Reduces Gefitinib-Induced Drug Resistance in Non-Small-Cell Lung Cancer by Targeting Apoptosis and Autophagy

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Received 13 March 2019; Revised 21 May 2019; Accepted 1 July 2019

Grant sponsor: National Natural Science Foundation of China, Grant number 81573780

Additional Supporting Information may be found in the online version of this article.

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Published online 14 August 2019 in Wiley Online Library (wileyonlinelibrary.com)

DOI: 10.1002/cyto.a.23869

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• Abstract

High incidence and mortality rates for non-small-cell lung cancer (NSCLC) lead to low survival rates. Epidermal growth factor receptor-tyrosine kinase inhibitors (EGFR-TKI) are commonly first prescribed for NSCLC patients with *EGFR* mutations. However, most patients with sensitizing *EGFR* mutations become resistant to EGFR-TKI after 9–13 months treatment. Yiqi Chutan Tang (YQCT) has been prescribed as a treatment to this issue for over 20 years. In this report, high-performance liquid chromatography (HPLC) analysis, flow cytometry, western blot analysis, and functional annotation analysis were applied to uncover the molecular mechanisms of YQCT. Our results show the application of YQCT reduces gefitinib-induced drug resistance, induces slight cell cycle arrest, enhances gefitinib-induced apoptosis, and activates the autophagy. These results indicate that at the molecular level YQCT can reduce drug resistance and improve anti-cancer effects when associated with gefitinib, which could be a result of enhancement of apoptosis and autophagy in the EGFR-TKI resistant cells of NSCLC. This research provides a new treatment strategy for patients with EGFR-TKI resistance in NSCLC. © 2019 The Authors. *Cytometry Part A* published by Wiley Periodicals, Inc. on behalf of International Society for Advancement of Cytometry.

• Key terms

non-small-cell lung cancer; flow cytometry; molecular mechanism; epidermal growth factor receptor-tyrosine kinase inhibitors; drug resistance

The Global Cancer Observatory 2018 shows that lung cancer has the highest incidence and mortality rates in Asian patients. Non-small-cell lung cancer (NSCLC) is the most common subgroup of lung cancer (1) with platinum-based chemotherapy being the first-line therapy of choice (2), while treatments with epidermal growth factor receptor-tyrosine kinase inhibitors (EGFR-TKI) have been shown to be more effective with higher survival rates compared to chemotherapy in patients with EGFR-mutated NSCLC (3). However, after 9–13 months of EGFR-TKI therapy, most patients with sensitizing *EGFR* mutations become resistant to EGFR-TKI, which greatly reduces its effectiveness (4). Therefore, there is an urgent need for new strategies to treat NSCLC patients with EGFR-TKI resistance.

One such strategy is the use of Traditional Chinese Medicine (TCM). Its therapy is an important source of effective anti-tumor treatments as well as reducing drug resistance for NSCLC (5). Yiqi Chutan Tang (YQCT) is a TCM formula used to treat NSCLC, which consists of American Ginseng (Xi Yang Shen), Bulbus *Fritillariae Thunbergii* (Zhe Bei Mu), Radix *Ranunculi Ternati* (Mao Zhua Cao), *Bombyx Batryticatus* (Jiang Can), Herba *Sarcandrae* (Zhong Jie Feng), Indian *Iphigenia Bulb* (Shan Ci Gu), Rhizoma *Pinelliae* (Ban Xia), and *Lucid Ganoderma* (Ling Zhi). It has been shown to inhibit tumor growth in mice (6), reduce drug resistance in lung cancer cells (7,8), prolong the median survival time (9), and reduce chemotherapy-related fatigue in NSCLC patients (10).

Our previous research suggests that YQCT can inhibit EGFR-TKI-resistant tumor growth *in vivo*, and the mechanism may be related to the regulation of the endoplasmic reticulum stress (ER stress) response by up-regulating CHOP/GADD153 and GADD34 protein expression (11). CHOP is important in ER stress-induced apoptosis, and with CHOP^{-/-} mice have shown to have a low apoptosis rate in response to ER stress (12). Since the PERK/eIF2 α /CHOP pathway is essential for inducing autophagy associated with ER stress (13), CHOP also plays an important role in regulating autophagy, with CHOP being able to induce transcription of several autophagy-related genes (ATG). Furthermore, dysregulated autophagy may also trigger ER stress as a feedback mechanism (14). It appears that the regulation of ER stress, apoptosis and autophagy is reflected in more than aspect of YQCT's overall effect. Our previous research has discussed the anti-cancer mechanism of YQCT via ER stress and apoptosis (11,15). In this study, we focus on drug resistance reduction of YQCT in gefitinib-resistant human NSCLC cells H1975 and explore the underlying molecular mechanisms associated with apoptosis and autophagy.

MATERIALS AND METHODS

Reagents

Dimethylsulfoxide (DMSO) and A 3-(4, 5-dimethylthiazol-2-yl)-2, 5-diphenyltetrazolium bromide (MTT) were provided by Sigma-Aldrich (St. Louis, MO). Bicinchoninic acid (BCA) Kit, Radio-Immunoprecipitation Assay (RIPA) lysis buffer, Cell cycle analysis kit, and annexin V-fluorescein isothiocyanate detection kit were obtained from Beyotime Institute of Biotechnology (Haimen, Jiangsu, China). Cell-light 5-ethynyl-2'-deoxyuridine (EdU) apollo 488 *in vitro* kit was obtained from Guangzhou Ribo Bio Co., Ltd (Guangzhou, Guangdong, China). Primary antibodies atg3, atg12, β -actin, and secondary antibodies were obtained from Cell Signaling Technology, Inc (Danvers, MA). Western blot detection reagents were provided by Bio-Rad Laboratories (Hercules, CA). Gefitinib was obtained from Selleck Chemicals (Houston, TX).

YQCT Preparation

Herbs were purchased from Guangdong Kang Mei Pharmaceutical Company Ltd (Jieyang, Guangdong, China). Herbs were soaked in double distilled water (1 l) for 30 min, mixed and boiled in eight volumes of water (v/w) for 2 h, and finally re-boiled in eight volumes of water for 1 h. The extracts were filtered and dried by lyophilization. The resulting supernatant was diluted in the cell culture media and filtered with 0.22 μ M filter.

High-Performance Liquid Chromatography Analysis

The samples solutions were put into the HPLC (Agilent 1200 HPLC system, Santa Clara, CA) and separated on the chromatographic column C18 (4.6 mm \times 250 mm, 2.7 μ m). The mobile phase consisted of acetonitrile (A) and 25 mM acetic acid with ammonia (B). The gradient elution program was as follows: 0%–0% A at 0–10 min, 40%–90% A at 35–45 min,

90%–100% A at 45–50 min, 0%–0% A at 51–58 min. The flow rate was 1 ml/min and the detection wavelength was at 254 nm. The injection volume was 10 μ l and the column temperature was maintained at 30°C.

Cell Culture

Human *EGFR* mutated lung cancer cells H1975 was obtained by the Chinese Academy of Science (Shanghai, China). Cells were cultured in Roswell Park Memorial Institute–1,640 medium (Thermo Fisher Scientific, MA) with 10% fetal bovine serum (Thermo Fisher Scientific) and 1% penicillin/streptomycin in a 5% CO₂ incubator at 37°C.

Cell Viability Assay

Briefly, 4×10^3 H1975 cells were seeded in 96-well plates for 24 h and then were incubated with YQCT and gefitinib. After 48 h of incubation, the effects of YQCT and gefitinib on cell viability were detected by the MTT assay. Each well was added with 100 μ l of MTT stock solution (0.5 mg/ml) and was incubated for 4 h. Finally, 150 μ l of DMSO was added into each well, and the plates were shaken for 10 min for crystal dissolution. Absorbance and cell viability were then determined.

EdU Incorporation and Immunofluorescence Staining

Each well was added with 100 μ l of 1:1,000 dilution of EdU-labeling reagent after 48 h cell culture for EdU labeling. The culture medium was discarded after 2 h followed by the addition of 50 μ l of cell fixative reagent to each well and incubation at room temperature for 30 min. The medium was discarded and 50 ml (2 mg/ml) glycine was added to each well before further incubation in a shaker for 5 min. About 100 μ l of 1 \times Apollo reagent was added into the culture medium and incubated in a dark shaker for 30 min. The medium was again discarded and 100 μ l of 0.5% TritonX-100 was added. Finally, 100 μ l of 1 \times Hoechst 33342 reagent was added and then incubated in a dark shaker for 30 min. Cells were detected by Leica spectral confocal fluorescent microscopy (Wetzlar, Germany) at 488 nm.

Cell Cycle Distribution Analysis

H1975 cells were seeded in six-well plates overnight. Following adding 12.5 μ M of gefitinib combined with or without 0.5 mg/ml YQCT for 48 h incubation. Cells were then re-suspended in 1 ml of phosphate-buffered saline (PBS) containing 1 mg/ml of RNase and 50 μ g/ml of propidium iodide (PI), and then were incubated in dark for 30 min at room temperature. A total of 1×10^4 cells were acquired by BD FACSAria™ III Cell Sorter (BD Biosciences, San Diego, CA) at 488 nm to determine cell cycle distribution under the drug treatments. Data were analyzed by FlowJo software (v7; FlowJo LLC, Ashland, OR).

Cell Apoptosis Analysis

Apoptotic cells were quantitated using the annexin V: PI apoptosis detection kit. Cells were treated with 12.5 μ M gefitinib combined with or without 0.5 mg/ml YQCT for 48 h, then were trypsinized, washed, and re-suspended at a concentration

of 1×10^6 cells/ml. Then cells were gently re-suspended in $1 \times$ binding buffer with 2.5 μ l of annexin V: PI in a total volume of 100 μ l and incubated in dark for 15 min at room temperature. Apoptotic cells were quantified by BD FACSAria™ III Cell Sorter (BD Biosciences) and data were analyzed by FlowJo software (v7; FlowJo LLC).

Western Blot Analysis

Cell lysate was prepared in RIPA lysis buffer containing 1% phenylmethanesulfonyl fluoride and 1% phosphatase inhibitor. The soluble protein fractions were collected after centrifugation at 1.35×10^4 g for 10 min. Protein concentrations were detected by BCA kit. About 30 mg of proteins were separated on 8–12% dodecyl sulfate, sodium salt-Polyacrylamide gel electrophoresis (SDS-PAGE) and were incubated with different antibodies overnight at 4°C. Membranes were incubated with the appropriate secondary antibodies. Signals were measured by an ECL chemiluminescence detection agent.

Data Processing and Functional Annotation

PubChem IDs were submitted into Bioinformatics Analysis Tool for Molecular mechANism (BATMAN) system (16) to identify genes that are regulated by nine major bioactive components in YQCT with a cut-off score of 20. After identifying highly relevant genes, functional enrichment analysis were performed based on Kyoto Encyclopedia of Genes and Genomes (KEGG) and Gene Ontology (GO) terms using cluster Profiler (v3.5) (17).

Statistical Analysis

SPSS 24.0 software (IBM, NY) was used to performed statistical analysis. Statistical comparisons were performed using Independent-Samples T test or one-way ANOVA test. Data measurement was expressed as mean values \pm standard deviation. The value of $P < 0.01$ was considered significantly statistically significant.

RESULTS

Chemical Composition of YQCT

HPLC was used to characterize alcohol extractions of YQCT, which reveals nine major chemical compounds: Rosmarinic Acid, Resorcinol, Isofraxidin, Ganoderic Acid B, Ganoderic

Acid C2, Ganoderic Acid A, Peimine, Peiminine, and Beta-Sitosterol (Fig. 1).

YQCT Inhibits Cell Viability, DNA Synthesis and Reduces Gefitinib-Induced Drug Resistance in H1975 Cell Line

The H1975 cell line was used in this research as it has *EGFR* mutations of exon 21 *L858R* and exon 20 *T790M* (18), mutations which are resistant to EGFR-TKI. Gefitinib is a small molecule inhibitor that suppresses *EGFR* tyrosine kinase activity and is the first generation of EGFR-TKI. As shown in Figure 2a, a high dose of gefitinib (50 μ M) did not inhibit cell viability in H1975, but it could effectively inhibit cell viability in EGFR-TKI sensitive NSCLC cell line A549. This reveals that the H1975 is more resistant to gefitinib than EGFR-TKI sensitive NSCLC cell line.

EdU is a thymidine analog used to detect cell proliferation. The specific reaction of fluorescent dyes of EdU monitors DNA replication activity and synthesis steps (19,20). In Figure 2b, Hoechst 33342 labeled the nucleus in blue fluorescence, indicating the total number of cells, while the EdU labeled the number of proliferating cells in green fluorescence.

The EdU assay showed that YQCT significantly suppressed the cell proliferation with increasing dose (Fig. 2b), indicating that the application of YQCT inhibited DNA synthesis *in vitro* in a dose-dependent fashion. MTT cell viability assay showed that the use of YQCT significantly inhibited H1975 cell viability in a dose-dependent fashion in 48 h (Fig. 2c). Hence, 0.5 mg/ml of YQCT was used for the study, as this concentration did not show obvious cytotoxicity and could inhibit DNA synthesis as shown in Figure 2b,c.

Compared to the treatment with gefitinib by itself, the treatment with gefitinib combined with YQCT significantly decreased H1975 cell viability in 48 h (Fig. 2d). These results indicate that YQCT may inhibit cell viability, cell proliferation, and DNA synthesis, as well as improving the anti-cancer effect and reducing gefitinib-induced drug resistance in H1975 cells when combined with gefitinib.

YQCT Induces Cell Cycle Arrest, Enhances Gefitinib-Induced Apoptosis while Activating the Autophagy

EdU is incorporated into replicated chromosomal DNA during the S phase of the cell cycle DNA synthesis (19,20). As its

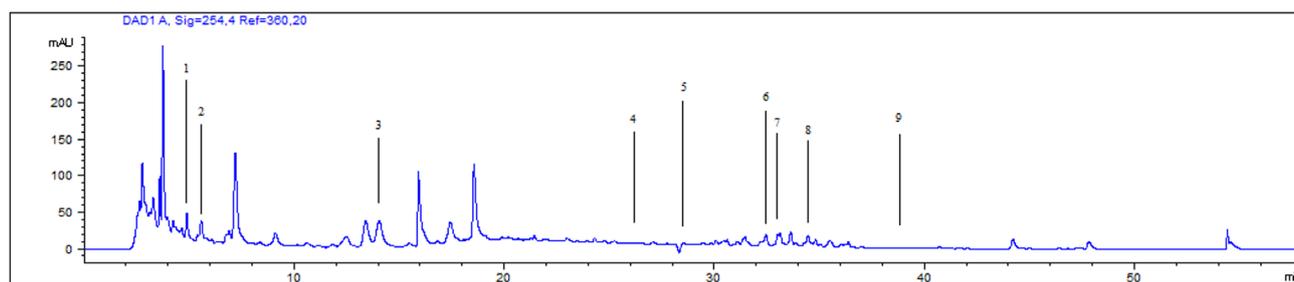


Figure 1. Alcohol extractions of YQCT were qualitatively analyzed with HPLC. The numbers in the chromatograms indicate the constituent peaks 1. Rosmarinic acid, 2. Resorcinol, 3. Isofraxidin, 4. Ganoderic acid B, 5. Ganoderic acid C2, 6. Ganoderic acid a, 7. Peimine, 8. Peiminine and 9. Beta-Sitosterol. A typical chromatogram is shown ($n = 3$). [Color figure can be viewed at wileyonlinelibrary.com]

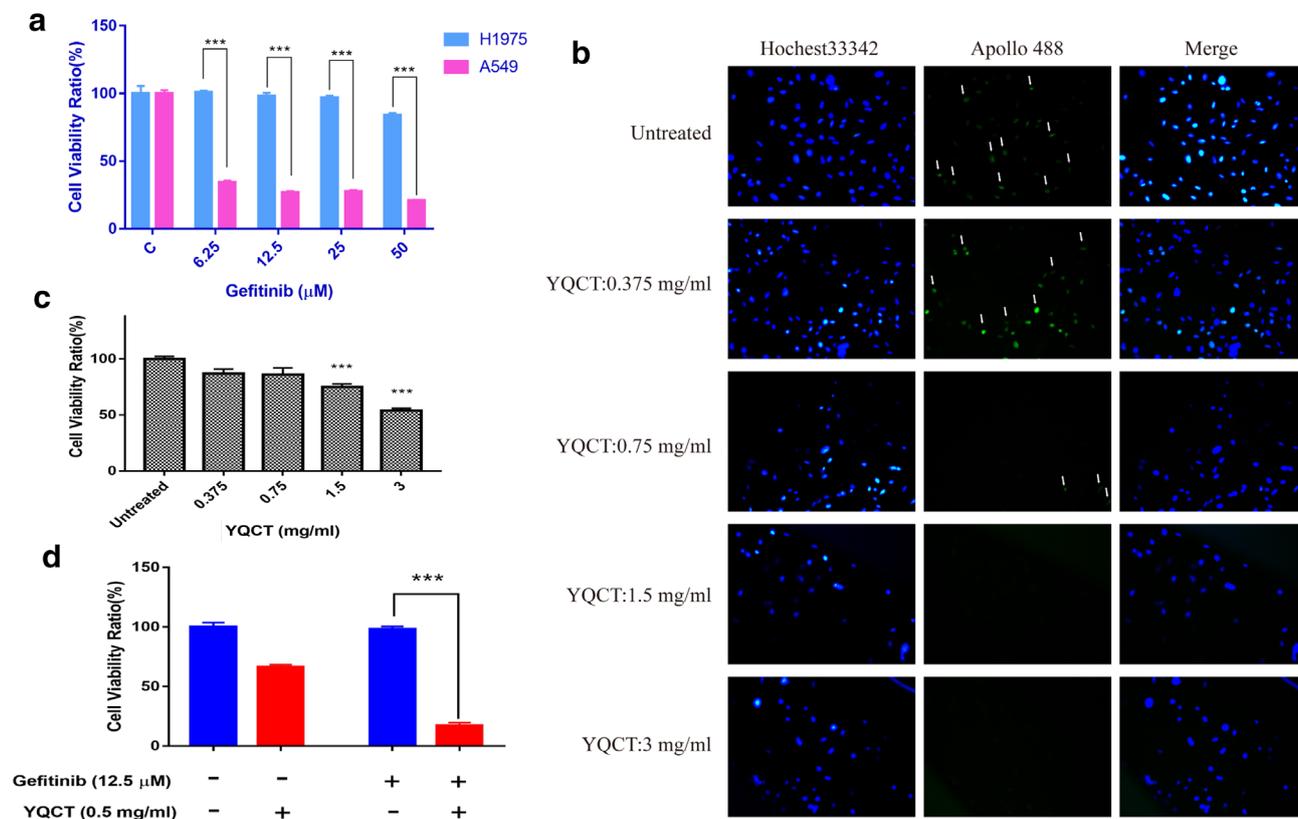


Figure 2. Effects of YQCT on H1975 cells. (a) MTT assay for cell viability ratio. H1975 and A549 cells were seeded in 96-well plates (4×10^3 cells/well) overnight and subsequently were treated with 6.25, 12.5, 25, and 50 μM gefitinib for 48 h. (b) EdU assay for DNA synthesis. H1975 cells were seeded in 96-well plates (4×10^3 cells/well) overnight and subsequently were treated with 0.375, 0.75, 1.5, and 3 mg/ml YQCT for 48 h, then were stained for EdU and visualized by a fluorescence microscope. (c) MTT assay for cell viability ratio. H1975 cells were seeded in 96-well plates (4×10^3 cells/well) overnight and subsequently were treated with 0.375, 0.75, 1.5, and 3 mg/ml YQCT for 48 h. (d) MTT assay for cell viability ratio. Cells were seeded in 96-well plates (4×10^3 cells/well) overnight and treated with 12.5 μM gefitinib for 48 h with or without 0.5 mg/ml YQCT. One-way ANOVA test and independent-samples T test were used for analysis, *** indicates $P < 0.01$ ($n \geq 3$). [Color figure can be viewed at wileyonlinelibrary.com]

incorporation is cell cycle dependent, we used flow cytometry to determine whether YQCT can modulate the cell cycle in NSCLC. H1975 cells were treated with 12.5 μM gefitinib either with or without the addition of 0.5 mg/ml YQCT for 48 h. The YQCT combined with gefitinib group (combined group) and YQCT group showed a slight G2/M phase arrest in H1975 cell line compared to the gefitinib group (Fig. 3a,b).

Gefitinib-induced apoptosis in the presence and absence of YQCT was measured in H1975 cells (Fig. 3c,d). Apoptotic cells were detected by flow cytometric analysis. The percentage of late apoptotic cells in the combined group was 1.7 folds higher than gefitinib group in 48 h, indicating YQCT enhanced apoptosis of gefitinib, which revealed that apoptosis might be one of the molecular mechanisms of YQCT for reducing gefitinib-induced drug resistance.

In addition, autophagy occurs upstream of apoptosis and activates it, therefore inducing apoptosis indirectly (21,22). Hence, we examined whether autophagy was also related to apoptosis after YQCT treatment. Atg3 and atg12, key transcription factors for microtubule-associated protein 1A/1B-light chain 3 (LC3) expression, were detected by western blot analysis (Fig. 3e). We observed up-regulated protein expression of atg3

and atg12 in H1975 cells in the combined group compared to gefitinib alone at 48 h, indicating that autophagy of gefitinib was enhanced by YQCT, which revealed that autophagy might be the other molecular mechanism of YQCT for reducing gefitinib-induced drug resistance.

Therefore, it is reasonable to believe that YQCT reduces gefitinib-induced drug resistance in NSCLC by targeting apoptosis and autophagy.

Potential Molecular Mechanisms

To characterize the potential molecular mechanisms of YQCT anti-cancer activity, we submitted the PubChem IDs of the nine principal compounds (Supporting Information Table S1) to the BATMAN (16) database to identify genes that were regulated by these bio-active components. Two hundred and sixty nine genes (gid.csv) were associated with these nine compounds (Supporting Information Table S2), in which 19 genes were relevant to cancer (Fig. 4a and Supporting Information Table S3).

We carried out functional enrichment analysis for these genes based on GO terms and KEGG (Fig. 4b,c and Supporting Information Tables S4 and S5). Significantly over-

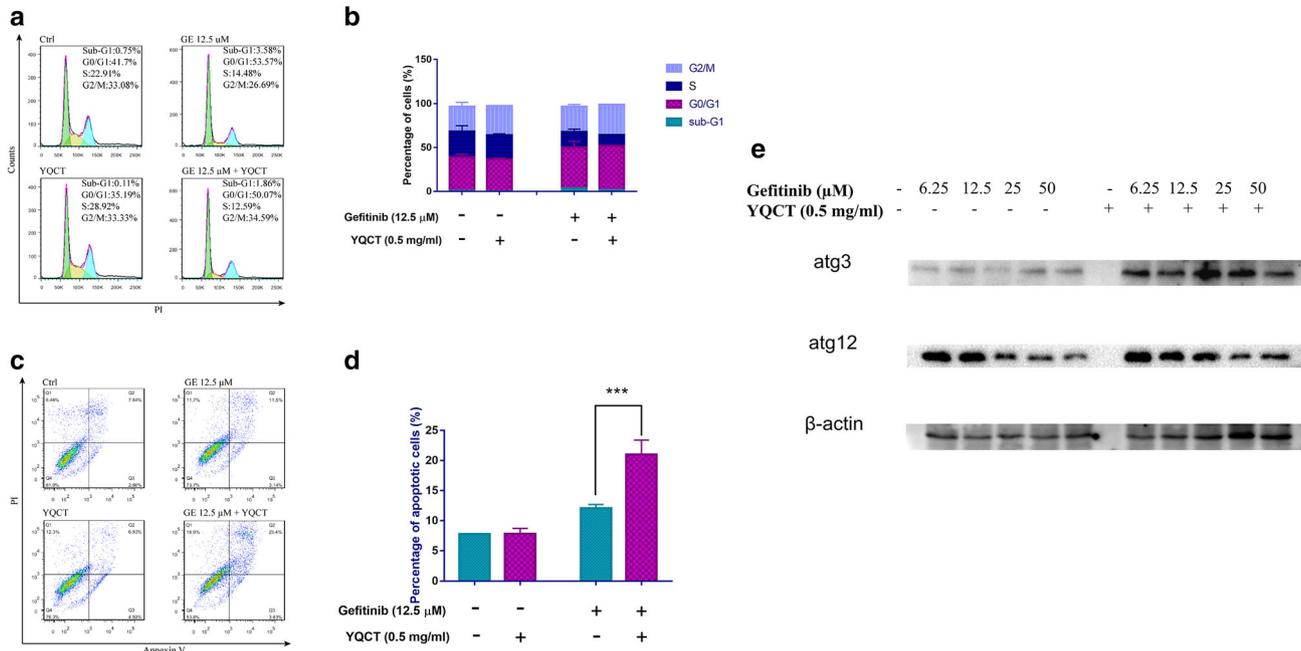


Figure 3. YQCT induces cell cycle arrest, enhances apoptosis and autophagy. (a) Effect of YQCT on the cell cycle. Fluorescence-activated cell sorting (FACS) detection of PI stained cells was used to measure the distribution of specific cell populations in Sub-G1, G0/G1, S, and G2/M phases in H1975 cells. Cells were treated with 12.5 μ M gefitinib with and without 0.5 mg/ml YQCT for 48 h and then analyzed by flow cytometry. (b) Plots the data from (a) to better illustrate the quantitative changes in cell cycle phases. Data were the mean \pm SD of independent experiments. (c) YQCT induced apoptotic cell death in H1975 cells. Cells were incubated with gefitinib at 12.5 μ M in the presence and absence of 0.5 mg/ml YQCT for 48 h, then analyzed by flow cytometry. (d) Plots the data from (c) to better illustrate the quantitative changes in late apoptosis. Data represented the mean \pm SD of independent experiments. One-way ANOVA test and independent-samples T test was used for analysis, *** indicates $P < 0.01$. (e) Western blot for autophagy proteins. H1975 cells were incubated with gefitinib at 6.25, 12.5, 25, and 50 μ M in the presence or absence of 0.5 mg/ml YQCT for 48 h. Atg3, atg12, and β -Actin (dilution ratio: 1:1,000) were visualized via western blot analysis. [Color figure can be viewed at wileyonlinelibrary.com]

represented GO and KEGG functional terms in protein-coding genes were shown in the Supporting Information Tables S6 and S7. We found that apoptosis and cell cycle categories were shown in the GO terms (Fig. 4b). Meanwhile, NSCLC related pathways identified as significantly affected by YQCT were shown in Figure 4c. From the analysis we focused on specific pathways related to cancer, pathways in cancer and pathways in NSCLC were shown in Figure 5a,b.

DISCUSSION

The nine bio-active compounds of YQCT were reported to have anti-cancer effect (23) and reversal of drug resistance (24) by causing cell cycle arrest (25), inducing apoptosis (26) and activating autophagy (27). However, the mechanism of YQCT on drug resistance has not been studied.

EdU is an indicator of cell proliferation (19,20). According to the EdU and MTT assays, 0.5 mg/ml of YQCT can inhibit cell proliferation but shows no obvious cell cytotoxicity. Therefore, its effect of reducing drug resistance appears to be based solely on cell proliferation inhibition. Cell cycle is the basic mechanism of proliferation, differentiation, and cell death. Cell cycle arrest leads to DNA breaks, which ultimately leads to the inhibition of cell proliferation (28). YQCT group and combined

group showed arrest in G2/M phase on H1975 cells, which indicates that the YQCT group and combined group could inhibit tumor cell proliferation via G2/M phase arrest, which is also consistent with the result of the EdU assay.

In the treatment of cancer, a promising treatment is manipulating apoptosis by modulation of the key regulators of apoptosis (29). Gefitinib has an effect on apoptosis regulation by competitively binding to the tyrosine kinase domain of EGFR, leading to the EGFR signaling pathway being blocked. The lack of gefitinib binding to the TKI domain in EGFR-TKI resistant cells leads to a reduction in apoptosis, which reduces the effectiveness of NSCLC treatment (30). Therefore, YQCT combined with gefitinib could be an effective therapy for EGFR-TKI resistance in NSCLC, as it sensitizes the apoptosis induced by gefitinib.

It is reported that loss of autophagy might cause the acquired EGFR-TKI resistance (31). The autophagy-related genes ATG3 and ATG12 are involved in tumorigenesis and cancer progression, they also perturb early autophagy pathway, which contributes to autophagosome maturation and formation processes, respectively (32). Therefore, our results indicate YQCT induces autophagy by up-regulating atg3 and atg12, which maybe one of the mechanisms of reducing the acquired EGFR-TKI resistance.

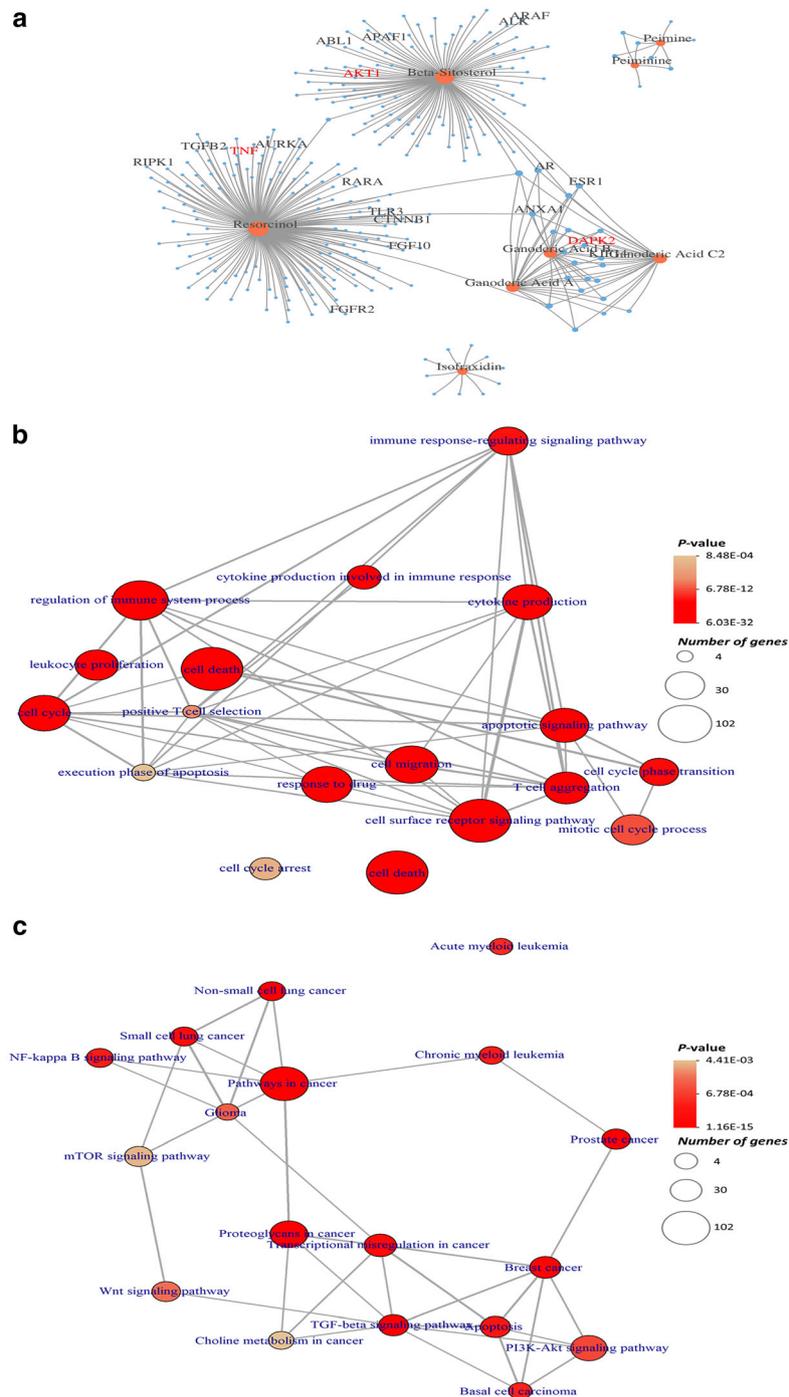


Figure 4. Potential molecular mechanisms of YQCT. (a) Genes regulated by YQCT. Orange nodes represented chemical components and blue nodes represented genes. (b) GO term enrichment results. The color of each node indicated the significance of the enriched term, the redder meant the higher relevance. The size of each node represented the number of GO term associated genes, the bigger meant the higher association. The names of most significant terms in each cluster were shown. (c) KEGG pathway enrichment results. The color of each node indicated the significance of the enriched term, the redder meant the higher relevance. The size of each node represented the number of KEGG term associated genes, the bigger meant the higher association. The names of most significant terms in each cluster were shown. [Color figure can be viewed at wileyonlinelibrary.com]

To find out potential drug resistance reduction mechanisms of YQCT, we find that 269 genes show significant relationship (score > 20) with these nine compounds in YQCT. Three of these

genes, *APAF1*, *TNF*, and *DAPK2*, are reported to mediate apoptosis, inhibit cell proliferation and metastasis (33–35). GO terms also show a significant relationship between YQCT and both apoptosis

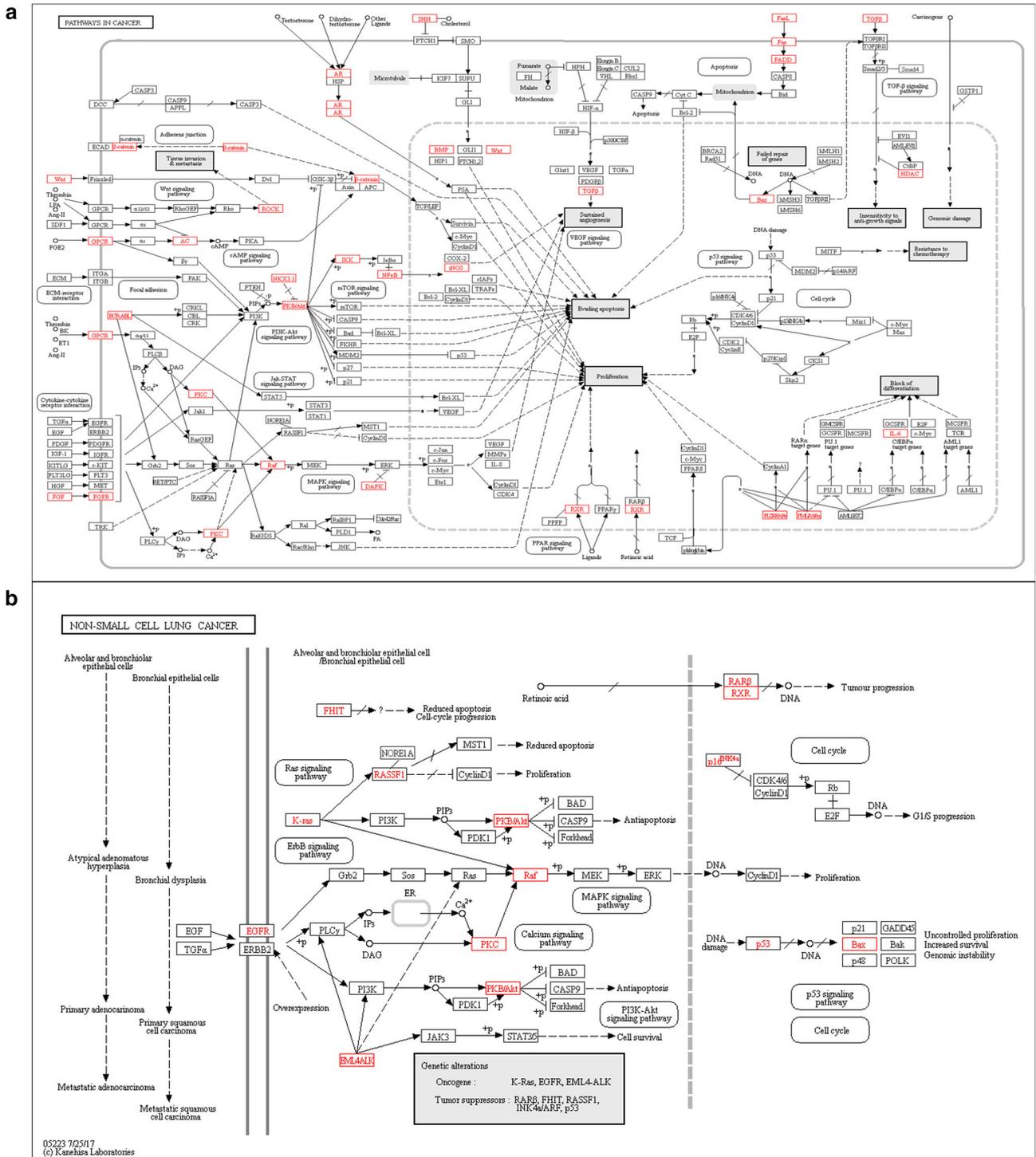


Figure 5. Pathways relevant to YQCT. (a) Pathways in cancer. (b) Pathways in NSCLC. Potential factors that relevant to YQCT were colored in red. [Color figure can be viewed at wileyonlinelibrary.com]

and cell cycle, as shown in Figure 4b, which is also consistent with the result of the flow cytometry and western blot analysis.

In the pathways in cancer and, specifically NSCLC, the FGF-FGFR and EGF-EGFR pathways are of interest as they are relevant to YQCT. Both of them are upstream effectors of the

PI3K-Akt pathway, which is relevant to apoptosis. As our previous study indicates that YQCT down-regulates p-akt in A549 NSCLC cells (36), and KEGG enrichment analysis suggests that the PI3K-Akt signaling pathway was affected by YQCT. From this, we speculate that YQCT down-regulates the PI3K-Akt

pathway and up-regulates apoptosis by affecting both the FGF-FGFR and EGF-EGFR pathways. These speculation and results provide a potential research direction to screen the relevant pathways in more comprehensive studies.

In summary, we demonstrate YQCT can inhibit cell proliferation, slightly arrest cell cycle at G2/M phase, induce apoptosis, and activate the autophagy. Together these results indicate YQCT has the ability to reduce gefitinib-induced drug resistance, we speculate that this might be through up-regulation of apoptosis and autophagy in EGFR-TKI resistant NSCLC cells.

Asia is the district, which has highest lung cancer new cases in 2018. Although EGFR-TKI are very effective in patients with EGFR mutations on lung cancer (37), acquired drug resistance leads to low efficacy and survival rate. Our findings may help in the development of a new strategy for reducing gefitinib resistance during treatment in NSCLC patients with EGFR mutations.

ACKNOWLEDGMENTS

We are very grateful to James Galbraith from the University of Adelaide (Australia) and Gee Tang for taking the time to read manuscript in full and offer helpful comments. This work was supported by the National Natural Science Foundation of China (grant number: 81573780).

CONFLICT OF INTERESTS

The authors declare that they have no conflict of interest.

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