

## Effect of thymoquinone on endoplasmic reticulum (ER) stress in NRK-52e cells

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**Abstract:** Thymoquinone (TQ), the active component of *Nigella sativa*, has many beneficial effects. The endoplasmic reticulum involved in the quality control of protein translocation and folding can vary under different conditions, the phenomenon of causing the accumulation of unfolded or misfolded proteins within the ER lumen is termed ER stress. This *in vitro* study was planned to investigate the effect of TQ on ER stress at proliferative (Tp) and toxic (TQ<sub>IC50</sub>) concentrations on NRK-52E cells at 24th, 48th hours. The expression of important genes in the ER stress pathway (ATF4, ATF6, BIP, CHOP, IRE1, XBP1, PERK) was analyzed. Expression of all genes except CHOP and XBPI increased at 24 hours and BIP at 48 hours for Tp. In the IC<sub>50</sub>, the CHOP and XBPI gene expressions increased at the 24th hour, and the CHOP and ATF4 genes increased at the 48th hour. As a result, it was determined that the expression of ER stress genes had significant changes with the TQ induction, depending on time and concentration, especially in the proliferative concentration. It is thought that TQ may have varying effects on healthy kidney cells, and it is important to investigate the mechanism of this effect in further studies.

**Keywords:** Thymoquinone, endoplasmic reticulum stress, kidney, *in vitro*.

### INTRODUCTION

Herbal medicines have attracted attention and are being used more and more as an alternative and supplement to chemical medicines in recent years. *Nigella sativa* and its most important chemical composition, TQ, have been researched for this purpose, and many studies have been carried out. (Usta *et al.*, 2018a; Usta *et al.*, 2018b, Yüksek, 2021). *Nigella sativa* seeds have been used traditionally for centuries in the treatment of various diseases, such as in the Middle East, Asia, and our country. TQ, the main component of *Nigella sativa*, is a potent inducer of apoptosis in cancer cells, has an antioxidant effect, is anti-diabetic, antitumoral, and anticarcinogenic, is anti-inflammatory, anti-allergic, antibacterial, antifungal, and antiparasitic (Kurt *et al.*, 2014; Majdalawieh *et al.*, 2017; Mollazadeh *et al.*, 2017; Ullah *et al.*, 2017; Usta and Dede, 2017; Goel *et al.*, 2018; Ansary *et al.*, 2021).

In addition, it is thought that TQ has a nephroprotective effect by improving many damages that cause nephrotoxicity due to its antioxidant, antiproliferative and proapoptotic activities (Mollazadeh *et al.*, 2017; Hosseinian *et al.*, 2019; Özer *et al.* 2020; Ansary *et al.*, 2021).

The endoplasmic reticulum (ER) is a network system found in the cytoplasm of cells. It provides for the

exchange of substances between cells and the production of substances in some regions. ER stress occurs when the balance between the protein folding capacity of the ER and the processed protein load increases in the direction of misfolded or unfolded protein. Infections, ambient temperature, oxidative stress, etc. are factors that affect the folding of proteins. These causes trigger the stress response, ER stress genes are activated, and eventually, cell death occurs. There have been studies showing that ER stress is involved in the etiology of many diseases (Manalo and Medina, 2018; Almanza *et al.*, 2019; Chadwick and Lajoie, 2019; Kara and Oztas, 2019; Tatar and Tatar, 2019; Sicari *et al.*, 2020; Lee and Lee, 2022).

Excessive ER stress leads to apoptosis, causing ischemic acute kidney injury and thus various kidney diseases. Therefore, approaches to reduce ER stress with various pharmacological agents have been investigated to prevent kidney damage and develop new treatment strategies (Ricciardi and Gnudi, 2020; Li and Chen, 2021; Ni *et al.*, 2021).

This study was planned to investigate the time-dependent effect of TQ, which is known to have many beneficial effects, on normal kidney cells at beneficial (proliferative) and toxic (IC<sub>50</sub>) concentrations, under *in vitro* conditions. Gene expressions (ATF4, ATF6, BIP, CHOP, IRE1, PERK, XBP1) that play a role in ER stress at beneficial (proliferative) and toxic (IC<sub>50</sub>) concentrations of TQ were investigated by RT-qPCR, at 24 and 48 hours.

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## MATERIALS AND METHODS

### Cell culture

Rat kidney epithelial NRK-52E (ATCC® CRL-1571™) cells were used as study material. Cells were cultured *in vitro* in RPMI 1640 as described previously (Korkmaz *et al.*, 2022).

### Cytotoxicity (MTT cell viability) test

NRK-52E cells were seeded at 7000 cells per culture plate under appropriate conditions. Cells were incubated for 24 hours at 37°C in a CO2 incubator. After incubation, the medium on the cells was removed, and TQ prepared at different concentrations using cell medium was added. TQ master stock concentration was dissolved in DMSO. It was prepared in cell medium at different final concentrations (1µM-100µM). TQ prepared at these concentrations was applied to the cells. After 24 and 48 hours, 100µl of cell medium (with 10µl of MTT solution) was added to each well and incubated. Then, MTT lysis solution (100µl) was added to each well, and the optical densities of the cells were read (570 nm). TQ IC50 and proliferation concentrations were determined according to the absorbance values obtained. While determining the percentage of cell viability, the viability of the control group was evaluated as 100%. Thus, proliferative and IC50 values of TQ at 24 and 48 hours were determined by MTT cell viability test (Korkmaz *et al.*, 2022).

### Preparation of study groups

The applications to be made to the study groups are summarized in table 1.

### RNA extraction

Cells were centrifuged, and the medium was removed. 1ml of cold PBS (phosphate buffer solution) was added to the underlying cell lysate, and the cells were well suspended. This mixture was transferred to a new sterile tube and centrifuged at 300xg for 5 minutes, and the supernatant was discarded. By adding 1ml of cold trizol reagent to the tube, the cell was homogenized and centrifuged at 3500 rpm for 10 minutes. The supernatant collected on top was transferred to a new tube. Cold chloroform was added to new tubes, incubated, and centrifuged at 12000xg for 15 minutes.

**Table 1:** Study plan

	Groups	Application
1	Control (C)	Cell medium
2	TQp	Proliferative concentration
3	TQ <sub>IC50</sub>	IC <sub>50</sub> concentration

750000 cells per flask were seeded for the study groups. Study groups were prepared as control and experimental groups, with the crossover between these groups.

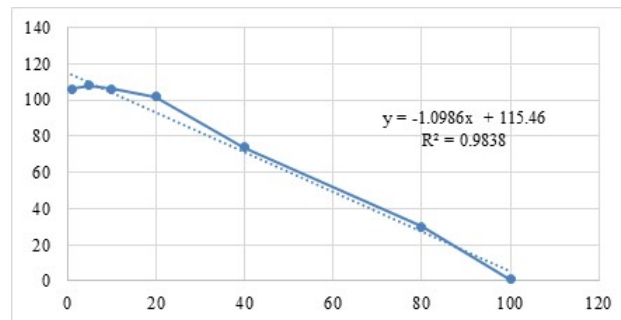
The upper clear phase was carefully removed, transferred to a new sterile tube, and mixed well by adding isopropyl alcohol. It was centrifuged at 12000 x g for 10 minutes. The supernatant was completely discarded, and the remaining RNA was washed by vortexing with 75% ethanol. It was centrifuged at 7500 x g for 5 minutes. The remaining pellet was dried in a laminar cabinet for 15 minutes, leaving the tube open. RNA was dissolved in 30-50µl of water and stored at -80°C for the cDNA step (Chomczynski and Mackey, 1995).

### cDNA (Complementary DNA) synthesis

To be used for gene expression analysis in real-time PCR, cDNA synthesis from the obtained RNAs was performed according to the protocol (WizScript, Cat No. W2211, Wizbio).

### Real-time polymerase chain reaction (RT-qPCR)

In this study, BIP (including immunoglobulin heavy chain-binding protein), XBP1 (X-box binding protein 1), CHOP (C/EBP [CCAAT/enhancer-binding protein]-homologous protein), PERK (PKR-like endoplasmic reticulum kinase), IRE1 (inositol-requiring 1), ATF6 (activating transcription factor 6), ATF4 (activating transcription factor 4) genes were expressed. The primer list of target genes is given in table 2. Evaluation of target gene products was performed according to the 2-ΔΔCt method (Livak and Schmittgen, 2011). Differences between groups were evaluated according to the comparison of the increase-decrease fold changes in the expression of the control gene.



**Fig. 1:** MTT results (24th, 48th h)

### Data analysis

CT values were exported to an Excel file. CT values, Glyceraldehyde-3-phosphate dehydrogenase (GAPDH), were used as reference gene. The fold change was calculated using the delta delta CT data analysis method. Differences were considered significant when p<0.05 (Yezdani *et al.*, 2016).

Paired sample t-test was used to determine whether there was a significant difference between groups according to time and concentration. The statistical significance level was taken as 5% in the calculations (SPSS ver. 22).

**Table 2:** The primers

Genes	L (5' to 3')	R (5' to 3')
BIP	rn-BIP-100bp-ID25617-F	ACCAAGACATTTGCCCCAGA
	rn-BIP-100bp-ID25617-R	CAACTGCATGGGTGACCTTC
XBP1	rn-XBP1-177bp-ID289754-F	CAGCAAGTGGTGGATTTGGA
	rn-XBP1-177bp-ID289754-R	CCTTACTCCATTCCCCTTGGGA
CHOP	rn-CHOP-103bp-ID29467-F	AACCTGAGGAGAGAGAAACCG
	rn-CHOP-103bp-ID29467-R	TCATACCAGGCTTCCAGCTC
PERK	rn-PERK-162bp-ID29702-F	CTGAAGGACGAAAGCACAGAC
	rn-PERK-162bp-ID29702-R	ACAGGAAATGCCCACTGAGA
IRE1	rn-IRE1-265bp-ID498013-F	TGCGCAGGTGCAATGAC
	rn-IRE1-265bp-ID498013-R	GTAAAGGGAAGTTTCGTCAGGC
ATF6	rn-ATF6-217bp-ID304962-F	AGCCCCTCATTAACACGACA
	rn-ATF6-217bp-ID304962-R	TCACTCCCAGAATTCCTACTGATG
ATF4	rn-ATF4-135bp-ID79255-F	AGACACCGGCAAGGAGGAT
	rn-ATF4-135bp-ID79255-R	AACGTGGCCAAAAGCTCATC
GAPDH	rn-GAPDH-77bp-ID24383-F	AGTGCCAGCCTCGTCTCATA
	rn-GAPDH-77bp-ID24383-R	GGTAACCAGGCGTCCGATAC

**RESULTS**

**MTT results**

TQ concentrations determined for the 24th and 48th hours as a result of the MTT test are given in table 3.

**Table 3:** Determined TQ concentrations

	24th hours	48th hours
TQp (µM)	10	10
TQ <sub>IC50</sub> (µM)	60	60

**The determination of TQ concentrations**

*ERS gene expression results*

The Ct plot and melting curve results obtained in RT-qPCR analyses for all target genes are given in Fig. 2. These plots show that the primers specifically designed for each target gene bind appropriately, and the regions are amplified (fig. 2).

Gene expression results obtained at 24 and 48 hours at Tp and TIC50 concentrations are summarized in tables 4-7.

**Table 4:** Time-dependent variation of TQ<sub>IC50</sub> concentration

Genes	24 (X±SD)	48 (X±SD)	P
ATF4	5.032±0.132	0.207±0.038	≤0.001
ATF6	0.593±0.030	4.517±0.343	≤0.001
BIP	0.300±0.035	0.198±0.033	≤0.005
CHOP	4.517±0.279	15.000±1.414	≤0.001
IRE1	55.333±8.042	1.028±0.091	≤0.001
PERK	0.598±0.036	0.210±0.034	≤0.001
XBP1	8.000±0.369	0.698±0.034	≤0.001

**Table 5:** Time-dependent variation of Tp concentration

Genes	24	48	P
ATF4	0.598±0.037	0.910±0.071	≤0.001
ATF6	0.298±0.035	12.933±0.779	≤0.001
BIP	0.503±0.035	0.987±0.046	≤0.001
CHOP	6.467±0.463	59.167±3.312	≤0.001
IRE1	2.000±0.261	1.000±0.071	≤0.001
PERK	0.2000±0.034	14.750±1.541	≤0.001
XBP1	9.167±0.931	1.517±0.136	≤0.001

Up and down regulation of gene expression was done according to the control gene. It was determined that the ATF4 gene was down-regulated 0.6 times in the TQp group and 0.2 times in the TQ<sub>IC50</sub> group at the 24th hour. At 48 hours, it up regulated 5 times in the TQp group and down regulated 0.9 times in TQ<sub>IC50</sub> group.

It was determined that the ATF6 gene expression in the TQp group decreased by 0.3 at the 24th hour, and decreased by 0.6 times in the TQ<sub>IC50</sub> group. At 48 hours, a 13-fold increase in the TQp group and a 4.5-times increase in TQ<sub>IC50</sub> were detected.

The expression level of the BIP gene was down-regulated by 0.5 times in the TQp group and 0.3 times in the TQ<sub>IC50</sub> group for the 24th hour. There was a change in the TQp (0.99) and TQ<sub>IC50</sub> (0.2) groups for the 48th hour. The CHOP gene was upregulated 6.5 times in the TQp group, 4.5 times in the TQ<sub>IC50</sub> group at 24 hours. There was an increase in 48 hours, 59 times in the TQp group and 15 times in the TQ<sub>IC50</sub>.

The expression level of the IRE1 gene was 2 times up-regulated in the TQp group at the 24th hour and 55-fold at

the 48th hour. However, there was no change in the TQ<sub>IC50</sub> group at the 24th and 48th hours. The PERK gene was down-regulated by 0.2-fold in the TQp group and 0.6-fold in the TQ<sub>IC50</sub> group at the 24th hour. For the 48th hour, it was found to be 15 times up-regulated in the TQp group and 0.2 times up-regulated in the TQ<sub>IC50</sub>.

**Table 6:** Difference between concentrations at 24th hour

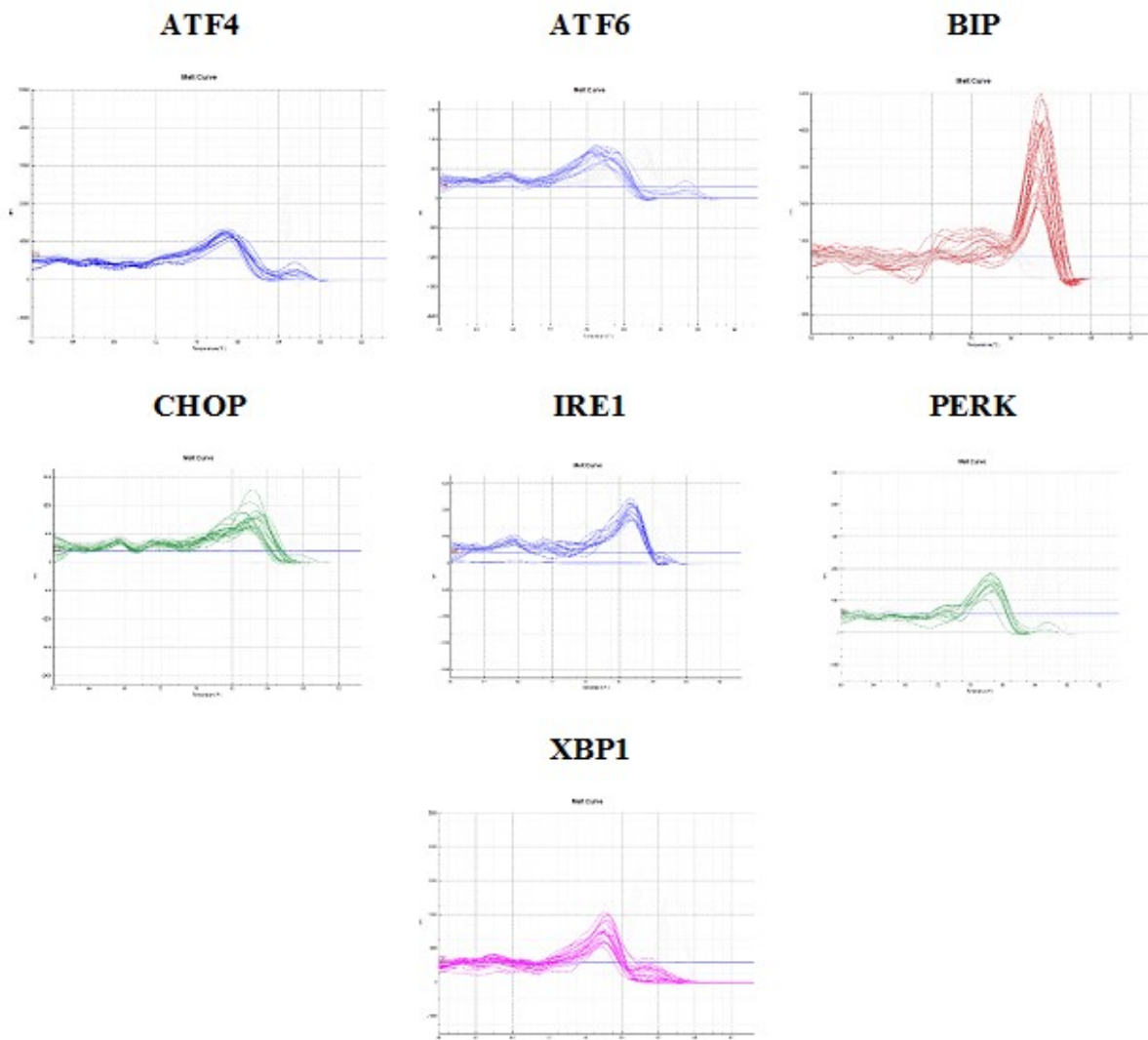
Genes	TQp (X±SD)	TIC50 (X±SD)	P
ATF4	0.598±0.037	5.032±0.132	≤0.001
ATF6	0.298±0.035	0.593±0.030	≤0.001
BIP	0.503±0.035	0.300±0.035	≥0.05
CHOP	6.467±0.463	4.517±0.279	≤0.005
IRE1	2.000±0.261	55.333±8.042	≤0.001
PERK	0.2000±0.034	0.598±0.036	≤0.005
XBP1	9.167±0.931	8.000±0.369	≥0.05

**Table 7:** Difference between concentrations at 48th hour

Genes	TQp (X±SD)	TIC50 (X±SD)	P
ATF4	0.910±0.071	0.207±0.038	≤0.001
ATF6	12.933±0.779	4.517±0.343	≤0.001
BIP	0.987±0.046	0.198±0.033	≤0.005
CHOP	59.167±3.312	15.000±1.414	≤0.001
IRE1	1.000±0.071	1.028±0.091	≤0.001
PERK	14.750±1.541	0.210±0.034	≤0.001
XBP1	1.517±0.136	0.698±0.034	≤0.001

\*Significant in comparison to other groups ( $p \leq 0.05$ ). X. mean; SD. Standard deviation

The XBP1 gene was expressed 9 times more in the TQp group and 8 times more in the TQ<sub>IC50</sub> group at the 24th hour. At 48 hours, it was found to be 1.5 times up-regulated in the TQp group, and 0.7 times up-regulated in TQ<sub>IC50</sub>.



**Fig. 2:** Melting curve plot of the products obtained for each target gene.

## DISCUSSION

TQ has been shown to affect numerous molecular and signalling pathways in many inflammatory and degenerative diseases, including cancer. There are many studies on the effect of TQ on ER stress-mediated apoptosis (Zhang *et al.*, 2018; Liou *et al.*, 2019; Landucci *et al.*, 2021).

ER stress plays a role in the emergence of various kidney diseases. There are studies suggesting that the endoplasmic reticulum (ER) plays a role in the emergence of acute kidney injury (AKI) and, leads to unfolded protein response (UPR) or ER stress. Various kidney diseases such as inflammation, ischemia-reperfusion, genetic mutations of kidney proteins, proteinuria, diabetic nephropathy caused by cyclosporine A treatment, renal fibrosis, and kidney damage have been reported to occur due to ER stress-induced apoptosis (Taniguchi and Yoshida, 2015; Maekawa and Inagi, 2017; Yan *et al.*, 2018; Mo *et al.*, 2019).

ER stress-induced ATF6, PERK and, IRE1 signaling pathways initiate pathways that promote cell survival. In addition, in cases where ER stress is chronically prolonged, it also causes cellular dysfunction and, thus, the induction of apoptosis pathways (Sarvani *et al.*, 2017; Adams *et al.*, 2019).

Genes that are important in the occurrence of ER stress are UPR genes, BIP (including immunoglobulin heavy chain-binding protein), XBP1 (X-box binding protein 1), CHOP (C/EBP [CCAAT/enhancer-binding protein]-homologous protein), IRE1 (inositol-requiring 1), ATF6 (activating transcription factor 6), and ATF4 (activating transcription factor 4) (Limonta *et al.*, 2019; Tatar and Tatar, 2019; Nakada *et al.*, 2021).

Induction of ER stress can be both cytoprotective and, cytotoxic by activating apoptosis in the cell (Cybulsky, 2017). In fact, the PERK-ATF4-CHOP pathway of the ER stress response is proapoptotic in some kidney diseases. Thus, the ER stress response protects against some kidney diseases. Removal of unfolded proteins by autophagy is also protective for some ER stress-induced kidney diseases (Taniguchi and Yoshida, 2015; Wei *et al.*, 2021). As a matter of fact, in the present study, it was determined that CHOP and, XBP1 gene expressions were significantly increased in the kidney epithelial cells of TQ at both proliferative and, IC50 concentrations at 24 hours. Other genes were found to be slightly down-regulated. On the other hand, IRE1 increased its expression 2-fold only at the proliferative concentration.

At the 48th hour, it was observed that all genes were up-regulated at the TQp concentration, and even the CHOP and IRE1 concentration increased more than 50 times.

Although CHOP and ATF6 were significantly increased at TQ<sub>IC50</sub> concentration, other genes were found to be slightly down-regulated.

Some genetic mutations are also considered to cause kidney diseases by inducing ER stress, protein misfolding, and disruption of protein traffic (Park *et al.*, 2019). Therefore, normalization of ER stress using various pharmacological agents for the treatment of kidney diseases may be promising to prevent or arrest the progression of kidney disease (Cybulsky, 2017). This stress signal network may be a target for interventions aimed at improving CKD (Maekawa and Inagi, 2017). Compounds that can mimic ER stress inhibitors, may provide regulatory effects on ER stress-induced apoptosis. Studies have shown that some substances used as preservatives may be important as potential therapeutic agents by inhibiting ER stress (Liu *et al.*, 2018; Mo *et al.*, 2019; Tatar and Tatar, 2019; Jeon Gómez-Sierra *et al.*, 2020).

In this study, it is thought that the time-dependent increases in TQp concentration may activate the mitochondrial pathway of apoptosis by stimulating the ER stress response in the healthy cell line. There are studies where TQ is used as a preventative against kidney disorders. It has been shown to have anti-inflammatory and antioxidant properties in animal and *in vitro* models, especially against various kidney diseases caused by inflammation and oxidative stress (Jalili *et al.*, 2017; Shaterzadeh-Yazdi *et al.*, 2018; Dera *et al.*, 2019b; Hosseinian *et al.*, 2019; Aslan *et al.*, 2020b; Hashem *et al.*, 2020; Özer *et al.*, 2020). The protective effects of TQ are thought to be due to increased antioxidant capacities and the mediation of the reduction of ER stress and apoptosis (Bouhleb *et al.* 2018).

Studies have been conducted to show that thymoquinone, known for its antioxidant, anti-inflammatory, and renal protective effects, may cause nephropathy. TQ increases cell viability up to a certain concentration. An increase in the causes of kidney damage (Yukse, 201), mitochondrial damage (Stelmashook *et al.*, 2020). Oral administration of TQ to rats can cause liver and kidney damage at certain concentrations (60 mg/kg) (Kurt *et al.*, 2014). Although black cumin and its bioactive components are relatively well tolerated, in some cases they can lead to oxidative stress and disrupt signaling pathways (Hannan *et al.*, 2021). It has been reported that TQ has strong cytotoxicity, especially in cancer cells, and a weaker killing effect against normal cells (Alaufi *et al.*, 2017).

The unfolded protein response (UPR) pathway regulates proteostasis and cell fate through the activity of the transcription factors ATF4, ATF6, and XBP1 (Yang *et al.*, 2020). The increase in CHOP in kidney tissue inhibits

and protects against the inflammatory response to kidney damage. ATF4 and CHOP directly induce protein synthesis and genes involved in the UPR. However, under conditions where ATF4 and CHOP increase protein synthesis, oxidative stress and cell death may result (Bujisic *et al.*, 2017; Almanza *et al.*, 2019). The fact that TQ increased 5 times at the proliferative concentration at the 48th hour in this study can be considered evidence of the TQ protective effect on kidney tissues.

In this study, the expression levels of genes activated due to ER stress were determined. Based on these results, it has been shown that ER stress occurs in normal kidney cells under normal conditions due to TQ administration. Especially at TQp concentration, activation of ER stress factors, which starts at the 24th hour, peaks at the 48th hour. TQ, which is often used for its protective and therapeutic properties, has been found to activate ER stress factors even at proliferative concentration. It was determined that the activating effect of TQ applied at the IC50 concentration on the expression of ER stress genes was more limited than the proliferative concentration, and this situation continued at the 48th hour.

It has been determined that the genes are up-regulated at the TQp concentration, i.e., while driving the cell to proliferation. It was determined that only ATF6 and CHOP genes increased while killing the cell at the TQ<sub>IC50</sub> concentration. Here, it was determined that the XBP1 gene was high in the first stage for both concentrations, but decreased at 48 hours and thus behaved differently from other ER stress genes. It is noteworthy that the genes involved in ER stress are activated or decreased by different mechanisms according to TQ concentration and time.

## CONCLUSION

As a result, it was determined that the stimulation of ER stress can be effective both cytoprotectively and cytotoxicity by activating apoptosis in kidney cells, and TQ can provide protection against some kidney diseases by stimulating ER stress at the appropriate dose. However, it has been concluded that it can be harmful as well as beneficial. It has been observed that TQ, used with the expectation of full benefit, may have varying effects on the kidney, including ER stress, depending on time and concentration. In order to reveal the molecular basis underlying the mechanism of this effect, it is thought that it would be beneficial to carry out further studies, including new and supportive parameters and additional concentrations and times.

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