



Research article

CGA alleviates LPS-induced inflammation and milk fat reduction in BMECs through the NF- κ B signaling pathway

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ABSTRACT

Mastitis is an easy clinical disease in dairy cows, which seriously affects the milk yield and quality of dairy cows. Chlorogenic acid (CGA), a polyphenolic substance, is abundant in *Eucommia ulmoides* leaves and has anti-inflammatory and anti-oxidative stress effects. Here, we explore whether CGA attenuated lipopolysaccharide (LPS)-induced inflammation and decreased milk fat in bovine mammary epithelial cells (BMECs). 10 μ g/mL LPS was used to induce mastitis in BMECs. QRT-PCR, Western blotting, oil red O staining, and triglyceride (TG) assay were used to examine the effects of CGA on BMECs, including inflammatory response, oxidative stress response, and milk fat synthesis. The results showed that CGA repaired LPS-induced inflammation in BMECs. The expression of IL-6, IL-8, TNF- α , IL-1 β , and iNOS was decreased, and the expression levels of CHOP, XCT, NRF2, and HO-1 were increased, which reduced the oxidative stress level of cells and alleviated the reduction of milk fat synthesis. In addition, the regulation of P65 phosphorylation by CGA suggests that CGA may exert its anti-inflammatory and anti-oxidative effects through the NF- κ B signaling pathway. Our study showed that CGA attenuated LPS-induced inflammation and oxidative stress, and restored the decrease in milk fat content in BMECs by regulating the NF- κ B signaling pathway.

1. Introduction

As one of the most common mammary gland diseases in dairy cows, mastitis seriously affects animal health and is closely related to the decline in milk yield and quality [1–4]. It is related to the important economic production factors of dairy cows and has attracted extensive attention from production and scientific researchers [5,6]. The dairy cow mammary gland is very susceptible to various bacterial pathogens, and bacterial infection further leads to the inflammatory response [7]. The main component of the cell wall of Gram-negative bacteria is LPS, after the death and lysis of Gram-negative bacteria, they act on the mammary epithelial cells of dairy cows, which can induce an inflammatory response [8,9]. At present, intramammary injection of antibiotics is often used to treat

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mastitis in dairy cows. However, with the increase in public concerns about antibiotics, especially the emergence of drug resistance and antibiotic residues, it is urgent to use safer and more reliable alternative drugs [3,10].

Traditional Chinese medicine and its extracts are good alternatives to antibiotics, and some plants and their extracts have antibacterial and anti-inflammatory effects [10]. Chlorogenic acid (CGA) is a polyphenolic substance that is abundant in nature and widely exists in traditional Chinese medicinal herbs such as honeysuckle, *Eucommia ulmoides* leaves, and chrysanthemum [11–13]. It has been reported that chlorogenic acid, one of the most studied phenolic compounds in the past decade, has a variety of functions, including anti-inflammatory, antibacterial, and antioxidative stress functions [14,15]. Studies have shown that CGA protects jejunal cell integrity by alleviating inflammation and apoptosis induced by DON in IPEC-J2 cells [12]; mice show inhibited inflammation and apoptosis after oral administration of CGA to alleviate colitis inflammation [14]. CGA can also inhibit the occurrence of neuro-inflammation and oxidative stress, thereby protecting neurons and improving posttraumatic stress disorder [16]. The addition of CGA to the basal diet of weanling pigs can effectively improve the intestinal barrier, which is achieved by inhibiting the TLR4/NF- κ B signaling pathway and activating the NRF2/HO-1 signaling pathway to inhibit inflammation and oxidative stress [11]. At present, CGA has been proven to be able to regulate intestinal homeostasis, alleviate renal inflammation, improve posttraumatic stress disorder, and improve the antioxidant capacity of liver tissue [16–19].

Previous studies have shown that CGA can act on mammary epithelial cells of dairy cows, alleviate the inflammatory response caused by *Staphylococcus aureus*, and reduce the growth rate and invasion rate of *Staphylococcus aureus* [20]. This study suggests that CGA may be an effective drug for the treatment of bovine mastitis. However, the specific role and mechanism of CGA in LPS-induced bovine mammary epithelial cell inflammation still needs to be explored. Here, an inflammation model of LPS-induced BMECs was established. After adding CGA, the expression levels of related inflammatory factors, milk fat synthesis-related genes, and oxidative stress-related genes were measured, and the changes in related signaling pathways were further analyzed to explore the effects of CGA on inflammation, and milk fat synthesis in LPS-induced BMECs.

2. Materials and methods

2.1. Cell culture

BMEC cells were purchased from Shanghai Qingqi Biological Co., LTD (Shanghai, China). The composition of the culture medium consisted of DMEM/F12 medium (BI, Kibbutz Beit Haemek, Israel), 10 % FBS (LONSERA, Shanghai, China) and 1 % penicillium-streptomycin solution (HyClone, South Logan, UT, USA). During cell culture, the carbon dioxide concentration was maintained at 5 % in constant temperature incubator at 37 °C. LPS (Sigma, St. Louis, Missouri, USA) was prepared using sterile PBS (Solarbio, Beijing, China) to concentration of 1 mg/mL. According to our previous study, the concentration of LPS was set at 10 μ g/mL for 24 h [21]. A 50 mg/mL CGA solution was prepared by dissolving 20 mg CGA (Solarbio, Beijing, China) in 400 μ L DMSO. After the cells were treated with LPS, CGA (0, 10, 20, 30, 40, and 50 μ g/mL) was added to the medium and cultured for 24 h. The final concentration of CGA was set at 10 μ g/mL.

2.2. The CCK-8 assay of cell viability

Using a 96-well plate, 5000 cells/well were seeded, covered with 100 μ L of medium, and incubated for 24 h at 37 °C. Then, the medium was converted to CGA containing medium. After 24 h of culture, 10 μ L CCK-8 (Beyotime, Shanghai, China) was added and treated for 1 h. Absorbance values at 450 nm were determined with a microplate reader (Tecan, Safire, Austria). Each concentration had three replicate wells.

2.3. RNA extraction and QRT-PCR

Total RNA was extracted from BMECs cultured in 12-well plates using TRIzol reagent (Invitrogen, Carlsbad, CA, USA). RNA concentration was determined and quality was evaluated using NanoDrop2000 spectrophotometer (Thermo, Waltham, MA, USA). The extracted total RNA was reverse transcribed into cDNA by a reverse transcription kit (Tiangen, Beijing, China). According to the concentration of RNA, different volumes were added to synthesize an equal amount of cDNA. QRT-PCR was performed using a 20 μ L system with 1 μ L cDNA, 1 μ L primer mixture, and SYBR Green (Tiangen, Beijing, China). The relative expression levels of all genes were determined by the $2^{-\Delta\Delta C_t}$ method. The sequences were shown in [Supplementary Table 1](#).

2.4. Western blotting

BMECs were seeded on a six-well plate and cultured. RIPA cell lysate (Solarbio, Beijing, China) was mixed with trypsin inhibitor 100:1 to prepare the lysate. The total protein concentration of BMECs was determined using the BCA Protein Assay kit (Beyotime, Shanghai, China). Equal amounts of protein were loaded into each well, and protein separation was performed using 10 % SDS-PAGE electrophoresis. Proteins were subsequently transferred to PVDF (Sigma Aldrich, St. Louis, Missouri, USA) membranes. PVDF membranes were blocked for 1 h at room temperature in a shaker using 5 % BSA and TBST buffer. The primary antibodies with membranes were diluted at a ratio of 1:1000 and incubated overnight at 4 °C. Next, the PVDF membrane was washed with TBST buffer for 5 min for a total of four times. The 1:3000 dilution of anti-rabbit IgG (ab205718, Abcam, Cambridge, UK) was incubated with PVDF membrane for 1 h at room temperature and washed again four times. Finally, the protein bands were visualized by chemiluminescence substrate

(Yamei, Shanghai, China) and analyzed by ImageJ.

NRF2 (Bioworld, Beijing, China), FASN (3180, CST, MA, USA), P-P65 (WL02169, Wanleibio, Shenyang, China), PPAR γ (2443, CST, MA, USA), SREBP (ab28481, Abcam, Cambridge, UK), P65 (8242, CST, MA, USA), and α -tubulin (ab52866, Abcam, Cambridge, UK) were used.

2.5. Oil red O staining

Cells were cultured in 12-well plates, washed twice with PBS after the medium was discarded, fixed, permeabilized with 60 % isopropanol, washed, and then oil red O dye was added to soak the cells for 20 min. Distilled water was used to remove the dye solution, and hematoxylin dye solution was added to dye the nucleus for 1 min. Distilled water was added again to wash away the multisuccinic dye solution, and the cells were then fixed. A distilled water coating cover was added, observed, and photographed under an inverted microscope (Nikon, Tokyo, Japan), and the results were collected.

2.6. Determination of triglycerides

The mammary epithelial cells of dairy cows were lysed by a triglyceride enzyme assay kit (Pulilia, Beijing, China) to measure the triglyceride content in the cells. The cells were washed twice with PBS before lysis. After adding lysis buffer, the cells were shaken thoroughly and incubated for 10 min. The supernatant was split in half, half of which was used to determine triglyceride content, and the other half was used to determine total protein content by a BCA kit. Finally, the triglyceride content was normalized to protein concentration per mg.

2.7. Statistical analysis

At least three replicates were performed for each experiment. The mean $\pm$ SD was used to represent all the experimental data. GraphPad Prism 9.0 software was used to perform the multiple comparisons of one-way ANOVA. $P < 0.05$ was considered statistically significant; $P < 0.01$, the difference was considered significant; $P > 0.05$ was considered that there was no statistical significance.

3. Results

3.1. Concentration screening of CGA

To determine whether CGA affected the viability of BMECs, we stimulated cells at different CGA concentrations (0, 10, 20, 30, 40, 50 μ g/ml) for 24 h, and detected by CCK-8 (Fig. 1). Compared with the control group, 10 μ g/mL CGA increased cell viability significantly ($P = 0.0012$). In contrast, 50 μ g/mL CGA inhibited cell viability ($P = 0.0473$).

3.2. CGA reduces LPS-induced inflammation

To explore the effect of CGA on LPS-induced inflammation in BMECs, we measured changes in inflammatory factors in cells after LPS stimulation and LPS + CGA treatment. Compared with the control group, the mRNA expression levels of the inflammatory factors

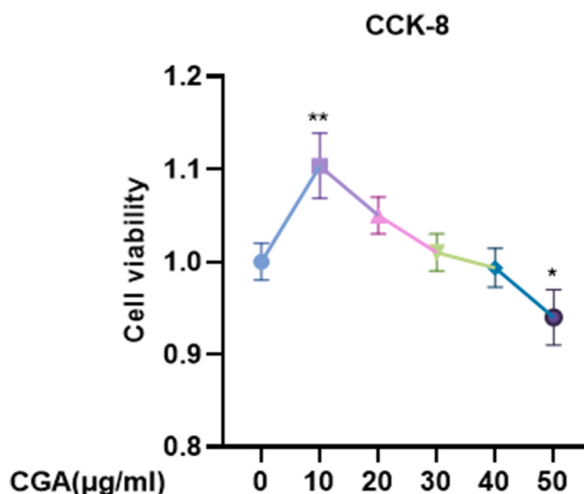


Fig. 1. Effect of CGA on the viability of Bovine mammary epithelial cells. All experiments were performed in triplicate. The data are shown as the mean $\pm$ SD. $P = 0.0012$ between 10 vs 0 μ g/mL, $P = 0.0473$ between 50 vs 0 μ g/mL.

IL-6 ($P < 0.0001$) (Fig. 2A), *IL-8* ($P < 0.0001$) (Fig. 2B), *TNF- α* ($P < 0.0001$) (Fig. 2C), *IL-1 β* ($P = 0.0001$) (Fig. 2D), and *iNOS* ($P = 0.0022$) (Fig. 2E) were significantly increased after LPS treatment. Compared with the LPS alone group, LPS + CGA treatment was performed. The expression of the inflammation-related genes *IL-6* ($P = 0.0012$), *IL-8* ($P < 0.0001$), *TNF- α* ($P < 0.0001$), *IL-1 β* ($P = 0.0021$) and *iNOS* ($P = 0.0003$) was decreased (Fig. 2A–E).

3.3. CGA reduces oxidative stress

To investigate the effect of CGA on oxidative stress in cells by detecting oxidative stress factors in cells. Compared with the control group, the expression levels of *CHOP* ($P = 0.1831$) (Fig. 3B) and *XCT* ($P = 0.2492$) (Fig. 3C) were decreased after LPS treatment, and the expression levels of *NRF2* ($P = 0.0070$) (Fig. 3A), *HO-1* ($P = 0.0007$) (Fig. 3D) and *GPR78* ($P = 0.0006$) (Fig. 3E) were significantly decreased. The expression levels of *CHOP* ($P < 0.0001$) (Fig. 3B), *XCT* ($P = 0.0005$) (Fig. 3C), *NRF2* ($P = 0.0005$) (Fig. 3A), *HO-1* ($P = 0.0087$) (Fig. 3D) and *GPR78* ($P = 0.1125$) (Fig. 3E) in the BMECs treated with CGA were increased. At the same time, the results of Western blotting also further verified the results at the gene level. As shown in Fig. 3F, LPS induced significantly reduced expression of *NRF2* in cells ($P = 0.0472$). Co-treatment with CGA and LPS significantly increased *NRF2* expression compared with LPS alone ($P = 0.0345$) (Fig. 3F).

3.4. The reduction in the synthesis of milk fat was reversed by CGA

Further experiments showed that CGA could alleviate the decrease in milk fat in BMECs caused by LPS to a certain extent. The TG concentration were used for determination. LPS stimulation caused a decrease in TG secretion in BMECs ($P = 0.0047$), while CGA could significantly save the phenomenon of reduced TG synthesis in cells ($P = 0.0033$) (Fig. 4A). The lipid droplets in BMECs were significantly reduced after LPS addition, and this situation was alleviated after CGA addition (Fig. 4B). The results of QRT-PCR showed that the mRNA expression levels of *SREBP* ($P = 0.0360$), *FASN* ($P = 0.0328$), and *PPAR γ* ($P = 0.0468$) in cells treated with LPS were significantly decreased. However, CGA could restore this decrease. The expression levels of *SREBP* ($P = 0.4450$), *FASN* ($P = 0.0006$), and *PPAR γ* ($P = 0.0224$) were significantly increased (Fig. 4C–E). LPS treatment significantly reduced the protein levels of *SREBP* ($P =$

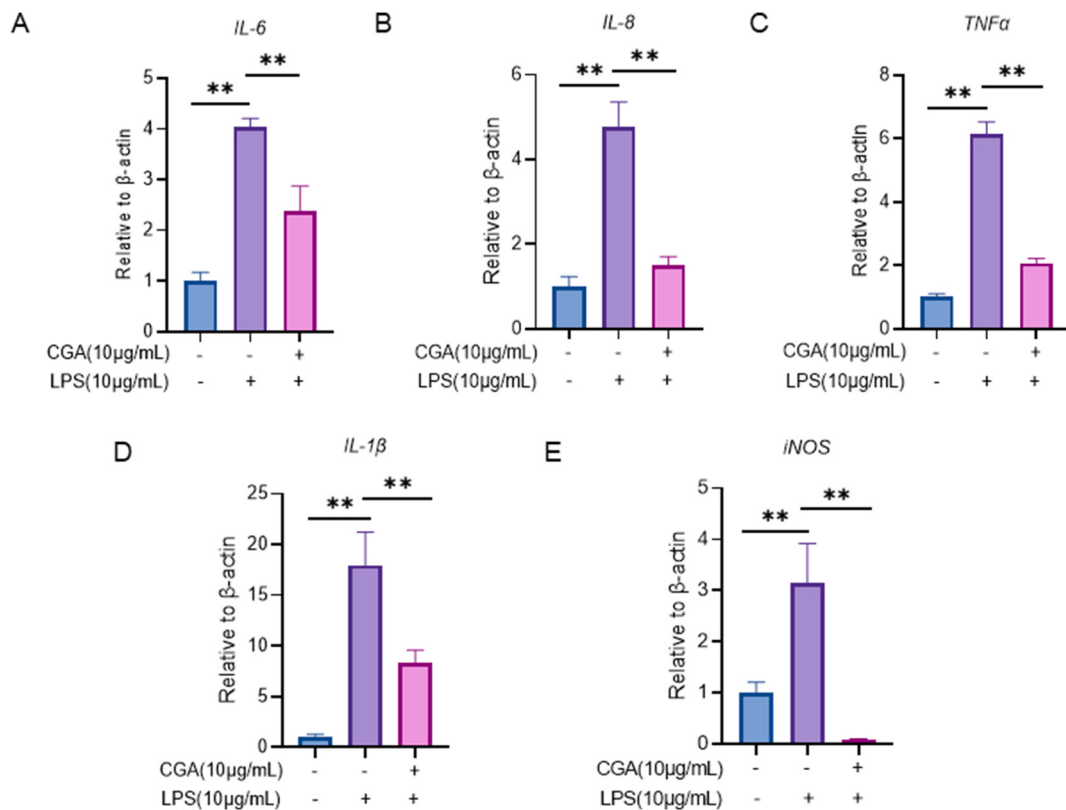


Fig. 2. CGA can alleviate LPS induced inflammatory response of Bovine mammary epithelial cells. (A) *IL-6* mRNA level. $P < 0.0001$ between CGA⁻LPS⁻ vs CGA⁻LPS⁺, $P = 0.0012$ between CGA⁻LPS⁺ vs CGA⁺LPS⁺. (B) *IL-8* mRNA level. $P < 0.0001$ between CGA⁻LPS⁻ vs CGA⁻LPS⁺, $P < 0.0001$ between CGA⁻LPS⁺ vs CGA⁺LPS⁺. (C) *TNF α* mRNA level. $P < 0.0001$ between CGA⁻LPS⁻ vs CGA⁻LPS⁺, $P < 0.0001$ between CGA⁻LPS⁺ vs CGA⁺LPS⁺. (D) *IL-1 β* mRNA level. $P = 0.0001$ between CGA⁻LPS⁻ vs CGA⁻LPS⁺, $P = 0.0021$ between CGA⁻LPS⁺ vs CGA⁺LPS⁺. (E) *iNOS* mRNA level. $P = 0.0022$ between CGA⁻LPS⁻ vs CGA⁻LPS⁺, $P = 0.0003$ between CGA⁻LPS⁺ vs CGA⁺LPS⁺. The data are shown as the mean $\pm$ SD.

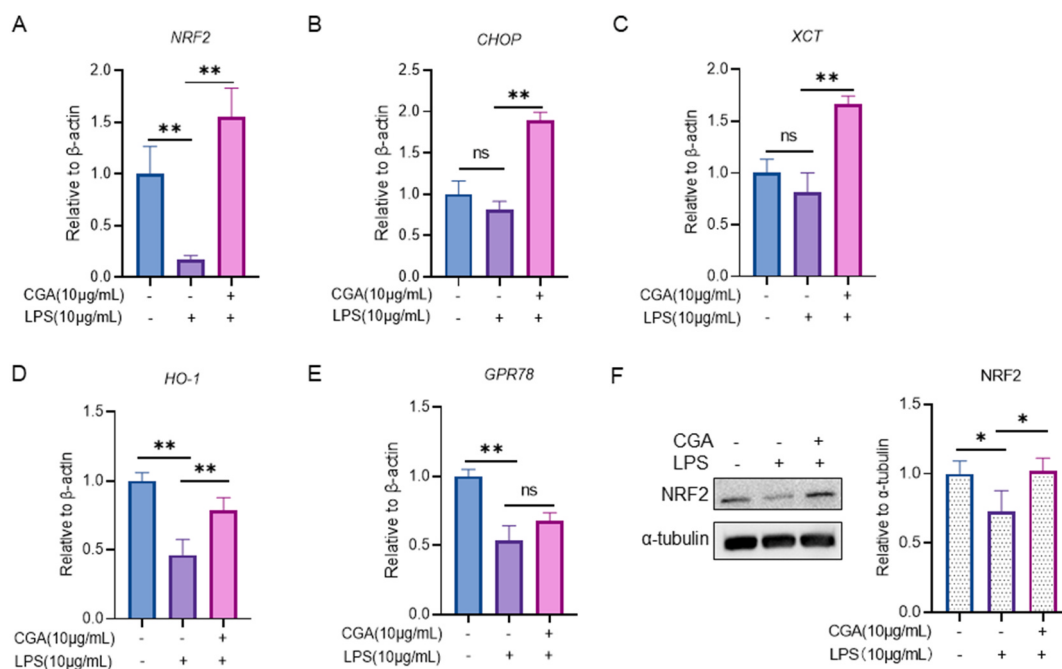


Fig. 3. CGA can improve oxidative stress caused by LPS. (A) *NRF2* mRNA level. $P = 0.0070$ between $\text{CGA}^- \text{LPS}^-$ vs $\text{CGA}^- \text{LPS}^+$, $P = 0.0005$ between $\text{CGA}^- \text{LPS}^+$ vs $\text{CGA}^+ \text{LPS}^+$. (B) *CHOP* mRNA level. $P = 0.1831$ between $\text{CGA}^- \text{LPS}^-$ vs $\text{CGA}^- \text{LPS}^+$, $P < 0.0001$ between $\text{CGA}^- \text{LPS}^+$ vs $\text{CGA}^+ \text{LPS}^+$. (C) *XCT* mRNA level. $P = 0.2492$ between $\text{CGA}^- \text{LPS}^-$ vs $\text{CGA}^- \text{LPS}^+$, $P = 0.0005$ between $\text{CGA}^- \text{LPS}^+$ vs $\text{CGA}^+ \text{LPS}^+$. (D) *HO-1* mRNA level. $P = 0.0007$ between $\text{CGA}^- \text{LPS}^-$ vs $\text{CGA}^- \text{LPS}^+$, $P = 0.0087$ between $\text{CGA}^- \text{LPS}^+$ vs $\text{CGA}^+ \text{LPS}^+$. (E) *GPR78* mRNA level. $P = 0.0006$ between $\text{CGA}^- \text{LPS}^-$ vs $\text{CGA}^- \text{LPS}^+$, $P = 0.1125$ between $\text{CGA}^- \text{LPS}^+$ vs $\text{CGA}^+ \text{LPS}^+$. (F) Detection of *NRF2* levels by Western blotting. Protein grayscale analysis. α -tubulin was used as the loading control. $P = 0.0472$ between $\text{CGA}^- \text{LPS}^-$ vs $\text{CGA}^- \text{LPS}^+$, $P = 0.0345$ between $\text{CGA}^- \text{LPS}^+$ vs $\text{CGA}^+ \text{LPS}^+$. The data are shown as the mean $\pm$ SD.

0.0499) and *FASN* ($P = 0.0102$) in mammary epithelial cells of dairy cows, while CGA could reverse the decrease in the protein levels of *SREBP* ($P = 0.0197$) and *FASN* ($P = 0.0409$), which was consistent with our QRT-PCR results (Fig. 4F).

3.5. Chlorogenic acid inhibits inflammation and restores milk fat synthesis through *NF-κB*

We further explored whether CGA exerted its effects through the *NF-κB* pathway. Western blot was used to measure the phosphorylation of *NF-κB*/P65 (Fig. 5A). In BMECs, LPS significantly increased the phosphorylation of P65 ($P = 0.0088$), and this increase was significantly reduced by CGA ($P = 0.0478$) (Fig. 5A and B). Similarly, Toll-like receptor 4 (TLR4), a major molecule downstream of *NF-κB*, was also altered, and CGA treatment attenuated TLR4 protein increased by LPS (Fig. 5A–C).

4. Discussion

LPS is an endotoxin that acts as an important pathogenic component of the cell wall of Gram-negative bacteria [8]. Previous studies have shown that after the bacterial cell wall is damaged, LPS is released from the bacterial membrane, leading to the release of proinflammatory cytokines [22]. When it directly acts on the mammary epithelial cells of dairy cows, mastitis can be induced [7,9,23]. Previous studies have shown that monomeric components of traditional Chinese herbal medicines, such as vanillin, can alleviate LPS-induced mastitis [24]. Vanillin inhibits the LPS-induced inflammatory response by inhibiting the *MAPK/NF-κB* signaling pathways to protect breast cells. CGA is also a rich monomer in nature and has anti-inflammatory and antioxidant effects [25–27]. CGA can inhibit the activation of *TLR4/NF-κB* signaling pathway and reduce inflammation in *E. coli* endometritis [28]. Studies have also shown that CGA can protect the integrity of the intestine and reduce mucosal damage and the inflammatory response caused by indomethacin [29]. Previous studies have also shown that CGA can alleviate mastitis caused by *Staphylococcus aureus* and reverse the decline in milk yield and quality [20].

It is generally accepted that cytokines are important players in the inflammatory response [12]. On the one hand, the synthesis and release of pro-inflammatory cytokines (*TNF-α*, *IL-6*, and *iNOS*) mark the occurrence of inflammation, which is a kind of self-protection response [30]. On the other hand, overexpression of inflammatory cytokines (*IL-6*, *TNF-α*, and *IL-1β*) can also cause mammary inflammation [31]. For example, *IL-1β* induces an inflammatory response, often by activating neutrophils, macrophages, and monocytes [32]. Therefore, inhibiting these factors alleviates LPS-induced breast inflammation [33]. According to previous studies, LPS activate the *MyD88/NF-κB* pathway by binding to the *TLR4* receptor to increase the release of proinflammatory cytokines in cells

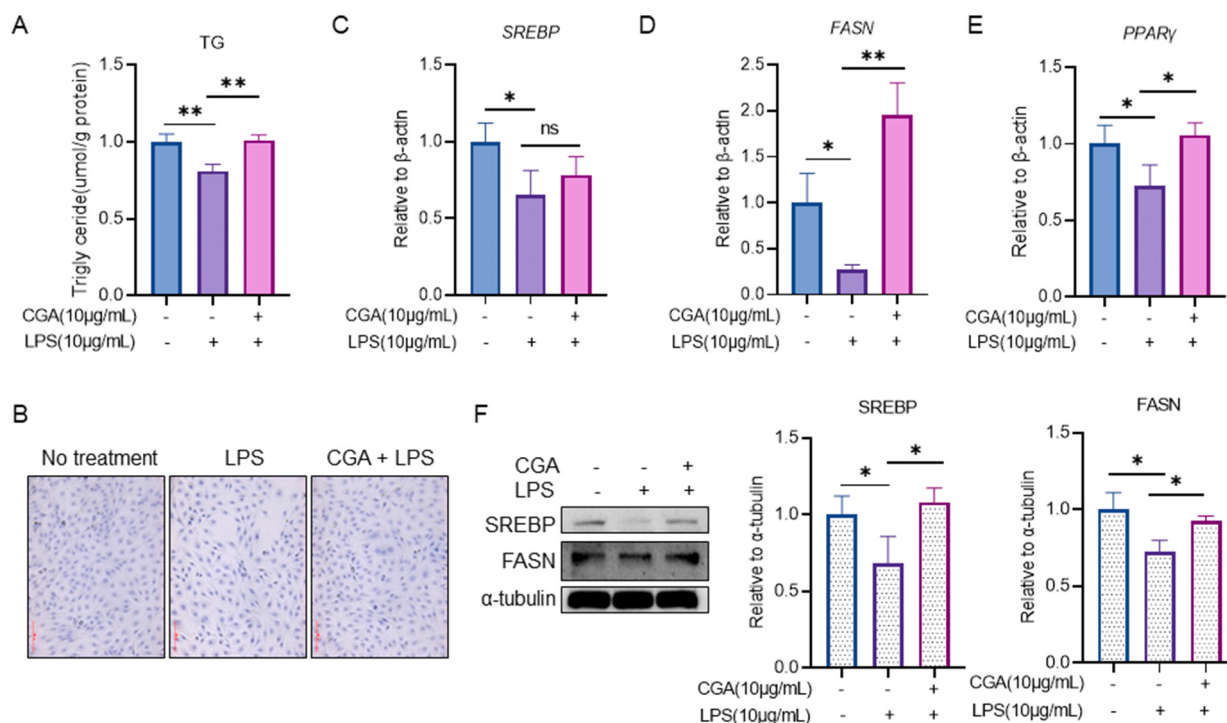


Fig. 4. CGA can improve oxidative stress caused by LPS. (A) Results of the measurement of triglyceride content. $P = 0.0047$ between CGA⁻LPS⁻ vs CGA⁻LPS⁺, $P = 0.0033$ between CGA⁻LPS⁺ vs CGA⁺LPS⁺. (B) Oil red O staining results, scale bar = 100 μm. (C) *SREBP* mRNA level. $P = 0.0360$ between CGA⁻LPS⁻ vs CGA⁻LPS⁺, $P = 0.4450$ between CGA⁻LPS⁺ vs CGA⁺LPS⁺. (D) *FASN* mRNA level. $P = 0.0328$ between CGA⁻LPS⁻ vs CGA⁻LPS⁺, $P = 0.0006$ between CGA⁻LPS⁺ vs CGA⁺LPS⁺. (E) *PPARγ* mRNA level. $P = 0.0468$ between CGA⁻LPS⁻ vs CGA⁻LPS⁺, $P = 0.0224$ between CGA⁻LPS⁺ vs CGA⁺LPS⁺. (F) Detection of *SREBP* and *FASN* levels by Western blotting. Protein grayscale analysis. α-tubulin was used as the loading control. *SREBP*: $P = 0.0499$ between CGA⁻LPS⁻ vs CGA⁻LPS⁺, $P = 0.0197$ between CGA⁻LPS⁺ vs CGA⁺LPS⁺. *FASN*: $P = 0.0102$ between CGA⁻LPS⁻ vs CGA⁻LPS⁺, $P = 0.0409$ between CGA⁻LPS⁺ vs CGA⁺LPS⁺. The data are shown as the mean ± SD. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

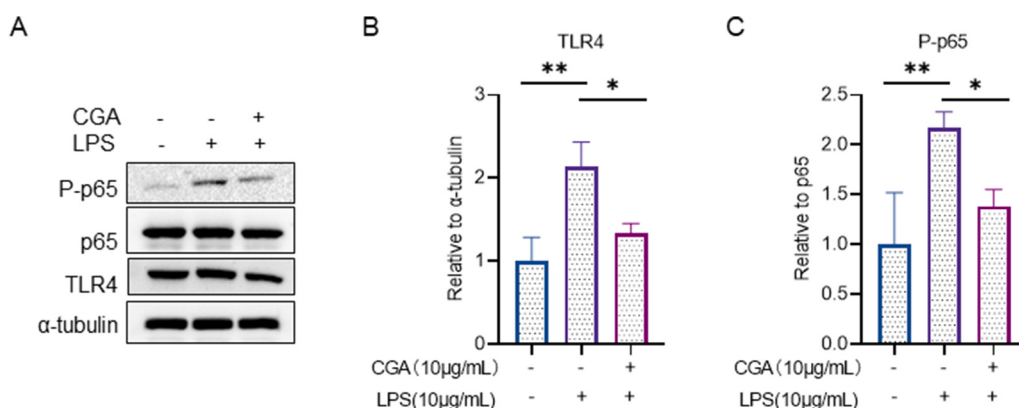


Fig. 5. CGA inhibited LPS-induced activation of NF-κB signaling pathway. (A) Western blot of P-p65, p65, and TLR4. (B) P-p65/p65 protein abundance analysis. $P = 0.0088$ between CGA-LPS⁻ vs CGA-LPS⁺, $P = 0.0478$ between CGA-LPS⁺ vs CGA + LPS⁺. (C) TLR4 relative protein abundance analysis. $P = 0.0011$ between CGA⁻LPS⁻ vs CGA⁻LPS⁺, $P = 0.0243$ between CGA⁻LPS⁺ vs CGA⁺LPS⁺. Data are presented as mean ± SD deviation.

[34]. Therefore, in our study, CGA reduced TLR4 expression in LPS-stimulated BMECs by inhibiting the activation of MyD88/NF-κB signaling pathway, and ultimately reduce the expression of proinflammatory cytokines, thereby alleviating breast inflammation.

Before and after calving, the feed consumption and energy demand of dairy cows will change dramatically [35]. In a high metabolic period, the mismatch between free radicals and antioxidant capacity in dairy cows will lead to oxidative stress [36,37]. Continuous oxidative stress can damage the breast, affect the production and quality of milk, and even cause mastitis [38,39]. The reduction of

cellular oxidative stress can reduce the activation of NF- κ B pathway, further reducing the production of proinflammatory cytokines and thereby alleviating the inflammatory response [30]. Studies have shown that CGA can reduce the oxidative stress and mitochondrial dysfunction of hepatocytes induced by a high-fat diet by activating SIRT1 [40]. Previous studies have also shown that CGA can inhibit apoptosis, activate the NRF2/HO-1 signaling pathway, and alleviate the pathological progression of osteoporosis [41]. It has also been reported that CGA plays a role in scavenging reactive oxygen species and reactive nitrogen species, reducing oxidative stress between cells, and inhibiting the NF- κ B signaling pathway, to produce anti-inflammatory effects [30]. NRF2 is an antioxidant transcription factor that regulates the expression of multiple protective genes in cells, such as HO-1 [42]. The HO-1 gene is closely related to oxidative stress, and its upregulation can inhibit the expression of inflammatory cytokines to a certain extent, thereby protecting tissue cells [43]. LPS can inhibit NRF2 and HO-1 in the brain, further inducing oxidative stress and acute neuroinflammation [44]. Therefore, we hypothesized that CGA may attenuate LPS-induced oxidative stress by increasing the expression of NRF2 and HO-1.

After inflammation in the mammary gland of dairy cows, intracellular lipase activity increases, and the membrane of milk fat globules is destroyed, which induces milk fat to be degraded by lipoprotein lipase, thereby reducing the milk fat content [45]. Studies have shown that fats and fatty acids in breast milk can be used as important regulators of immunity and metabolism to reduce the occurrence of inflammation to a certain extent [46]. In addition, lactating cows are prone to lipid oxidation, accumulate a large number of lipid peroxides, and regulate inflammation by affecting the development of oxidative stress [37]. Thus, lipid metabolism is closely related to inflammation; some lipid metabolism enzymes, such as P450 and COX2, are regulated in the process of inflammation, and the lack of certain oxygen lipids also promotes oxidative stress [37]. Studies have shown that LPS can be used to induce breast inflammation, downregulate the expression of PPAR γ and FASN genes related to milk fat synthesis, reduce intracellular TG content and reduce milk fat synthesis [47]. Our study shows that CGA can rescue the LPS-induced reduction in milk fat synthesis, which may be by upregulating the expression of the milk fat synthesis genes SREBP, FASN, and PPAR γ , thereby promoting the synthesis of fatty acids and increasing the content of TG.

As a transcription factor, NF- κ B exists in the cytoplasm and can activate the transcription of the proinflammatory factors (IL-6, IL-1 β , and TNF- α) after being activated and transferred to the nucleus [27,48]. In the liver, inflammatory signaling factors can also aggravate inflammation and oxidative stress by activating the downstream NF- κ B signaling pathway [25]. It has been reported that LPS can further activate IKK by activating the TLR4 receptor on the membrane of endometrial epithelial cells so that I κ B is phosphorylated, releasing and activating NF- κ B, the phosphorylation and nuclear translocation of P65, which initiates the transcription of inflammatory cytokines [49]. CGA can reduce the inflammatory response by reducing the expression of TLR4 [28,50]. Therefore, we speculated that CGA may inhibit the activation of P65/NF- κ B by downregulating the expression of the TLR4 receptor in mammary epithelial cells of dairy cows, thereby protecting against LPS-induced mastitis.

In summary, CGA can repair LPS-induced mammary inflammation, alleviates oxidative stress, and restores milk fat synthesis by inhibiting the NF- κ B signaling pathway. CGA can be used as a potential therapeutic drug to alleviate LPS-induced injury of bovine mammary gland cells and decreased milk fat synthesis by improving oxidative stress and alleviating inflammation.

Data availability statement

Data will be made available on request.

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CRediT authorship contribution statement

Chen-Chen Lyu: Writing – original draft, Software, Methodology, Data curation, Conceptualization. **Xing-Yu Ji:** Writing – original draft, Formal analysis, Data curation, Conceptualization. **Hao-Yu Che:** Formal analysis. **Yu Meng:** Formal analysis. **Hong-Yu Wu:** Formal analysis. **Jia-Bao Zhang:** Writing – review & editing, Resources. **Yong-Hong Zhang:** Writing – review & editing. **Bao Yuan:** Writing – review & editing.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Bao Yuan reports financial support was provided by The Chinese Agricultural Science Research System. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.heliyon.2024.e25004>.

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