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ARTICLE INFORMATION	Fill in information in each box below
Article Type	Research article
Article Title (within 20 words without abbreviations)	Danggui buxue decoction Protects Against Lipopolysaccharides- Induced Mastitis in bovine mammary epithelial cells in Vitro
Running Title (within 10 words)	Danggui buxue decoction Protects Against LPS-Induced Mastitis in BMECs in Vitro
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Competing interests	No potential conflict of interest relevant to this article was reported.
Funding sources	This research work was supported by National Natural Science
State funding sources (grants, funding sources,	Animal Perioductive Physiology and Perioductive Pegulation
grant if available	(20.IR10RA563)
grant il available.	
Acknowledgements	Not applicable.
Availability of data and material	Upon reasonable request, the datasets of this study can be available
	from the corresponding author.
Authors' contributions	Conceptualization: Wang J, Zhang Y
Please specify the authors' role using this form.	Data curation: Wang J, Yao D
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	Investigation: Gao Y
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	Writing - review & editing: Wang J, Gao Y, Cheng C, Li Y, Zhang X,
	Yao D, Zhang Y
Ethics approval and consent to participate	This article does not require IRB/IACUC approval because there are
	no numan and animal participants.

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#### 7 Abstract

8 Bovine mastitis (BM) is a prevalent and recurring disease in dairy farming. Danggui Buxue Decoction (DBD) 9 possesses significant anti-inflammatory, antioxidative stress, and immune system regulatory effects. However, its 10 application in the clinical prevention and treatment of bovine mastitis has not been explored. This study aimed to 11 assess the effectiveness and mechanism of DBD on bovine mastitis through an in vitro model using 12 lipopolysaccharide (LPS)-stimulated bovine mammary epithelial cells (BMECs). LPS stimulation led to increased 13 expression of inflammatory markers (TNF-α, IL-1β, IL-6, and IL-8), damage indicators (BNBD5, GM-CSF, CCL2, 14 and GADD-45 $\alpha$ ), and oxidative stress markers (COX-2, PPAR $\gamma$ , and iNOS) in the BMECs. Conversely, treatment 15 with DBD counteracted these effects. Additionally, a lactate dehydrogenase (LDH) release assay indicated that DBD 16 diminished the cellular damage caused by LPS. The Total antioxidant capacity (T-AOC), Glutathione (GSH), 17 Superoxide dismutase (SOD), Malondialdehyde (MDA), Nitric Oxide (NO) content assay, and Reactive Oxygen 18 Species (ROS) staining demonstrated that DBD mitigated cellular oxidative stress triggered by LPS. Moreover, 19 DBD suppressed the mRNA and protein expression of TLR4 and NF-kB. These results imply that DBD exerts anti-20 inflammatory, wound healing, and antioxidative stress effects on BMECs following LPS exposure, suggesting its 21 potential as an effective treatment for bovine mastitis.

### 22 Keywords:

23 Bovine mastitis (BM); Danggui Buxue Decoction (DBD); bovine mammary epithelial cells (BMECs); toll-like

24 receptor 4 (TLR4); inflammation

## 26 Introduction

27 Mastitis in bovine cows represents the most widespread disease within the contemporary cattle industry, leading 28 to significant economic losses. These losses severely hinder the development of dairy farming as well as the hygiene 29 and safety of human food [1]. Currently, the global treatment for dairy cow mastitis predominantly involves 30 antibiotics, whose prolonged and extensive use may result in internal flora dysfunction, organism resistance, and 31 antibiotic residues in milk [2]. Consequently, the quest for new alternative therapies and treatments is a challenge 32 that must be addressed by veterinary practitioners and researchers collaboratively. Traditional Chinese herbs offer 33 several benefits over antibiotics, including reduced side effects, a lower likelihood of bacterial resistance, minimal 34 toxicity, negligible residue, and no dependency. Many traditional Chinese medicines or traditional Chinese medicine 35 extracts have been shown to be effective in the treatment of BM. Wang J used the flavonoid compound Morin 36 isolated from Moraceae Chinese herbal medicine to act on LPS-induced BMECs. He found that Morin could 37 significantly reduce the gene expression of inflammatory factors and inhibit the activation of NF-KB and MAPK 38 signaling pathways, thereby achieving the anti-inflammatory effect of treating cow mastitis [3]. Jirao S used 39 S.haemolyticus to induce the inflammatory response of BMECs. He found that the mRNA and protein levels of 40 inflammatory factors in BMECs were significantly reduced after paeoniflorin (PF) treatment, and the activation of 41 TLR2 and NF-KB signaling pathway-related genes and protein expression were inhibited, indicating that PF is 42 expected to be a potential drug for the treatment of BM [4]. In addition, Safia A found the bacteriostatic effect of 43 Chinese herbal medicine. He tested the bacteriostatic effect of squaw mint, catnip, and lemon balm on the 44 pathogenic bacteria of BM. The results showed that essential oil and some herbal plant extract had significant 45 bacteriostatic activity against S.aureus and E.coli, and pointed out that lemon balm and peppermint oil could be used 46 as alternative methods for the treatment of mastitis [5]. These research results show that traditional Chinese 47 medicine has great potential in the treatment of mastitis. Furthermore, the treatment of mastitis with Chinese herbal 48 medicine focuses on enhancing blood circulation in the udder, clearing blocked vessels, relieving stagnation, and 49 boosting the body's immunity, thereby providing both symptomatic relief and addressing the root cause of the 50 disease. This approach offers fresh perspectives in the search for alternative therapies.

51 Danggui buxue decoction (DBD) was obtained from Li Dongyuan's Discussion of Internal and External Injuries 52 and is known as a classic formula for tonifying qi and generating blood [6]. DBD was made by decocting *Astragalus* 53 and *Angelicae* at a ratio of 5:1 in two volumes of water and filtering and concentrating the mixture [7]. In the 54 formula, *Astragalus* can strengthen the spleen, act as a diuretic, and detoxify qi, the main treatment for qi and blood deficiency. *Angelica sinensis* can enhance blood production, prevent thrombosis, relieve pain, and treat blood deficiency. *Angelica* and *Astragalus* complement each other, facilitating the tonification of qi and the generation of blood. Several studies have shown that DBD has biological functions, such as anticancer, antitumor, antioxidant, antifibrosis, accelerated hematopoiesis, and immunomodulatory activities [8–14]. However, the efficacy of DBD on mastitis in dairy cows has not been reported.

60 Bovine mastitis is identified by a diverse array of pathogenic factors and a complex pathogenesis. The expression 61 of inflammatory factors such as TNF- $\alpha$ , IL-1 $\beta$ , and IL-6, among others, is elevated in the mastitis tissues of dairy 62 cows compared to healthy tissues [15]. Subsequent research has indicated a close association between cell damage, 63 oxidative stress, and the progression of mastitis. Upon cellular inflammation, an increase in LDH release is observed 64 alongside the upregulation of BNBD5, GM-CSF, CCL2, and GADD-45 $\alpha$  expression. LDH serves as a crucial 65 indicator of the extent of cellular damage; GM-CSF and CCL2 facilitate the convergence of macrophages to damage 66 sites and modulate an organism's immune response; BNBD5 represents a potential local defense gene for breast 67 tissue; and GADD-45 $\alpha$ , which is inducible by various damage factors, is a DNA damage-responsive gene. 68 Additionally, LPS-induced cellular inflammation may lead to an increase in ROS and the upregulation of COX-2, 69 PPAR $\gamma$ , and iNOS expression [16,17]. COX-2, which is typically not expressed under resting conditions, can be 70 rapidly upregulated during inflammation, while prolonged activation of iNOS may result in excessive NO 71 production and oxidative stress, causing tissue damage [18,19]. T-AOC, GSH, SOD, MDA and NO can reflect the 72 body's oxidation and antioxidant [20]. It has been noted that in mastitis induced by gram-negative bacteria, TLR4 73 specifically recognizes LPS, mediates MyD88 signaling, activates NF-kB, initiates the transcription of related 74 factors, and promotes cytokine release [21,22]. These findings highlight key molecules as potential therapeutic 75 targets for bovine mastitis. Research has demonstrated the modulatory effects of DBD on several of the 76 aforementioned factors. For instance, Li Chengyin reported that DBD treatment diminished the production of IL-1β, 77 IL-6, IL-10, and TNF- $\alpha$  in a mouse model of inflammatory bowel disease (IBD) induced by dextrose sodium sulfate 78 (DSS), effectively improving inflammation and pathological conditions [23]. Zhang Yan's study suggested that 79 DBD, in combination with conventional therapy, could lower TNF- $\alpha$  and IL-6 levels in diabetic nephropathy mice, 80 mitigating the inflammatory response [24]. Research by Kun Liu indicated that DBD notably decreased LDH levels 81 in mice with cardiac injury and downregulated NF-KB protein expression in cardiac tissues [25]. Amy G. W. Gong 82 identified the main components of the DBD and formulated an herbal soup, "DBTAfa," which was found to decrease 83 ROS formation and enhance the transcriptional activity of antioxidant genes in H9C2 cells [26]. Wang Jiepeng proposed that the therapeutic effects of DBD on rats with bleomycin-induced pulmonary fibrosis (PF) might occur through the inhibition of the TLR4/NLRP3 signaling pathway [27]. Additionally, the inhibition of NF- $\kappa$ B activity by DBD was shown to reduce inflammation-related damage [28]. The experimental findings of Amy GW Gong demonstrated that the modulation of the NF- $\kappa$ B signaling pathway by DBD has immunomodulatory effects [29]. This finding suggests the potential of DBD to treat mastitis by inhibiting the production of these factors.

The aim of this study was to investigate the efficacy and mechanism of action of DBD in treating bovine mastitis and to fill this research gap in the field of DBD treatment for bovine mastitis. We used LPS to induce inflammation in BMECs, which was used to establish an in vitro cellular model of bovine mastitis, to evaluate the protective effect of DBD on BMECs in terms of inflammation, injury and oxidative stress to conduct preliminary studies on the molecular mechanisms involved. Our experimental results provide basic information for further research on the mechanism of action of DBD in mastitis in dairy cows and provide a reference for the use of DBD in the prevention and treatment of bovine mastitis.

## 96 Materials and Methods

### 97 Reagents

98 BMECs were preserved at the Veterinary Obstetrics Lab of Gansu Agricultural University (Lanzhou, China). RPMI 99 1640 medium was obtained from Gibco (New York, USA, C11875500BT). LPS (From Escherichia coli O55:B5) 100 was obtained from Solarbio (Beijing, China, L8880). Astragalus membranaceus (ASR) and Angelica sinensis (AR) 101 were obtained from the Yellow River Herbal Market (Lanzhou, China). TRIzol was obtained from Ambion (Tesax, 102 USA, 15596-026). An Evo M-MLV RT Kit with gDNA Clean for qPCR was obtained from Accurate 103 Biotechnology (Changsha, China, AG11728). 2×SYBR Green qPCR Master Mix was obtained from Selleck 104 (Shanghai, China, B21203). A bovine LDH Cytotoxicity Assay Kit was obtained from Sino Best Biological 105 (Shanghai, China, YX-22476B). The CCK-8(C0042), ROS assay kit (S0033S) and NO assay kit (S0021S) were 106 obtained from Beyotime (Shanghai, China). The T-AOC assay kit (BC1315)was obtained from Solarbio (Beijing, 107 China). The GSH assay kit (A006-2-1), SOD assay kit (A001-3) and MDA assay kit (A003-1) were obtained from 108 Nanjing Jiancheng (Jiangsu China). The GS-Prestained Protein Ladder was obtained from Genesand (Beijing, China, 109 PM901). Cell lysis buffer (P0013) and QuickBlock<sup>™</sup> Blocking Buffer (P0252) were obtained from Beyotime 110 (Shanghai, China). Rabbit anti-IL-1β antibody (bs-20449R) (1:2000), rabbit anti-IL-8 antibody (bs-0780R) (1:2000) 111 and rabbit anti-NF-κB p65 antibody (bs-0465R) (1:1000) were obtained from Bioss (Beijing, China). A rabbit anti-112 IL-6 antibody (21865–1-AP) (1:1000) was obtained from Proteintech (Wuhan, Hubei). Rabbit anti-TNF- $\alpha$  antibody

113 (AF-7014) (1:2000) was obtained from Affinity Bio (Burnet Ave, USA). Rabbit Anti-GM-CSF antibody (CPA2949)

114 (1:1000), Rabbit Anti-CCL2 antibody (CQA3687) (1:1000), Rabbit Anti-GADD-45α antibody (CQA1970) (1:1000),

115 Rabbit Anti-TLR4 antibody (CPA2171) (1:1000), Rabbit Anti-NF-κB p50 antibody (CPA4479) (1:1000), Mouse

116 Anti-β-actin antibody (CPA9100) (1:10000) was from Cohesion Bio(London, UK). HRP\* goat anti-mouse IgG

117 (H+L) (RS0001) (1:10000) and HRP\* goat anti-rabbit IgG (H+L) (RS0002) (1:10000) were purchased from

118 ImmunoWay Bio (Plano, USA).

### 119 **Preparation of DBD**

120 DBD was extracted from AR and ASR at a ratio of 5:1, and these herbs were obtained from Gansu Province (China). 121 The herbal liquid was soaked in distilled water (1:8; v/w) for 30 min and boiled in water for 1 h, after which the 122 residue from the first extraction was boiled in water (1:6; v/w) for 1 h. To prepare the DBD solution, after being 123 mixed twice, the solution was subjected to concentration using a rotary evaporator [30]. Subsequently, the DBD 124 solution was concentrated using a rotary evaporator at 60 °C and 60 rpm/min, and the concentrated drug solution 125 was freeze-dried at -50 °C to obtain the DBD powder. Before use, the DBD powder was dissolved in RPMI 1640, 126 and the DBD medium was heated at 50 °C, sonicated for 15 min, and filtered through a 0.22 µm filter. The desired 127 concentrations were prepared as needed.

### 128 Cell culture

The cells were cultured at 37  $^{\circ}$ C in a 5% CO<sub>2</sub> cell culture incubator, 0.25% trypsin was used for digestion, RPMI 130 1640 medium supplemented with 10% FBS was used for passaging culture, and RPMI 1640 medium without FBS 131 was used for preparation of the required drugs.

#### 132 Effects of DBD and LPS on cell proliferation

133 A total of 100  $\mu$ L of the BMECs suspension at a concentration of 5  $\times$  10<sup>4</sup> cells/mL was inoculated into a 96-well 134 plate, and subsequent studies were performed after the cells had grown to confluency. BMECs were grown in 96-135 well cell culture plates, 100 µL of DBD at final concentrations of 10, 25, 50, 100, 250, 500, 1000, 2500, 5000, 136 10000, 25000, 50000, and 100000 µg/mL was added to the DBD group, and LPS was added to the LPS group at 137 final concentrations of 0.1, 1, and 10 µg/mL. The culture plate was incubated at 37 °C for 24 h. A total of 10 µL of 138 CCK-8 reagent was added to each well 4 h before the end of the incubation, after which the cells were incubated. 139 After the incubation was completed, the OD450 of each well was measured with an enzyme labeler, and the cell 140 viability was calculated (unit: %). When the cell viability was less than 100%, the cell inhibition rate (IR) was

- 141 calculated as follows:  $IR = (100 \text{-cell viability}) \times 100\%$ , and the  $IR \le 10\%$  criterion was used to establish the upper limit
- 142 of the supplied concentration of DBD medium.

#### 143 LPS-treated cells

144 2 mL of BMECs cell suspension at a concentration of  $5 \times 10^5$  cells/mL was inoculated into a 6-well plate, and 145 subsequent studies were performed after the cells had grown to the wall. LPS is a component of the cell wall of 146 gram-negative bacteria. LPS induces an inflammatory response in cells, and LPS-treated cell models are widely used 147 in inflammation studies. To establish an in vitro cellular model of bovine mastitis, we stimulated BMECs for 24 h 148 with LPS at final concentrations of 0.1, 1, and 10 µg/mL. The mRNA and protein of the cells were collected, and the 149 expression of TNF- $\alpha$ , IL-1 $\beta$ , IL-6, and IL-8 at the transcriptional and protein levels was analyzed via qPCR and WB.

## 150 Cell Treatments

151 To observe the effects of DBD on the expression of TNF-α, IL-1β, IL-6, IL-8, BNBD5, GM-CSF, CCL2, GADD-

45α, COX-2, PPARγ, iNOS, TLR4, and NF-κB in LPS-stimulated BMECs, the cells were cultured for 24 h with 1 µg/mL LPS as the LPS group, and the cells were cocultured for 24 h with 100 µg/mL DBD and 1 µg/mL LPS as the LPS+DBD group. For analysis of protein and mRNA expression, the cells in 6-well plates were collected. Bovine LDH cytotoxicity and NO analyses were performed using the cell culture supernatant collected from 6-well plates.

156 Walled cells were subjected to reactive oxygen species staining.

## 157 Total RNA isolation and qRT–PCR

158 Total RNA was extracted with TRIzol, and the A260/A280 ratio of RNA was determined to be between 1.8 and 2.0 159 before reverse transcription. An Evo M-MLV RT Kit with gDNA Clean was used to reverse transcribe the RNA to 160 cDNA. The internal reference gene was GAPDH; the target genes were TNF- $\alpha$ , IL-1 $\beta$ , IL-6, IL-8, BNBD5, GM-161 CSF, CCL2, GADD-45α, COX-2, PPARγ, iNOS, TLR4, NF-κB p65 and NF-κB p50. The reaction mixture 162 contained 10 µL of 2×SYBR Green qPCR Master Mix, 1 µL of each forward and reverse primer, and 1 µL of cDNA, 163 for a total volume of 20 μL. The reaction conditions were 95 °C for 600 s, 45 cycles of 95 °C for 15 s, and 60 °C for 164 45 s. A LightCycler®96 real-time detection system (Roche, Basel, Switzerland) was used to carry out the reaction 165 program. The  $2^{-\Delta\Delta CT}$  method was utilized to determine the relative expression of the target genes. Table 1 166 summarizes the sequences of the primers used in this study.

### 167 Western Blotting Analysis

BMECs were inoculated into 6-well plates, and at the end of the treatment, an appropriate amount of cell lysis buffer
was added. The lysate was centrifuged at 10,000 rpm/min for 10 min at 4 °C, after which the precipitate was

170 removed to obtain protein samples. The protein concentration was determined using a BCA protein assay kit, and an 171 equal amount of protein was added to a protein electrophoresis gel and separated via SDS-PAGE. The proteins were 172 then electrotransferred onto a PVDF membrane via wet transfer, and the resulting PVDF membrane was incubated 173 with QuickBlock<sup>TM</sup> Blocking Buffer for 1 h at room temperature. The membranes were incubated with rabbit 174 polyclonal antibodies against TNF-α, IL-1β, IL-6, GM-CSF, CCL2, GADD-45α, TLR4, NF-κB p50, and NF-κB p65 175 and mouse polyclonal antibodies against IL-8 and  $\beta$ -actin overnight at 4 °C. After the membrane was washed, the 176 sections were incubated with HRP\* goat anti-mouse IgG (H+L) and HRP\* goat anti-rabbit IgG (H+L). 177 Immunoreactivity was observed on an Amersham ImageQuant 800 (Cytiva, Japan) after the dropwise addition of 178 ECL reagent to the PVDF membranes, and the gray values were analyzed using ImageJ software (National Institutes 179 of Health, Bethesda, MD, USA).

#### 180 LDH Release Assay

181 For the LDH release assay, the cell culture fluid was centrifuged. According to the instructions, 50 µL of LDH 182 standards at different concentrations (0, 30, 60, 120, 240, and 480 U/L) were added to the standard wells to construct 183 a standard curve, and 10 µL of cell culture solution from different treatments and 40 µL of sample diluent were 184 added to the sample wells. Then, 100 µL of HRP-conjugate reagent was added to each well, and the mixture was 185 allowed to stand at 37 °C for 60 min. The substance was removed, and the plate was rinsed five times with washing 186 solution. Then, 50 µL of Chromogen Solution A and 50 µL of Chromogen Solution B were added to each well, 187 which was incubated for 15 min at 37 °C in the dark. Afterward, 50 µL of Stop Solution was added, and the OD 188 value of each well was measured at 450 nm using an enzyme meter. A standard curve was plotted with the OD at 189 450 nm as the horizontal coordinate and the concentration of LDH (U/L) as the vertical coordinate, and the 190 concentration of LDH in the sample was determined.

### **191** Total antioxidant capacity (T-AOC)

192 Cells in 6-well plates were collected and lysed by adding a proper amount of pre-cooled extract and centrifuged at 193 10000 rpm/min for 10 min. The supernatant was taken to determine the protein concentration and detect T-AOC. 40 194  $\mu$ mol/mL FeSO<sub>4</sub> standard solution was prepared and diluted to various concentrations. Standard tube (100  $\mu$ L FeSO<sub>4</sub> 195 solution + 100  $\mu$ L reagent 2) , blank tube (24  $\mu$ L distilled water + 180  $\mu$ L mixture) and determination tube (6  $\mu$ L

- sample + 18 μL distilled water + 180 μL mixture) were set up. After fully mixed, 200 μL was added to the 96-well
- 197 plate after 10 min, and the OD value was measured at 593 nm.
- 198 Glutathione (GSH) Content

199 The standard dilution was used to prepare 20  $\mu$ M GSH standard solution, and then 100  $\mu$ L of cell protein sample 200 was mixed with 100  $\mu$ L precipitation solution. After centrifugation, the supernatant was taken for testing. 100  $\mu$ L 201 precipitation liquid was added to the blank well, 100  $\mu$ L 20  $\mu$ M GSH was added to the standard well, and 100  $\mu$ L 202 supernatant was added to the determination well. 100  $\mu$ L buffer and 25  $\mu$ L chromogenic agent were added to each 203 well and mixed. After standing for 5 min, the OD value of 405 nm was measured, and the GSH content (mol/gprot) 204 in each group was calculated.

#### 205 Superoxide dismutase (SOD) activity

The appropriate dilution ratio of cell protein was selected in the pre-experiment. According to the instructions of SOD assay kit, the control well, the control blank well, the determination well, and the determination blank well were set up. After adding the corresponding reagents to each well, mixing well, and standing at 37 °C for 20 min, the OD value of each well at 450 nm was measured. The SOD inhibition rate (%) and SOD activity (U/mgprot) in each group were calculated.

#### 211 Malondialdehyde (MDA) content

According to the instructions of the MDA assay kit, a blank tube (100  $\mu$ L anhydrous ethanol), standard tube (100  $\mu$ L 10 nM tetraethoxypropane) and determination tube were set up. Add 4 mL of pre-prepared working solution to each tube and mix well, boil for 40 minutes, and then rinse with water to cool. The cooled samples were centrifuged at 3500 rpm/min for 10 min. The supernatant obtained from 200  $\mu$ L was added to a 96-well plate, and the OD value was measured at 532 nm to calculate the MDA content (nmol/mg prot) of each group.

## 217 Nitric oxide (NO) content

For the NO content assay, the cell culture fluid was centrifuged. The method was carried out in accordance with the manufacturer's instructions after all the reagents were brought to room temperature. The 96-well plate was filled with 50  $\mu$ L of the test samples, 50  $\mu$ L of standards at various concentrations, and 50  $\mu$ L of each of the Griess Reagent I and Griess Reagent II. Within 10 min, the absorbance value at 540 nm was determined. A standard curve was plotted with the OD value at 540 nm as the horizontal coordinate and the concentration of NaNO2 ( $\mu$ M) as the vertical coordinate, and the final concentration of NO in the sample was obtained.

## 224 Reactive Oxygen Species Assay

1 mLof the BMECs suspension at a concentration of  $5 \times 10^5$  cells/mL was inoculated into glass-bottomed culture dishes and treated with drugs after the cell growth density reached 80%. The cells were incubated with Rosup (50  $\mu$ g/mL) at 37 °C for 30 min as a positive control for ROS accumulation. Using the in situ loading probe assay,

- 228 DCFH-DA at a concentration of 10 µmol/L was prepared with RPMI Medium 1640 basic, and 1 mL of DCFH-DA
- 229 was added to the cells, which were incubated at 37 °C for 30 min. The cells were subsequently washed three times
- with RPMI 1640 medium to minimize residual DCFH-DA. The cells in each well were observed by fluorescence
- 231 microscopy after the addition of an anti-fluorescence quencher.

## 232 Statistical analysis

- 233 Statistical analyses were performed using GraphPad Prism 8.4.2 software (GraphPad Software, San Diego,
- California, USA). Quantitative data are presented as the mean  $\pm$  SEM. Differences between groups were evaluated
- by one-way ANOVA, and p < 0.05 was considered to indicate statistical significance.

## 236 **Results**

237 DBD and LPS's effects on BMECs' ability to survive

The CCK-8 assay was used to measure the cytotoxicity of DBD and LPS on the BMECs to examine their impact on their viability. These findings demonstrated that whereas high amounts of DBD reduced cell growth, low quantities of DBD promoted cell growth. The maximum concentration limit for DBD-treated cells was found to be 1000  $\mu$ g/mL since the inhibition rate (IR) was greater than 10% at 2500  $\mu$ g/mL (Figure 1A). Moreover, we discovered that LPS suppressed cell proliferation in a concentration-dependent manner and that it could significantly limit cell growth at concentrations up to 1  $\mu$ g/mL (\*\* *p* < 0.01) (Figure 1B).

### 244 LPS-induced inflammation in BMECs

We used qRT–PCR and WB to measure the mRNA and protein levels of TNF- $\alpha$ , IL-1 $\beta$ , IL-6, and IL-8 in LPStreated cells to investigate the impact of LPS on the inflammatory response of BMECs. The findings demonstrated that at 1 µg/mL LPS, the mRNA (Figure 2A) and protein (Figure 2B, Figure 2C) expression of cellular inflammatory components was considerably upregulated. Thus, the inflammatory model in this work was established by treating cells with 1 µg/mL LPS for 24 h.

#### 250 In BMECs, DBD inhibits the inflammation induced by LPS

- 251 Using qRT-PCR and WB, we investigated the mRNA (Figure 3A) and protein (Figure 3B, Figure 3C) levels of
- 252 TNF-α, IL-1β, IL-6, and IL-8 following LPS treatment to explore the anti-inflammatory effects of DBD on BMECs.
- 253 Following LPS treatment, the expression levels of TNF-α, IL-1β, IL-6, and IL-8 were upregulated in comparison to
- those in the untreated group. On the other hand, the levels of these inflammatory factors decreased when DBD was
- 255 present.

### 256 In BMECs, DBD protects against injury induced by LPS

257 We observed the release of LDH within the fluid of LPS-treated cells, as well as the gene and protein expression of

- 258 BNBD5, GM-CSF, CCL2, and GADD-45α within cells, to explore the protective impact of DBD against cell injury.
- 259 LDH release was greater in the LPS group than in the control group. Similarly, the gene expression levels of

260 BNBD5, GM-CSF, CCL2 and GADD-45α were elevated, and the levels of GM-CSF, CCL2, and GADD-45α were

- 261 increased. However, in the presence of DBD, LDH release was reduced (Figure 4A), and the gene (Figure 4B) and
- 262 protein (Figure 4C, Figure 4D) levels of cell-associated damage factors were decreased.

#### 263 In BMECs, DBD prevents the oxidative damage induced by LPS

264 To investigate the ability of DBD to shield cells from oxidative damage, we detected the gene expression of COX-2, 265 PPARy, and iNOS in LPS-treated BMECs by DBD. At the same time, the contents of T-AOC, GSH, SOD and 266 MDA in the cells were determined, the amount of NO in the cell culture supernatant was determined, and the 267 reactive oxygen species staining was performed. The findings demonstrated that cells in the LPS group had 268 increased COX-2, PPARy, and iNOS gene expression; the content of T-AOC, GSH, and SOD in cells decreased 269 significantly; while the content of MDA in cells increased, the concentration of NO in cell culture supernatant 270 increased, and the level of reactive oxygen species increased. However, in the presence of DBD, the content of T-271 AOC, GSH and SOD in cells increased, while the content of MDA in cells decreased, the release of NO in cell 272 culture medium decreased (Figure 5A), the level of ROS in cells decreased (Figure 5C), and the expression of 273 oxidative stress-related factors decreased (Figure 5B).

#### 274 DBD reduces TLR4 and NF-kB expression in LPS-treated BMECs

We evaluated the levels of NF- $\kappa$ B and TLR4 in vitro to determine the defense mechanisms of DBD on the mammary epithelial cells of inflamed cows. Cells in the LPS group exhibited increased TLR4 and NF- $\kappa$ B expression. On the other hand, TLR4 and NF- $\kappa$ B expression was downregulated when DBD was present (Figure 6A, Figure 6C).

## 278 **Discussion**

Mastitis in dairy cows is a highly prevalent disease in the cattle industry that harms the wellbeing of cows, leading to decreased milk production, increased treatment costs, and compromised productivity [31]. In order to find a new alternative therapy for the treatment of BM, we used LPS to infect BMECs to establish an in vitro model of mastitis, and on this basis, we studied the protective effect of DBD on cells. Firstly, we observed the effects of 14 different concentrations of DBD on cell growth. The results showed that a low concentration of DBD could promote cell proliferation, while the high concentration of DBD could inhibit cell proliferation. The results of Roy C. Y. Choi showed that DBD treatment could induce the proliferation of MG-93 cells and increase the number of cells compared with the treatment without DBD [32]. LI Ying-dong 's study also showed that DBD could alleviate the decrease of cardiomyocyte viability induced by hydrogen peroxide and significantly increase cell viability [33]. Other studies have shown that DBD can also directly promote the growth of megakaryocytes [34], which is similar to our results. Therefore, we conclude that the active ingredients of traditional Chinese medicine in DBD can promote the absorption of nutrients by cells, and thus promote the proliferation of BMECs. The high concentration of DBD nutrients is too high, which will cause certain stimulation to the cells, cause the cell absorption burden, and thus inhibit cell proliferation.

293 Numerous investigations have demonstrated that mastitis is associated with an increase in the expression of 294 intracellular inflammatory factors, including TNF- $\alpha$ , IL-1 $\beta$ , IL-6, and IL-8; therefore, mastitis is often used as an 295 important indicator of the level of inflammation in dairy cows with mastitis [35-37]. In our study, we also found that 296 LPS treatment upregulated the expression of TNF- $\alpha$ , IL-1 $\beta$ , IL-6, and IL-8 in BMECs. Several studies have 297 confirmed the positive effects of herbal components on the control of mastitis in dairy cows. For example, Liuxue L 298 investigated the ability of matrine to prevent inflammation in BMECs and the underlying molecular mechanism, and 299 the results showed that matrine pretreatment downregulated the expression of IL-1 $\beta$ , IL-6, IL-8, and TNF- $\alpha$  during 300 inflammation in BMECs [38]. Jie S investigated the effect of the ethanol extract of Artemisia annua (AAE) on LPS-301 induced inflammatory injury in BMECs and demonstrated that AAE treatment reduced the levels of several 302 inflammatory factors in LPS-stimulated BMECs [39]. Another study revealed that LBP pretreatment significantly 303 reduced the expression of TNF- $\alpha$  and IL-1 $\beta$  in cells stimulated with *E. coli* [40]. DBD, a traditional Chinese herbal 304 formula, can exert potential immunoprotective effects by fighting inflammation, preventing injury and reducing 305 oxidative stress and has been recognized as an effective immunomodulator [35,41,42]. Li-Wen Fang reported that 306 DBD suppressed skin inflammation and reduced the cellular levels of IL-4, IL-5, and TNF- $\alpha$  during the course of 307 evaluating whether DBD could alleviate symptoms of atopic dermatitis (AD) [43]. Our study showed that DBD 308 downregulated the expression of TNF- $\alpha$ , IL-1 $\beta$ , IL-6, and IL-8 after LPS-induced BMEC infection.

309 Cells experiencing injury exhibit increased LDH release and elevated expression of BNBD5, GM-CSF, CCL2, 310 and GADD-45 $\alpha$  [44–48]. Various studies have explored alterations in factors associated with injury in BMECs 311 during inflammation and the impacts of pharmacological interventions. For example, BMECs are damaged by 312 rupture of the cell membrane and release of LDH from the cytoplasm into the extracellular space, leading to 313 increased LDH levels in cell cultures; however, in deoxynivalenol-induced inflammatory injury in mammary 314 epithelial cells, treatment with taraxasterol strongly reduced LDH release [49]. In addition, BNBD5 is an important 315 molecule in the innate defense system that activates the body's first defense barrier and is considered a candidate 316 gene for treating mastitis [50]. Studies have shown that BNBD5 is significantly upregulated in mastitis. GM-CSF 317 acts as a "messenger" that promotes macrophage recruitment to the site of inflammation and increases the secretion 318 of TNF- $\alpha$  and IL-6, directly inducing tissue injury [51]. CCL2 is a macrophage chemokine that functions by 319 targeting immune cells for chemotaxis. Breast tissue injury occurs after S. aureus and E. coli infection, which leads 320 to an intrinsic immune response in which the mRNA transcript level of CCL2 is upregulated [52]. Additionally, 321 GADD-45a is a growth-blocking and DNA damage repair gene, and some studies have shown that LPS- or LTA-322 induced cellular inflammation in BMECs is accompanied by significantly increased expression of GADD-45 $\alpha$  and 323 DNA damage [53]. Therefore, researchers have noted that resistance to cellular damage is highly important for 324 alleviating the development of inflammation. Using our LPS-induced mastitis epithelial cell model, we found that 325 DBD reduced LDH release and downregulated the expression of the damage-associated factors BNBD5, GM-CSF, 326 CCL2, and GADD-45α. These findings suggested that DBD can effectively ameliorate cellular injury and that this 327 cellular injury is closely related to the generation of inflammation.

328 Recent investigations have established a strong relationship between oxidative stress levels and mastitis in dairy 329 cows. Chen Y highlighted the association between oxidative stress and bovine mastitis, noting that the excessive 330 production of ROS by BMECs triggers apoptosis and the release of inflammatory factors. This suggests that a 331 disruption in the intracellular redox balance impairs immune and anti-inflammatory functions in cows around the 332 time of parturition [54]. In the context of the ability of betaine to mitigate inflammation and serve as an antioxidant, 333 Nannan Z reported that betaine decreased the LPS-induced inflammatory response and oxidative damage by 334 reducing the expression of COX-2 and iNOS in LPS-stimulated BMECs [55]. Similarly, Kaiqiang F reported that 335 Tanshinone IIA significantly lowered ROS and MDA levels in LPS-treated BMECs [56]. Additionally, Maocheng 336 J's findings indicated that quercetin effectively shielded BMECs from LPS-induced oxidative and barrier damage 337 [57]. Li, D. found that DBD could down-regulate the expression of IL-6 and TNF- $\alpha$ , reduce the level of MDA and 338 increase the level of SOD in the process of using DBD to treat vascular aging in mouse with chronic intermittent 339 hypoxia [58]. Our findings demonstrate that DBD, when applied to LPS-treated BMECs, it could increase the T-340 AOC of the cells, increase the GSH content, improve SOD activity, reduce the intracellular production of ROS, 341 MDA, and NO, and down-regulate the expression of COX-2, PPARy, and iNOS in order to protect the cells from 342 oxidative stress damage. DBD has been used in China for more than 800 years. A large number of studies have 343 shown that the main components of DBD are saponins, flavonoids, volatile oils, organic acids, polysaccharides and

so on [13]. Ferulic acid is the main active component of DBD. Ferulic acid can not only reduce the formation of free radicals and ROS, increase the expression of antioxidant genes and the activity of antioxidant enzymes, but also promote the activity of G-CSF and accelerate the repair of damaged cells [26,59]. Total glucosides of DBD can improve pulmonary fibrosis and increase cell anti-fibrotic activity [60]. Quercetin in DBD belongs to flavonoids, which can inhibit the growth of cancer cells and prevent cancer [61]. Therefore, we believe that the antiinflammatory, anti-injury and anti-oxidation effects of DBD are achieved with the help of ferulic acid, saponins, quercetin and other effective substances.

351 Extensive research has underscored the pivotal roles of TLR4 and NF- $\kappa$ B in managing mastitis [21,22]. LPS 352 activation of NF-KB through the specific recognition of TLR4 suggested that NF-KB, an intracellular nuclear 353 transcription factor, regulates the release of multiple inflammatory factors, inhibits cell proliferation, and promotes 354 cellular inflammation. Consequently, TLR4 and NF-KB have been identified as potential therapeutic targets for 355 treating mastitis in dairy cows [62]. Wang Y reported that LPS stimulation of BMECs hindered cell proliferation, 356 promoted the release of inflammatory and apoptotic factors, and increased the expression of TLR4 and NF-KB p65 357 [63]. Our experiments also revealed LPS-induced upregulation of TLR4 and NF-kB expression. HaoYu C's work 358 with allicin showed that it could mitigate LPS-induced inflammation in BMECs by inhibiting the TLR4/NF-KB 359 signaling pathway [64]. Moreover,  $\beta$ -carotene was found to reduce LPS-induced inflammation in BMECs by 360 suppressing NF-κB expression [65]. In an investigation of artemisinin, it was observed that artemisinin blocked the 361 TLR4-mediated NF- $\kappa$ B signaling pathway and decreased the expression of TNF- $\alpha$ , IL-6, and IL-1 $\beta$  mRNA in E. 362 coli-induced BMECs, thus reversing the inflammatory response [66]. Our results indicated that DBD could 363 downregulate the expression of TLR4, NF-κB p50, and NF-κB p65 following LPS induction in BMECs.

364 In conclusion, this study established an in vitro model of bovine mastitis by stimulating BMECs with LPS to 365 explore the protective effects of DBD on these cells and achieved relatively satisfactory outcomes. DBD mitigated 366 the LPS-induced expression of the inflammatory markers TNF- $\alpha$ , IL-1 $\beta$ , IL-6, and IL-8; reduced the expression of 367 the damage indicators BNBD5, GM-CSF, CCL2, GADD-45 $\alpha$ , and the release of LDH; and in terms of oxidative 368 stress, DBD decreased the expression of COX-2, PPARy, and iNOS, increased the T-AOC, GSH content, and SOD 369 activity, lowered MDA content, and NO release, and attenuated the generation of ROS. These findings indicate that 370 DBDs exhibit significant anti-inflammatory effects, provide protection against cellular injury, and alleviate 371 oxidative stress. Additionally, DBD suppressed the expression of TLR4, NF-κB p50, and NF-κB p65, suggesting the 372 potential of DBD as an effective treatment for mastitis in dairy cows. However, given the complexity of the immune

- 373 response in animals, the in vitro model has certain limitations. Consequently, future research will involve validating
- 374 the therapeutic efficacy of DBD through animal models of mastitis and clinical trials to investigate the mechanism
- by which DBD affects dairy mastitis more thoroughly.

## 376 Conclusion

377 LPS treatment of BMECs resulted in cellular inflammation, injury, and oxidative stress. DBD exerted anti-378 inflammatory, anti-injury, and antioxidative stress effects on LPS-treated BMECs. Furthermore, DBD significantly 379 reduced the expression of TLR4 and NF- $\kappa$ B in these cells. These findings suggest the potential of DBD as an 380 innovative treatment for mastitis in dairy cows. Consequently, DBD has been proposed as a promising new 381 therapeutic option for managing dairy cow mastitis based on these findings.

## 382 Funding sources

- 383 This research work was supported by National Natural Science Foundation of China (U21A20262) and the Gansu
- 384 Key Laboratory of Animal Reproductive Physiology and Reproductive Regulation (20JR10RA563).



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# 608 Tables and Figures

609 Table 1. Primers used for qRT–PCR.

GenePrimers Sequences $(5' \rightarrow 3')$ TNF- $\alpha$ F:GTTCTCCCCATGACACCACCTG R:GGGAGAAGAGAGTCAGACAGGCIL-1 $\beta$ F:AGATGAAGAGAGCTGCATCCAACA R:AACTCGTCGGAGGACGTTTCIL-6F:CTTCACAAGCGCCTTCACTC R:GCGCTTAATGAGAGACTCGGIL-8F:ATGACTTCCAAGCTGGCTGTT R:AGCTGCCGTTGGAATATGGG R:CTCCTGCAGCATGGTACTCGGM-CSFF:GACTCCCAGGAACCAACGTG R:TCGTAGTGGGTGGCCATCATCCL2F:CGGCTGGAGGAGCAAAGACCGAAAG R:GAGCCACGTCCCTGTCGTCGTCTTCCOX-2F:TAAAGCCAGGGAGCAAAAGACCGAAAG R:TAGGGAAAGCCGGAAGAAPPAR $\gamma$ F:TCCGTTCCCAAGGAGCTACGA R:CCTTCTGGTGAAGCACGACACGTCAINOSF:CAGGATGACCCCAAACGTCA R:CCTTCTGGTGAAGCGTGACTACANF- $\kappa$ B p50R:CTGCACAGGACCACGACAAAACNF- $\kappa$ B p65R:GTCCACGAGGCTGCTTTTA R:CCAGCATCACCACACCACACCACCACCACACCACACACAGAPDHF:GGTCACCCAACCCCACTTGATRCTF:GGTCACCCACTGCTTTA R:CCAGCATCACCACTGACNF- $\kappa$ B p65R:CCCACCACCCCACTTGATR:CAGCATCACCACCACACCACACACACACACACACACACAC		
TNF- $\alpha$ F:GTTCTCCCCATGACACCACCTG R:GGGAGAAGAGAGAGAGACAGACAGGCIL-1 $\beta$ F:AGATGAAGAGCTGCATCCAACA R:AACTCGTCGGAGGACGTTCIL-1 $\beta$ F:AGATGAAGAGCTGCATCCAACA R:GCGCTTAATGAGAGCCTCACTCIL-6F:CTTCACAAGCGCCTTCACTC R:GCGCTTAATGAGAGCCTGGTIL-8F:ATGACTTCCAAGCTGGCTGTT R:GGTTTAGGCAGACCTCGTTCBNBD5F:AGCTGCCGTTGGAATATGGG R:CTCCTGCAGCATGGTACTCGGM-CSFF:GACTCCCAGGAACCAACGTG R:TCGTAGTGGGTGGCCATCATCCL2R:TTAGGAAAGCCGGAAGAA R:GAGCCACGTCCCTGTCGTCGTCGTCTTCCOX-2F:CGGCTGGAGGAGCAAAAGACCGAAAG R:TAAGCCAGGGGAGCACAAGGACCACGACPPAR $\gamma$ F:CAGGATGACCCCAAAGGCTGAC R:TCGTGGAGAGCACCCAAAGGCTGAC R:CTCTGGTGAAGGCGCCCCACTTiNOSF:CAGGATGACCCCAAAGGCTGAC R:GCGCTTCACTACAGGGACCATTILA4F:TGCCTTCACTACAGGGACCATA F:CAGGATGACCCCAAACGTCAPAR $\gamma$ F:CAGGATGACCCCAAACGTCA R:TGGGACACCACACGACAATAAC F:CTGGAAGCACCACACAACGTCA R:GCTGTAAACATGAGCCGTACCNF-kB p50R:GCTGTAAACATGAGCCGTACC R:ACAACCCCTTCCAAGTTCC R:CCCCAGAGGTCCCTTTA R:CCAGCATCACCCACTTACACGAPDHF:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCCACTTGAT	Gene	Primers Sequences $(5' \rightarrow 3')$
INF-aR:GGGAGAAGAGAGAGAGTCAGACAGGCIL-1 $\beta$ F:AGATGAAGAGCTGCATCCAACAR:AACTCGTCGGAGGACGTTTCIL-6F:CTTCACAAGCGCCTTCACTCR:GCGCTTAATGAGAGCTGGCTGTTIL-8F:ATGACTTCCAAGCTGGCTGTTBNBD5F:AGCTGCCGTTGGAATATGGGGM-CSFF:GACTCCCAGGAACCAACGTGR:TCGTAGTGGGTGGCCATCATCCL2F:CCTGGAGAAGAGCCGGAAGAAGADD-45 $\alpha$ F:CGGCTGGAGGAGCAAAAGACCGAAAGPAR $\gamma$ F:TCCTTCCTGCAGGCAGGGACCAACGTCINOSF:CAGGATGACCCCAAGGCGGACGAAAAGNF-kB p50F:CGGCTGGAAGCACGACGAAAACNF-kB p65F:CAGCACCACGTCCCTTCCAAGGCCGAACGAGAPDHF:GGTCACCAGGGCTGCTTTAACACACCCCAACGGCCACCACTTAF:CCCCAGGAGTCCCAATACCNF-kB p65F:CACCACAGGCCCAACGACCACACACACACACACACACAC	TNF-α	F:GTTCTCCCCATGACACCACCTG
IL-1βF:AGATGAAGAGCTGCATCCAACA R:AACTCGTCGGAGGACGTTTCIL-6R:ACTCGTCGGAGGACGTTCACTC R:GCGCTTAATGAGAGCTTCGGIL-8F:ATGACTTCCAAGCTGGCTGTT R:GGTTTAGGCAGACCTCGTTTCBNBD5F:AGCTGCCGTTGGAATATGGG R:CTCCTGCAGCATGGTACTCGGM-CSFF:GACTCCCAGGAACCAACGTG R:TCGTAGTGGGTGGCCATCATCCL2F:CCTGGGCAAGGAGCAAAGAGAA R:GAGCCACGTCCCTGTCGTCGTCTTCCOX-2F:TAAGGCAGGAGCAAAAGACCGAAAG R:TGGGGATACCGGAAGGACCAACGTCAPPARγF:CCGGCTGGAGAGCACAACGTCA R:TGGGATACCCCAAGGCTGCACTTTLR4F:CGGCTTCACTACAGGACCGAAAAC R:GCTGTAAACACACCACAACGTCANF-κB p50F:CAGCATCCCAAGGCTGCCTTTA R:CTCCCAAGAGCTGCCACTTCC R:CTCCCAAGAGCTGCCAACGACCACACACACACACACACAC		R:GGGAGAAGAGAGTCAGACAGGC
L-1pR:AACTCGTCGGAGGACGTTCIL-6F:CTTCACAAGCGCCTTCACTCIL-8F:ATGACTTCCAAGCTGGCTGTTBNBD5F:AGCTGCCGTTGGAATATGGGGM-CSFF:GACTCCCAGGAACCAACGTGR:TCGTAGTGGGTGGCCATCATCCL2F:CCTGGGCAAGGAGCTATGTGGADD-45 $\alpha$ F:CGGCTGGAGGAGCAAGAACAAAGACCGAAAGGADD-45 $\alpha$ F:CGGCTGGAGGAGCAACGACGAAGAAPPAR $\gamma$ F:TCCGTTCCCAAGGAGCTACGAR:TAGGGAAAGCCGGAAGCAAAAGACCGAAAGPPAR $\gamma$ F:CAGGATGACCCCAACGTCCINOSF:CAGGATGACCCCAAACGTCANF-xB p50F:CTGGAAGCACGAACGAAAGACCGAAAAGNF-xB p65F:ACAAACCCTTCCAAGGGCTGCTTCR:FGGTCACCAGGGCTGCTCTTCF:ACAAACCCCTTCCAAGATCACGAR:F-xB p65F:CAGGATCACCCCAAGTCCR:AACAACCCCTTCCAAGAGTCCF:AACAACCCCTTCCAAGTCCNF-xB p65F:ACAAACCCCTTCCAAGTCCR:GAPDHF:GGTCACCAGGGCTGCTTTAR:CCAGCATCACCCACGACTTGATF:GGTCACCAGGGCTGCTTTAR:CCAGCATCACCCCACTTAACCCF:ACAACCCCTTCCAAGTCCR:CCAGCATCACCACGACTTTAAF:CAGGATCACCACGAATTAAC	IL-1β	F:AGATGAAGAGCTGCATCCAACA
IL-6F:CTTCACAAGCGCCTTCACTCIL-8F:ATGACTTCCAAGCTGGCTGTTIL-8F:ATGACTTCCAAGCTGGCTGTTBNBD5F:AGCTGCCGTTGGAATATGGGGM-CSFF:GACTCCCAGGAACCAACGTGR:TCGTAGTGGGTGGCCATCATF:CCTGGGCAAGGAGTTATGTGCCL2F:CCTGGGCAGGAGCAAAAGACCGAAAGGADD-45αF:CGGCTGGAGGAGCAACGACGAAGAAPPARγF:TCCGTTCCCAAGGAGCTGACNOSF:CAGGATGACCCCAAGGGCTCCTLR4F:TGCCTTCACTACAGGGAACCAACGTCANF-κB p50F:CTGGAAGCACGAACGAAAGACCGAAAGANF-κB p65F:AACAACCCCTTCCAAGAGTCCGAPDHF:GGTCACCAGGGCTGCTTTAGAPDHF:GGTCACCAGGGCTGCTTTA		R:AACTCGTCGGAGGACGTTTC
L-0R:GCGCTTAATGAGAGCTTCGGIL-8F:ATGACTTCCAAGCTGGCTGTT R:GGTTTAGGCAGACCTCGTTTCBNBD5F:AGCTGCCGTTGGAATATGGG R:CTCCTGCAGCATGGTACTCGGM-CSFF:GACTCCCAGGAACCAACGTG R:TCGTAGTGGGTGGCCATCATCCL2F:CCTGGGCAAGGAGTATGTG R:CGGCTGGAGGAGCAAAGAACCGAAAGGADD-45αF:CGGCTGGAGGAGCAAAAGACCGAAAG R:GAGCCACGTCCCTGTCGTCGTCTTCCOX-2F:TAAAGCCAGGGGAGCTACGA R:TAAGCCTGGACGGAGCTACGAPPARγF:TTCCGTTCCCAAGAGCTGAC R:CCTTCTGGTGAAGCGTGCTCTINOSF:CAGGATGACCCCAAACGTCA R:CCTTCTGGTGAAGCGTGCTCTTLR4F:TGCCTTCACTACAGGGACCAATAAC F:CTGGAAGCACGAATGACAGANF-κB p50F:CTGGAAGCACGAATGACAGA R:GCTGTAAACATGAGCCGTACC R:TCCCAGAGTTCCGATTCAC R:CCCAGAGTTCCGATTCACGAPDHF:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCCACTTGAT	IL-6	F:CTTCACAAGCGCCTTCACTC
IL-8F:ATGACTTCCAAGCTGGCTGTT R:GGTTTAGGCAGACCTCGTTTCBNBD5F:AGCTGCCGTTGGAATATGGG R:CTCCTGCAGCATGGTACTCGGM-CSFF:GACTCCCAGGAACCAACGTG R:TCGTAGTGGGTGGCCATCATCCL2F:CCTGGGCAAGGAGTTATGTG R:TAGGGAAAGCCGGAAGAAGADD-45αF:CGGCTGGAGGAGCAAAAGACCGAAAG R:GAGCCACGTCCTGTCGTCGTCGTCTTCCOX-2F:TAAAGCCAGGGGAGCAAAAGACCGAAAG R:TAAGCCTGGACGGAGCTACGAPPARγF:TTCCGTTCCCAAGAGCTGAC R:CCTTCTGGTGAAGCGTGCTCTiNOSF:CAGGATGACCCCAAACGTCA R:CCTTCTGGTGAAGCGTGCTCTILR4F:TGCCTTCACTACAGGGACCATAAC R:GCGGAAGCACGAATGACAGANF-κB p50F:CTGGAAGCACGAATGACAGA R:GCTGTAAACATGAGCCGTACC R:TCCCAGAGTTCCGATTCACNF-κB p65F:AACAACCCCTTCCAAGTCC R:CTCCCAGAGTTCCACAC R:CCCCCCAGAGTTCCACCGAPDHF:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCCACTTGAT		R:GCGCTTAATGAGAGCTTCGG
L-5R:GGTTTAGGCAGACCTCGTTTCBNBD5F:AGCTGCCGTTGGAATATGGGGM-CSFF:GACTCCCAGGAACCAACGTGR:TCGTAGTGGGTGGCCATCATCCL2F:CCTGGGCAAGGAGTTATGTGGADD-45αF:CGGCTGGAGGAGCAAAAGACCGAAAGGADD-45αF:CGGCTGGAGGGAGCTACGAPPARγF:TTCCGTTCCCAAGAGCTGACINOSF:CAGGATGACCCCAAGGGGAGCTACGAR:TAGGGAAGCCCCAAACGTCAF:CAGGATGACCCCAACGTCAINOSF:CAGGATGACCCCAAACGTCAR:GGCTTCCACTACAGGGACTACGAR:CCTTCTGGTGAAGCGTGTCTTLR4F:TGCCTTCACTACAGGGACCATAACNF-κB p50F:CTGGAAGCACGAATGACAGANF-κB p65R:CTCCCAGAGTCCGATTCACGAPDHF:GGTCACCAGGGCTGCTTTAR:CCAGCATCACCCCACTTGATF:ACAGCATCACCCCACTTGAT	ΠQ	F:ATGACTTCCAAGCTGGCTGTT
BNBD5F:AGCTGCCGTTGGAATATGGG R:CTCCTGCAGCATGGTACTCGGM-CSFF:GACTCCCAGGAACCAACGTG R:TCGTAGTGGGTGGCCATCATCCL2F:CCTGGGCAAGGAGTTATGTG R:TTAGGGAAAGCCGGAAGAAGADD-45αF:CGGCTGGAGGAGCAAAAGACCGAAAG R:GAGCCACGTCCCTGTCGTCGTCTTCCOX-2F:TAAAGCCAGGGGAGCTACGA R:TAAGCCTGGACGGGACGATAPPARγF:TCCGTTCCCAAGAGCTGAC R:CCTTCTGGTGAAGCGTGCTiNOSF:CAGGATGACCCCAACGTCA R:CCTTCTGGTGAAGCGTGTCTTLR4F:TGCCTTCACTACAGGGACCTTT R:TGGGACACCACGACAATAACNF-κB p50F:CTGGAAGCACGAATGACAGA R:GCTGTAAACATGAGCCGTACC R:CTCCCAGAGTTCCAACCNF-κB p65F:CAGGATCACCAGGGCTGCTTTA R:CTCCCAGAGTTCCAACCGAPDHF:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCCACTTGAT	IL-8	R:GGTTTAGGCAGACCTCGTTTC
BNBD3R:CTCCTGCAGCATGGTACTCGGM-CSFF:GACTCCCAGGAACCAACGTG R:TCGTAGTGGGTGGCCATCATCCL2F:CCTGGGCAAGGAGGAGTATGTG R:TTAGGGAAAGCCGGAAGAAGADD-45αF:CGGCTGGAGGAGCAAAAGACCGAAAG R:GAGCCACGTCCCTGTCGTCGTCTTCCOX-2F:TAAAGCCAGGGGAGGAGCTACGA R:TAAGCCTGGACGGGACGATAPPARγF:TTCCGTTCCCAAGAGCTGAC R:CCTTCTGGTGAAGCGTGACINOSF:CAGGATGACCCCAAACGTCA R:CCTTCTGGTGAAGCGTGTCTTLR4F:TGCCTTCACTACAGGGACCGATAA R:GCTGTAAACATGAGCCGTACCNF-κB p50F:CTGGAAGCACGAATGACAGA R:GCTGTAAACATGAGCCGTACCNF-κB p65F:ACAAACCCCTTCCAAGTTCC R:CTCCCAGAGTTCCGATTCACGAPDHF:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCCACTTGAT	BNBD5	F:AGCTGCCGTTGGAATATGGG
GM-CSFF:GACTCCCAGGAACCAACGTG R:TCGTAGTGGGTGGCCATCATCCL2F:CCTGGGCAAGGAGGAGTATGTG R:TAGGGAAAGCCGGAAGAAGADD-45αF:CGGCTGGAGGAGCAAAAGACCGAAAG R:GAGCCACGTCCCTGTCGTCGTCTTCCOX-2F:TAAAGCCAGGGGAGCTACGA R:TAAGCCTGGACGGGACGATAPPARγF:TTCCGTTCCCAAGAGCTGAC R:TGGGGATACAGGCTGCTiNOSF:CAGGATGACCCCAAACGTCA R:CCTTCTGGTGAAGCGTGTCTTLR4F:TGCCTTCACTACAGGGACCATTA R:TGGGACACCACGACAATAACNF-κB p50F:CTGGAAGCACGAATGACAGA R:GCTGTAAACATGAGCCGTACCNF-κB p65F:AACAACCCCTTCCAAGTTCC R:CTCCCAGAGTTCCGATTCACGAPDHF:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCACTTGAT		R:CTCCTGCAGCATGGTACTCG
GMI-CSFR:TCGTAGTGGGTGGCCATCATCCL2F:CCTGGGCAAGGAGTTATGTGR:TTAGGGAAAGCCGGAAGAAGADD-45αF:CGGCTGGAGGAGCAAAAGACCGAAAGR:GAGCCACGTCCCTGTCGTCGTCTTCCOX-2F:TAAAGCCAGGGGAGCTACGAPPARγF:TTCCGTTCCCAAGAGCTGACiNOSF:CAGGATGACCCCAAACGTCAR:TGGGGACAGCCCCAAACGTCAR:TGGGACACCACGGGACGATAF:TLR4F:TGCCTTCACTACAGGGACTTTNF-κB p50F:CTGGAAGCACGAATGACAGANF-κB p65F:AACAACCCCTTCCAAGTCCGAPDHF:GGTCACCAGGGCTGCTTTAR:CCAGCATCACCCCACTTGAT	GM-CSF	F:GACTCCCAGGAACCAACGTG
CCL2F:CCTGGGCAAGGAGTTATGTG R:TTAGGGAAAGCCGGAAGAAGADD-45αF:CGGCTGGAGGAGCAAAAGACCGAAAG R:GAGCCACGTCCCTGTCGTCGTCTTCCOX-2F:TAAAGCCAGGGGAGCTACGA R:TAAGCCTGGACGGGACGATAPPARγF:TTCCGTTCCCAAGAGCTGAC R:TGGGGATACAGGCTCCACTTiNOSF:CAGGATGACCCCAAACGTCA R:CCTTCTGGTGAAGCGTGTCTTLR4F:TGCCTTCACTACAGGGACCATA R:GCTGTAAACATGAGCCGTACCNF-κB p50F:CTGGAAGCACGAATGACAGA R:CTCCCAGAGTTCCACACCNF-κB p65F:AACAACCCTTCCAAGTTCC R:CTCCCAGAGTTCCGATTCACGAPDHF:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCCACTTGAT		R:TCGTAGTGGGTGGCCATCAT
CCL2R:TTAGGGAAAGCCGGAAGAAGADD-45αF:CGGCTGGAGGAGCAAAAGACCGAAAG R:GAGCCACGTCCCTGTCGTCGTCTTCCOX-2F:TAAAGCCAGGGGAGCTACGA R:TAAGCCTGGACGGGACGATAPPARγF:TTCCGTTCCCAAGAGCTGAC R:TGGGGATACAGGCTCCACTTiNOSF:CAGGATGACCCCAAACGTCA R:CCTTCTGGTGAAGCGTGTCTTLR4F:TGCCTTCACTACAGGGACTTT R:TGGGACACCACGACAATAACNF-κB p50F:CAGGAAGCACGAATGACAGA R:GCTGTAAACATGAGCCGTACCNF-κB p65R:CTCCCAGAGTTCCAAGTTCC R:CTCCCAGAGTTCCAAGTTCCGAPDHF:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCCACTTGAT	CCL2	F:CCTGGGCAAGGAGTTATGTG
GADD-45αF:CGGCTGGAGGAGCAAAAGACCGAAAG R:GAGCCACGTCCCTGTCGTCGTCTTCCOX-2F:TAAAGCCAGGGGAGCTACGA R:TAAGCCTGGACGGGACGATAPPARγF:TTCCGTTCCCAAGAGCTGAC R:TGGGGATACAGGCTCCACTTiNOSF:CAGGATGACCCCAAACGTCA R:CCTTCTGGTGAAGCGTGTCTTLR4F:TGCCTTCACTACAGGGACTTT R:TGGGACACCACGACAATAACNF-κB p50F:CTGGAAGCACCACGAATGACAGA R:GCTGTAAACATGAGCCGTACCNF-κB p65F:AACAACCCCTTCCAAGTTCC R:CTCCCAGAGTTCCGATTCACGAPDHF:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCACTTGAT	CCL2	R:TTAGGGAAAGCCGGAAGAA
GADD-450tR:GAGCCACGTCCCTGTCGTCGTCTTCCOX-2F:TAAAGCCAGGGGAGCTACGAPPARγF:TTCCGTTCCCAAGAGCTGACPPARγF:TTCCGTTCCCAAGAGCTGACiNOSF:CAGGATGACCCCAAACGTCAiNOSF:CAGGATGACCCCAAACGTCTTLR4F:TGCCTTCACTACAGGGACTTTNF-κB p50F:CTGGAAGCACGAATGACAGANF-κB p65F:AACAACCCTTCCAAGTCCR:CTCCCAGAGTTCCGATTCACGAPDHF:GGTCACCAGGGCTGCTTTA	GADD-45α	F:CGGCTGGAGGAGCAAAAGACCGAAAG
COX-2F:TAAAGCCAGGGGAGCTACGA R:TAAGCCTGGACGGGACGATAPPARγF:TTCCGTTCCCAAGAGCTGAC R:TGGGGATACAGGCTCCACTTiNOSF:CAGGATGACCCCAAACGTCA R:CCTTCTGGTGAAGCGTGTCTTLR4F:TGCCTTCACTACAGGGACTTT R:TGGGACACCACGAATGACAGA R:GCTGTAAACATGAGCCGTACCNF-κB p50F:ACAAACCCTTCCAAGTCC R:GCTGTAAACATGAGCCGTACCNF-κB p65F:AACAACCCTTCCAAGTTCC R:CTCCCAGAGTTCCCAAGTTCACGAPDHF:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCACTTGAT		R:GAGCCACGTCCCTGTCGTCGTCTTC
COA+2R:TAAGCCTGGACGGGACGATAPPARγF:TTCCGTTCCCAAGAGCTGACR:TGGGGATACAGGCTCCACTTiNOSF:CAGGATGACCCCAAACGTCAR:CCTTCTGGTGAAGCGTGTCTTLR4F:TGCCTTCACTACAGGGACTTTNF-κB p50F:CTGGAAGCACGAATGACAGANF-κB p65F:AACAACCCTTCCAAGTCCR:CTCCCAGAGTTCCGATTCACGAPDHF:GGTCACCAGGGCTGCTTTAR:CCAGCATCACCCACTGAT	COX 2	F:TAAAGCCAGGGGAGCTACGA
PPARγF:TTCCGTTCCCAAGAGCTGAC R:TGGGGATACAGGCTCCACTTiNOSF:CAGGATGACCCCAAACGTCA R:CCTTCTGGTGAAGCGTGTCTTLR4F:TGCCTTCACTACAGGGACTTT R:TGGGACACCACGACAATAACNF-κB p50F:CTGGAAGCACGAATGACAGA R:GCTGTAAACATGAGCCGTACCNF-κB p65F:AACAACCCTTCCAAGTTCC R:CTCCCAGAGTTCCGATTCACGAPDHF:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCACTGAT	COX-2	R:TAAGCCTGGACGGGACGATA
FFARYR:TGGGGATACAGGCTCCACTTiNOSF:CAGGATGACCCCAAACGTCAiNOSR:CCTTCTGGTGAAGCGTGTCTTLR4F:TGCCTTCACTACAGGGACTTTR:TGGGACACCACGACAATAACF:CTGGAAGCACCACGAATGACAGANF-κB p50F:CTGGAAGCACCATGAGCCGTACCNF-κB p65F:AACAACCCTTCCAAGTTCCR:GCTGTAAACATGAGCCGTACCF:AACAACCCCTTCCAAGTTCCGAPDHF:GGTCACCAGGGCTGCTTTAR:CCAGCATCACCCACTTGAT	PPARγ	F:TTCCGTTCCCAAGAGCTGAC
iNOS F:CAGGATGACCCCAAACGTCA R:CCTTCTGGTGAAGCGTGTCT F:TGCCTTCACTACAGGGACTTT R:TGGGACACCACGACGACTAAC F:CTGGAAGCACCACGAATGACAGA R:GCTGTAAACATGAGCCGTACC F:AACAACCCCTTCCAAGTTCC R:CTCCCAGAGTTCCGATTCAC F:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCCACTTGAT		R:TGGGGATACAGGCTCCACTT
INOSR:CCTTCTGGTGAAGCGTGTCTTLR4F:TGCCTTCACTACAGGGACTTTR:TGGGACACCACGACAATAACF:CTGGAAGCACGAATGACAGANF-кВ p50F:CTGGAAGCACGAATGACCGTACCNF-кВ p65F:AACAACCCTTCCAAGTTCCR:CTCCCAGAGTTCCGATTCACF:GGTCACCAGGGCTGCTTTAGAPDHF:GGTCACCAGGGCTGCTTTA	iNOS	F:CAGGATGACCCCAAACGTCA
TLR4F:TGCCTTCACTACAGGGACTTT R:TGGGACACCACGACGACTAAC F:CTGGAAGCACGAATGACAGA R:GCTGTAAACATGAGCCGTACC F:AACAACCCCTTCCAAGTTCC R:CTCCCAGAGTTCCGATTCAC F:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCCACTTGAT		R:CCTTCTGGTGAAGCGTGTCT
ILR4R:TGGGACACCACGACAATAACNF-кВ p50F:CTGGAAGCACGAATGACAGANF-кВ p65R:GCTGTAAACATGAGCCGTACCNF-кВ p65F:AACAACCCCTTCCAAGTTCCGAPDHF:GGTCACCAGGGCTGCTTTAR:CCAGCATCACCCCACTTGAT	TLR4	F:TGCCTTCACTACAGGGACTTT
NF-кB p50 NF-кB p65 R:GCTGTAAACATGAGCCGTACC F:AACAACCCCTTCCAAGTTCC R:CTCCCAGAGTTCCGATTCAC F:GGTCACCAGGGCTGCTTTA R:CCAGCATCACCCCACTTGAT		R:TGGGACACCACGACAATAAC
NT-κB p50R:GCTGTAAACATGAGCCGTACCNF-κB p65F:AACAACCCCTTCCAAGTTCCGAPDHF:GGTCACCAGGGCTGCTTTAAR:CCAGCATCACCCCACTTGAT	NE 1/B n50	F:CTGGAAGCACGAATGACAGA
NF-κB p65 GAPDH F:AACAACCCCTTCCAAGTTCC R:CTCCCAGAGTTCCGATTCAC F:GGTCACCAGGGCTGCTTTTA R:CCAGCATCACCCCACTTGAT	мг-кырзо	R:GCTGTAAACATGAGCCGTACC
GAPDH R:CCAGCATCACCAGGGCTGCTTTA R:CCAGCATCACCCACTTGAT	NF-кВ р65	F:AACAACCCCTTCCAAGTTCC
GAPDH F:GGTCACCAGGGCTGCTTTTA R:CCAGCATCACCCCACTTGAT		R:CTCCCAGAGTTCCGATTCAC
R:CCAGCATCACCCCACTTGAT	GAPDH	F:GGTCACCAGGGCTGCTTTTA
		R:CCAGCATCACCCCACTTGAT





612Figure 1. DBD and LPS effects on the survival of the BMECs. (A) BMECs were treated with several doses of613DBD (10, 25, 50, 100, 250, 500, 1000, 2500, 5000, 10000, 25000, 50000, and 100000  $\mu$ g/mL) for 24 h. The CCK-8614test was utilized to evaluate the viability of the cells; (B) BMECs were exposed to several concentrations of LPS615(0.1, 1, and 10  $\mu$ g/mL) for 24 h. The CCK-8 test was utilized to evaluate the viability of the cells. The data are616shown as the mean ±SEM. \* p < 0.05, \*\* p < 0.01.





620 Figure 2. LPS-induced inflammation in BMECs. After 24 h, three different LPS doses (0.1, 1, and 10 μg/mL)

- 621 were applied to the cells. (A) qRT–PCR was used to measure the relative mRNA levels of TNF- $\alpha$ , IL-1 $\beta$ , IL-6, and
- 622 IL-8; GAPDH was used as the internal reference gene; (B) TNF-α, IL-1β, IL-6, and IL-8 expression was measured
- 623 via WB; (C) TNF-α, IL-1β, IL-6, and IL-8 quantification. The control utilized was β-actin. The data are shown as
- 624 the mean  $\pm$ SEM. \* p < 0.05, \*\* p < 0.01.



626Figure 3. In BMECs, DBD inhibits the inflammation induced by LPS. For 24 h, the cells were exposed to 100627µg/mL DBD and 1 µg/mL LPS. (A) qRT–PCR was used to measure the relative mRNA levels of TNF-α, IL-1β,628IL-6, and IL-8; GAPDH was used as the internal reference gene; (B) TNF-α, IL-1β, IL-6, and IL-8 expression was629measured via WB; (C) TNF-α, IL-1β, IL-6, and IL-8 quantification the control utilized was β-actin. The data are630shown as the mean ±SEM. \*p < 0.05 vs. Con group, \*\*p < 0.01 vs. Con group; #p < 0.05 vs. LPS group, ##p < 0.01</td>631vs. LPS group.





Figure 4. In BMECs, DBD protects against injury induced by LPS. For 24 h, the cells were exposed to 100 µg/mL DBD and 1 µg/mL LPS. (A) LDH assay for detecting LDH release from cell supernatants; (B) qRT–PCR was used to measure the relative mRNA levels of BNBD5, GM-CSF, CCL2, and GADD-45α; GAPDH was used as the internal reference gene; (C) GM-CSF, CCL2, and GADD-45α expression was measured via WB; (D) Quantification of GM-CSF, CCL2, and GADD-45α. The control utilized was β-actin. The data are shown as the mean ±SEM. \*p < 0.05 vs. Con group, \*\*p < 0.01 vs. Con group; #p < 0.05 vs. LPS group, ##p < 0.01 vs. LPS group.



Figure 5. DBD alleviates LPS-induced injury in BMECs. For 24 h, the cells were exposed to 100 µg/mL DBD and 1 µg/mL LPS. (A) The effect of DBD on intracellular oxidation and antioxidant index expression; (B) Relative COX-2, PPARγ and iNOS mRNA levels were determined via qRT–PCR; GAPDH was used as the internal reference gene; (C) Reactive oxygen staining was used to observe the production of reactive oxygen species in the BMECs. The data are shown as the mean  $\pm$ SEM. \**p* < 0.05 vs. Con group, \*\**p* < 0.01 vs. Con group; #*p* < 0.05 vs. LPS group, ##*p* < 0.01 vs. LPS group.



Figure 6. DBD reduces TLR4 and NF-κB expression in LPS-treated BMECs. For 24 h, the cells were exposed to 100 µg/mL DBD and 1 µg/mL LPS. (A) Relative TLR4 and NF-κB mRNA levels were determined via qRT–PCR; GAPDH was used as the internal reference gene; (B) TLR4 and NF-κB expression was measured via WB; (C) Quantification of TLR4 and NF-κB expression. The control utilized was β-actin. The data are shown as the mean ±SEM. \*p < 0.05 vs. Con group, \*\*p < 0.01 vs. Con group; #p < 0.05 vs. LPS group, ##p < 0.01 vs. LPS group.