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Xuanfei Baidu Formula attenuates LPS-induced acute lung injury by inhibiting the NF-κB signaling pathway

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1. Introduction

Acute lung injury (ALI) is mainly characterized by acute, progressive respiratory failure and hypoxemia and is clinically typical in thoracic surgery diseases [\(Yin et al., 2021\)](#page-13-0). Adult respiratory distress syndrome is characterized by a cascade of pro-inflammatory mediators due to immune system overactivation and is one of the most severe symptoms of ALI ([Liu et al., 2021b\)](#page-12-0). Because most researchers believe that inflammatory response plays a central role in ALI, treatment approaches are still focused on effective controlling the degree of the inflammatory response. Research on ALI pathogenesis has mainly focused on the nuclear factor-κB (NF-κB) inflammatory pathway [\(Ye et al., 2021](#page-13-0); [Liu](#page-12-0) [et al., 2021\)](#page-12-0). In clinical practice, commonly used anti-inflammatory drugs for treating ALI, such as glucocorticoids, cause symptoms such as skin atrophy, decreased bone density, and gastrointestinal discomfort. Although strategies for treating ALI are constantly improving, there remains a lack of specific drugs, and poor prognosis remains a significant challenge to supporting patients' health [\(Reichardt et al., 2021](#page-13-0)). Therefore, there is an urgent need to develop specific drugs for ALI treatment. At present, research on traditional Chinese medicine (TCM) has emerged as a novel area of research for developing ALI treatments, and the anti-inflammatory mechanism and influence on the immune

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function of various TCM components are continuously being explored.

Xuanfei Baidu (XFBD) is a prescription recommended by the State Administration of Traditional Chinese Medicine for the clinical treatment of COVID-19 [\(Zhao et al., 2021\)](#page-13-0). This prescription is a traditional Chinese medicine formula proposed by Academician Zhang Boli and Professor Liu Qingquan on the anti-epidemic front line. It is composed of 13 TCM compounds, listed as follows with their materials of origin: Semen Armeniacae Amarum from *Prunus sibirica* L., *Verbenae Herba* from *Verbena officinalis* L., *Ephedrae Herba* from *Ephedra sinica* Stapf, *Atractylodis Rhizoma* from *Atractylodes chinensis* (DC.) Koidz, *Glycyrrhizae Radix et Rhizoma* from *Glycyrrhiza uralensis* Fisch., *Descurainiae Semen* from *Descurainia sophia* (L.) Webb. ex Prantl., *Polygoni Cuspidati Rhizoma et Radix* from *Polygonum cuspidatum* Siebold & Zucc., *Phragmitis Rhizoma* from *Phragmites communis* Trin., *Coicis Semen* from *Coix lacryma-jobi* L. var *mayuen* (Roman.) Stapf, *Citri Grandis Exocarpium* from *Citrus grandis* (L.) Osbeck, *Artemisia Annua Herba* from *Artemisia annua* L., *Pogostemonis Herba* from *Pogostemon cablin* (Blanco) Benth., and *Gypsum Fibrosum*. Clinical trials have demonstrated that XFBD can restore white blood cell and lymphocytes levels to normal [\(Wu et al., 2020\)](#page-13-0). However, there are few studies on the active components of XFBD, and the mechanism of action of XFBD in treating ALI is unclear.

The lung is a critical organ for gas exchange, and airborne pathogens, allergens, and other toxins increase susceptibility ALI during lung infection or inflammation. The ALI response to severe pulmonary microbial infection is the result of the immunological recognition of pathogens responsible for inducing a pro-inflammatory immune response ([Rezoagli et al., 2017](#page-13-0)). ALI can cause signigicant tissue damage, and in severe cases, irreversible lung damage can lead to death. Macrophages play a crucial role in the pathogenesis of bacterial pneumonia and associated ALI([Wu et al., 2021](#page-13-0)). For example, in Gram-negative bacterial pneumonia, macrophages produce TNF-α, which induces granulocyte-macrophage colony-stimulating factor (GM-CSF) in AECs, causing proliferative signals in AECs through autocrine stimulation, thereby contributing to restoration of the alveolar epithelial barrier[\(Kumar, 2020](#page-12-0)). In this study, we used lipopolysaccharide (LPS; a unique component in the cell wall of gram-negative bacteria) to stimulate mouse mononuclear macrophage leukemia cells (RAW264.7) as a cell experimental model to verify that XFBD alleviates the acute mechanism of action in lung injury.

In this study, we analyzed the active components of XFBD, predicted and verified the targets of XFBD according to its active ingredients, and elucidated its mechanism of action in treating ALI. A graphical summary of this study is provided.

2. Materials and methods

2.1. Reagents and materials

XFBD powder was provided by Tianjin Modern TCM Innovation Center (Batch No: XF210204, HPLC detection: 1.21 mg/g for ephedrine and pseudoephedrine, 25.30 mg/g for naringin, and 1.83 mg/g for glycyrrhizic acid in XFBD powder). The production method is to soak the 13 TCM samples (Lepidium apetalum Willd bag decoction) in the prescription in water (1:4 ratio) for 30 min, heat the mixture to boiling, maintain the mixture overheat for 40 min, filter the decoction, and concentrate the filtrate to a relative density of 1.02–1.10 (60 ◦C), spray dried. Lianhua Qingwen Granules (LHQW) was purchased from Beijing Yiling Pharmaceutical Co., Ltd (Beijing, China). MS-grade methanol and acetonitrile were obtained from Thermo Fisher Scientific Co., Ltd (Shanghai, China). LC-MS/HPLC-grade formic acid was obtained from Anaqua Chemicals Supply (Wilmington, USA). Purified water was purchased from Watsons Co., Ltd (Guangdong, China). A CCK-8 Cell Proliferation Kit and BCA Protein Assay Kit were purchased from Beijing Solarbio Science & Technology Co., Ltd (Beijing, China). LPS was purchased from Sigma-Aldrich trading Co., Ltd (MO, USA). Dulbecco's modified Eagle medium (DMEM) was purchased from Meilunbio

(Dalian, China). IL-6, TNF-α, IL-1β, IL-10, monocyte chemotactic protein 1 (MCP-1), and fetal bovine serum (FBS) were purchased from ExCell Biotech Co., Ltd (Shanghai, China). The NO assay kit was purchased from Beyotime Biote Co., Ltd (Shanghai, China). Myeloperoxidase (MPO) and cyclooxygenase-2 (COX-2) were purchased from Shanghaimeilian Biotech Co., Ltd (Shanghai, China). BAY 11–7082 was purchased from Selleck. CN (Shanghai, China). All antibodies used in this study were purchased from Affinity Biosciences LTD (Jiangsu, China).

The following 37 standard compounds were used as reference standards (purity≥98%). Isoquercitrin, ephedrine, catechin, caffeic acid, vanillic acid, pseudoephedrine, vitexin, liquiritin, hesperidin, atractylenolide II, scopoletin, wogonin, amygdalin, adenosine, isochlorogenic acid C, polydatin, naringin, rhoifolin, atractylenolide III, hastatoside, physcion, verbenalin and glycyrrhetinic acid were purchased from China National Institute for Food and Drug Control (Beijing, China). Glycyrrhizic acid, scopolin, verbascoside, ferulic acid, ononin, apigenin-7-O-diglucuronide, vicenin-2, cryptochlorogenic acid, torachrysone 8- O-glucoside, liquiritin apioside, emodin and apigenin-7-O-glucoside were purchased from Shanghai Shidande Standard Technical Service Co., Ltd (Shanghai, China). Kaempferol 3-O-β-D-glucoside and naringenin were purchased from Chengdu Aifa Biological Technology Co., Ltd (Chengdu, China).

2.2. Ultra-high performance liquid chromatography with quadrupole time-of-flight mass spectrometry (UPLC-Q/TOF-MS)

The UPLC-Q/TOF-MS method employed for analyzing XFBD was the same as that used in our previous study [\(Wang et al., 2022](#page-13-0)).

2.3. Gene networks analysis

The identified compounds were imported into the traditional Chinese medicine ayatems pharmacology database and analysis platform (TCMSP; <https://old.tcmsp-e.com/tcmsp.php>), TargetNet [\(http://](http://targetnet.scbdd.com) targetnet.scbdd.com), and SwissTargetPrediction database ([http://www.](http://www) swisstargetprediction.ch/) to predict the active ingredient targets. The keyword "acute lung injury" was searched in the Gene Cards (<https://www.genecards.org/>, date of visit: December 24, 2021) and OMIM (<http://omim.org/>) databases to summarize disease targets. Overlap targets were screened by comparing ALI-associated targets with active compound targets to indentify potential targets for ALI treatmet. Kyoto Encyclopedia of Genes and Genomics (KEGG) pathway enrichment analysis and gene ontology (GO) analysis in the Metascape database [\(https://metascape.org](https://metascape.org)) were performed to investigate gene function. GO functionally annotated key genes as molecular functions (MFs), cellular components (CCs) and biological processes (BPs). Cytoscape 3.7.0 software (<http://www.cytoscape.org/>) and the String website ([http://www.string-db.org/\)](http://www.string-db.org/) were used to further analyze the overlapping targets and obtain hub targets [\(Wang et al., 2021\)](#page-13-0). The lowest interaction score in the protein-protein interaction (PPI) network is 0.900. According to previous research, nodes with a degree more than twice the median degree of all nodes were selected as hub nodes (Chen [et al., 2021\)](#page-12-0).

2.4. Cell experiments

2.4.1. Cell culture and treatment

RAW264.7 cells were obtained from the American Type Culture Collection (ATCC, Manassas, USA) and grown in DMEM containing 10% FBS in a humidified incubator at 37 $°C$ and 5% CO₂.

2.4.2. CCK-8 assay

Cells were seeded at a density of 1×10^4 cells/well in 96-well plates for 24 h. XFBD was dissolved in the medium, and 100 μL of medium was added at different concentrations (0, 25, 50, 100, 200, 400, 800 μg/mL) to culture cells for 24 h. After administration, 10 μL of the CCK-8

Fig. 1. Ultra-high performance liquid chromatography with quadrupole time-of-flight mass spectrometry (UPLC-Q/TOF-MS) analysis of Xuanfei Baidu Formula (XFBD). (A) Chromatogram of XFBD in 254 nm mode. (B) Base peak intensity chromatograms of XFBD in positive and (C) negative ESI mode.

solution was added to each well and incubated for 2 h. The 96-well plate was removed, and the absorbance was measure at 450 nm.

2.4.3. Detection of inflammatory cytokines

Cells were seeded in 96-well plates at a density of 1×10^4 cells/well for 24 h. The cells were divided into control, LPS, and administration groups (50, 100, and 200 μg/mL). The model group was cultured for 24 h in medium containing 5 μg/mL LPS, and the administration group was cultured for 24 h in the medium containing 5 μg/mL LPS and the corresponding concentration of XFBD, and the cytokines were measured after the culture. NO, IL-10, MPO, TNF-α, COX-2, IL-6, MCP-1, and IL-1β levels were observed according to the recommended instruction. Absorbance was measured using by an automatic microplate reader.

2.4.4. Immunofluorescence assay

For immunofluorescence analysis, cells were fixed, permeabilized, and blocked with 5% bovine serum albumin for 1 h. The cells were soaked in a 4 ℃ refrigerator with a p–NF–κB p65 (1:400) antibody for 12 h. Sections were washed 3 times with PBS to remove residual antibody, and then labelled with anti-rabbit IgG $(H + L)$ (Alexa Fluo 555) for 2 h at room temperature. The cleaning procedure was repeated, and the cells were stained with Hoechst 33342 for 10 min. After repeating the cleaning, images were acquired by Operetta CLS (PerkinElmer, USA) [\(Li](#page-12-0) [et al., 2020a,b\)](#page-12-0).

2.4.5. Western blot analysis

Cells were seeded in 96-well plates at a density of 1×10^4 cells/well for 24 h. The cells were divided into control, LPS, and treatment groups (50, 100, and 200 μg/mL). The model group was cultured for 24 h with the medium containing 5 μg/mL LPS, and the administration group was cultured with the medium containing 5 μg/mL LPS and the corresponding concentration of XFBD for 24 h. The cell proteins were then extracted for western blotting experiments. Western blotting was performed as previously described (Li et al., $2020a$, b). The following primary antibodies were used in the RAW264.7 cell experiments: Phospho–NF–κB-p65 (1:1000 dilution), NF-κB-p65 (1:1000 dilution), COX-2 (1:1000 dilution), and β-actin protein (1:10000 dilution).

2.5. Animal experiment

2.5.1. Model design

Male C57BL/6 mice ($n = 72$, body weight: 18–22 g, six weeks old) were obtained from SPF Biotechnology Co., Ltd. (license number: SCXK (Tianjin) 2019-0002). All experimental procedures were approved by the Animal Care and Use Committee of the Tianjin University of Traditional Chinese Medicine (authorization number: TCM-LAEC2021186). All mice were kept at 22–26 °C and 55 \pm 5% humidity with a light/dark cycle for 12 h, acclimated for 7 days before the experiment, and given free access to food and water.

The 72 mice were randomly divided into control, LPS (2 mg/mL), LPS + LHQW (2.3 g/kg), and LPS + XFBD (1.3, 2.6, and 5.2 g/kg) groups. Different groups of mice were administered XFBD by gavage according to the experimental design. On the 8th day, 1 h after gavage, LPS solution (0.5 μ L/g) was injected into the nasal cavity. Mice were anesthetized 6 h after instillation, and lung tissue, serum and bronchoalveolar lavage fluid (BALF) were collected. LPS, LHQW and XFBD administrations were formulated using deionized water.

2.5.2. Lung wet/dry weight (W/D) ratio

The surface layer of the upper lobe of the left lung was wiped dry and then weighed. Subsequently, the lung tissue was dried in an oven at 80 ℃ for 3 days and weighed again. The W/D ratios were recorded for all groups.

2.5.3. Protein concentration determination in BALF

After death, the chest of each mouse was opened, and the trachea was bluntly separated and exposed. A small "inverted V" cut was made in the trachea with surgical scissors, the catheter was carefully inserted through the incision, and lavage was performed with a 1 mL syringe. The lungs were lavaged 3 times with 500 μL of sterile PBS [\(An et al., 2021](#page-12-0)). The three lavages were pooled and centrifuged at 3000 rpm for 10 min at 4 ◦C, and the supernatant was used for BCA determination of total protein concentration.

Table 1

Chemical constituents identified in XFBD based on UPLC-Q/TOF-MS.

(*continued on next page*)

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Table 1 (*continued*)

A: *Ephedrae Herba*, B: *Glycyrrhizae Radix et Rhizoma*, C: *Armeniacae Semen Amarum*, D: *Coicis Semen*, E: *Polygoni Cuspidati Rhizoma et Radix*, F: *Artemisia Annua Herba*, G: Atractylodis Rhizoma, H: Pogostemonis Herba, I: Verbenae Herba, J: Citri Grandis Exocarpium, K: Descurainiae Semen Lepidii Semen, L: Phragmitis Rhizoma.
^a Indicates that the compound has been compared with the reference

314 nodes and 1905 edges

34 nodes and 501 edges

Fig. 2. Network pharmacology analysis of potential XFBD mechanisms in treating Acute lung injury (ALI). (A) Venn diagram showing overlap of ALI genes and predicted compound targets. (B) Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis. (C) Gene Ontology (GO) analysis of biological processes. (D) Protein-protein interaction (PPI) results and hub targets of compound targets were analyzed by Cytoscape software.

2.5.4. Inflammatory cytokines detections

Tissues were rinsed with pre-chilled PBS, the blood removed, and the tissues were dried with filter paper. Then, 1 g of tissue were weighed and homogenized by adding 1 ml of PBS. The prepared tissue homogenate was centrifuged at 4 ℃ and 10,000 rpm for 10 min. The sediment was discarded, and the supernatant was retained. NO, IL-10, MPO, TNF-α, COX-2, IL-6, MCP-1, and IL-1β levels were observed according to the recommended instructions. Absorbance value was measured using by an automatic microplate reader.

2.5.5. Histopathology evaluation

Lung tissue was soaked in 4% paraformaldehyde for 24 h. The tissue was dehydrated, embedded and sectioned (5 μm). The tissue sections were stained using the Hematoxylin and eosin staining (H&E) method ([Ying et al., 2013\)](#page-13-0). The structure of the lung tissues was photographed using a microscope (Leica, GER).

2.5.6. Immunohistochemistry assay

Immunohistochemical studies were performed to detect p-IKK, p–NF–κB p65, and iNOS expression. The lung tissue sections were deparaffinized, rehydrated, and incubated in 10 mM citric acid buffer at 120 ◦C for 5 min. Then, 10% goat serum was sectioned at room

temperature for 1 h and incubated with antibodies p-IKK, p–NF–κB p65, and iNOS (1:200 dilution) at 4 \degree C overnight. Finally, the sections were incubated with horseradish peroxidase (HRP)-conjugated secondary antibody (1:1000 dilution) was sectioned at room temperature for 1 h and photographed.

2.6. Statistical analysis

Statistical analysis was performed using the GraphPad Prism software (version 6.07, San Diego, CA, USA). Statistical analysis was performed using one-way analysis of variance (ANOVA) with post hoc Tukey's test. Data are shown as the mean \pm standard deviation. Statistical significance was set at P *<* 0.05.

3. Results

3.1. Compound identification

In total, 113 compounds were analyzed and identified from the XFBD by UPLC-Q/TOF-MS, including 48 flavonoids, 6 alkaloids, 4 triterpenes, 5 anthraquinones, 5 iridoid glycosides, 5 organic acids, 7 sesquiterpene glycosides, 6 coumarins, 11 phenylpropanoids class, 4 phenols, 9

Fig. 3. Effect of XFBD on lipopolysaccharide (LPS)-stimulated inflammatory cytokines in RAW264.7 cells. (A) XFBD cytotoxicity in RAW264.7 cells was determined by the CCK-8 assay. (B–F) Nitric oxide (NO), interleukin-10 (IL-10), tumor necrosis factor alpha (TNF-α), interleukin-6 (IL-6), and interleukin-1β (IL-1β) levels in RAW264.7 cells. Data are shown as mean ± standard deviation (SD) by one-way analysis of variance (ANOVA). n = 4. #p *<* 0.05, ##p *<* 0.01 vs control group, *p *<* 0.05, **p *<* 0.01 vs LPS group, ∧∧p *<* 0.01 vs administration group (50 μg/mL), ††p *<* 0.01 vs administration group (100 μg/mL).

glycosides, and 3 other compounds [\(Sun et al., 2021](#page-13-0); Xu et al., 2021; [Zhang et al., 2021;](#page-13-0) [Gao et al., 2021](#page-12-0); [Ming et al., 2021;](#page-13-0) [Dong et al., 2021](#page-12-0)). The results are presented in [Fig. 1](#page-3-0) and [Table 1.](#page-4-0) Of these, 37 were verified using reference materials.

1446 ALI-associated targets were retrieved. The 314 potential therapeutic targets of XFBD for ALI were identified using Venn diagrams ([Fig. 2A](#page-6-0)).

3.2. Compound and disease targets predictions

We explored the mechanisms by which XFBD treats ALI by querying several databases. Searching 113 chemical constituents through SwissTargetPrediction and TCMSP databases resulted in 856 candidate compound targets. By searching the OMIM and Gene Card databases,

3.3. Pathway enrichment analysis

KEGG analysis showed that 314 genes were enriched in 20 pathways, including disease pathways and biological communication ([Fig. 2](#page-6-0)B). GO analysis revealed that these molecular functions were primarily concentrated on multiple processes, such as protein kinase activity, transcription factor binding, leukocyte differentiation, and cytokine

Fig. 4. Effects of XFBD on inflammatory response in lung tissue of LPS-induced ALI model mice. (A) Wet/dry ratio. (B–G) TNF-α, IL-1β, IL-6, COX-2, MPO andMCP-1 levels in lung tissue. Data are shown as mean \pm SD by ANOVA. n = 5. $^{\#}p$ < 0.05, $^{\#}p$ < 0.01 vs control group, $^{\ast}p$ < 0.05, $^{\ast}p$ < 0.01 vs LPS group.

Fig. 5. Effects of XFBD on inflammatory response in bronchoalveolar lavage fluid (BALF) of LPS-induced ALI model mice. (A) Protein concentrations in BALF. (B–D) TNF-α, IL-1β, IL-6 levels in BALF. Data are shown as mean ± SD by ANOVA. n = 5. #p *<* 0.05, ##p *<* 0.01 vs control group, *p *<* 0.05, **p *<* 0.01 vs LPS group.

receptor binding ([Fig. 2](#page-6-0)C). The PPI network is interrelated for visualizing the role of diverse essential proteins in diseases, and targets with a higher degree have a more significant impact on central associations ([Zou et al., 2020](#page-13-0)). The 314 targets were screened by twice the median degree, and 34 hub targets were identified: SRC, TP53, PIK3R1, STAT3, MAPK3, HSP90AA1, GRB2, MAPK1, PIK3CA, AKT1, HRAS, RELA, PTPN11, CTNNB1, EGFR, LYN, JAK2, JUN, LCK, CREBBP, VEGFA, ESR1, MAPK8, HDAC1, STAT1, MAPK14, IL6, PTK2, JAK1, IL2, CCND1, RB1, NFKBIA, and TNF ([Fig. 2](#page-6-0)D). KEGG pathway enrichment analysis showed that the NF-κB pathway plays an important role in ALI and the PPI network revealed that the RELA (P65) gene occupies a central position in the composite target. RelA is a subunit of NF-κB, and upon release of NF-κB from an inhibitory interaction with IκB, the dimer containing RelA and cRel translocates to the nucleus, where it activates the transcription of specific NF-κB target genes. The combination of the two suggests that the NF-κB signaling pathway might be an effective way for XFBD action for treat XFBD-induced ALI. Therefore, the NF-κB pathway was selected for subsequent verification.

Fig. 6. Effects of XFBD on pathological changes to lung tissue in LPS-induced ALI model mice revealed by Hematoxylin and eosin Staining. (A) Serial sections of lung tissues were stained with H&E Scale bar = 100 μ m (magnification: x200). (B) Statistical results of lung pathological damage. Data are shown as mean \pm SD by ANOVA. n = 3. ##p *<* 0.01 vs control group, **p *<* 0.01 vs LPS group.

Fig. 7. Effects of XFBD on the expression of phosphorylated κB inhibits protein kinases (p-IKK), phosphorylated nucleus factor-κB (p–NF–κB) p65, and inducible nitric oxide synthase (iNOS) protein in LPS-induced ALI model mice. (A) Protein expression levels of p-IKK was determined by immunohistochemistry. (B) Protein expression levels of p–NF–κB p65 was determined by immunohistochemistry. (C) Protein expression levels of iNOS was determined by immunohistochemistry. Scale bar = 50 μm (magnification: x200). (D) Results were expressed of p–NF–κB p65. (E) Results were expressed of p–NF–κB p65. (F) Results were expressed of p–NF–κB p65. Data are shown as mean ± SD by ANOVA. n = 3. ##p *<* 0.01 vs control group, *p *<* 0.05, **p *<* 0.01 vs LPS group.

3.4. Effect of XFBD on LPS-stimulated inflammatory cytokines in RAW264.7 cells

The XFBD toxicity test showed that 0–200 μg/mL of XFBD had no significant effect [\(Fig. 3](#page-7-0)A). We examined the effect of XFBD on LPSstimulated inflammatory cytokines. After LPS stimulation, cellular NO, TNF- α , IL-6, and IL-1 β concentrations were significantly increased and IL-10 concentrations were decreased, indicating that cells in the LPS group exhibited severe inflammatory damage. XFBD can modulate these factors to reduce inflammatory damage. Moreover, the therapeutic effect of XFBD was found to be dose-dependent [\(Fig. 3](#page-7-0)B–F).

3.5. Effects of XFBD on W/D ratio of lung tissue in ALI model

The lung W/D ratio directly responds to the degree of pulmonary edema. As shown in [Figs. 4A and 6](#page-7-0) h after modelling, the lung W/D ratio in the model group increased. Treatment with XFBD (2.6 and 5.2 g/kg) and LHQW (2.3 g/kg) effectively reduced tissue edema.

3.6. Effects of XFBD on pulmonary inflammatory factors in ALI model mice

The levels of TNF- α , MPO, IL-1 β , MCP-1, IL-6, and COX-2 were examined to detect the inflammatory response to XFBD in LPSstimulated mice. The results indicated that TNF-α, MPO, IL-1β, MCP-1, IL-6, and COX-2 levels were notably increased in the model group. However, the increments were suppressed afte XFBD (1.3, 2.6, and 5.2 g/kg) and LHQW (2.3 g/kg) administration [\(Fig. 4](#page-7-0)B–G).

We also detected the protein concentration and inflammatory factors in mouse BALF. The results showed that the protein concentration, TNFα, IL-1β, and IL-6 content ([Fig. 5A](#page-8-0)–D) in BALF of model group mice increased, while XFBD (1.3, 2.6 and 5.2 g/kg) and LHQW alleviated these increased. These results indicate that XFBD significantly attenuated inflammatory damage in the lungs.

3.7. Effects of XFBD on pathological lung tissue in ALI model mice

We then examined the lung sections. Pathological damage, such as inflammatory cell infiltration, alveolar wall thickening, and alveolar destruction, was observed in the stained areas of the model group. However, treatment with XFBD (2.6 and 5.2 g/kg) and LHQW (2.3 g/kg) alleviated LPS-induced pathology damages [\(Fig. 6](#page-8-0)).

3.8. Effects of XFBD on the protein content of p-IKK, p–*NF*–*κB p65, and iNOS protein in ALI model mice*

Previous results have indicated that the NF-κB pathway is a crucial pathway for XFBD in ALI treatment. Therefore, we performed immunohistochemistry to investigate the levels of p-IKK, p–NF–κB p65 and iNOS. The results showed that more positive nuclear p-IKK, p–NF–κB p65 and iNOS staining was detected in LPS-induced mouse lung tissue (Fig. 7). However, the number of the above-mentioned positive cells decreased by XFBD (2.6 and 5.2 g/kg) and LHQW (2.3 g/kg) administration.

We revalidated the NF-κB pathway at the cellular level. As shown in [Fig. 8](#page-10-0), both immunofluorescence and western blotting results indicated that the inhibitory effect of XFBD on the NF-κB pathway was similar to that of BAY 11–7082, and they were both able to inhibit the protein levels of p–NF–κB and COX-2 in the model group. These results confirm that XFBD can alleviate ALI in mice by inhibiting the NF-κB pathway.

Fig. 8. Effect of XFBD on the expression of p–NF–κB p65 and COX-2 protein in LPS-induced RAW264.7 cells. (A) p–NF–κB p65 protein was determined by immunofluorescence staining. Scale bar = 100 μm. (B) Results were expressed of p–NF–κB p65. (C) Expression levels of p–NF–κB p65, NF-κB p65 and COX-2 were determined by western blotting. (D) Results were expressed as the ratios of p–NF–κB p65/NF-κB p65 and COX-2/β-actin, respectively. Data are shown as mean ± SD by ANOVA. n = 3. #p *<* 0.05, ##p *<* 0.01 vs control group, *p *<* 0.05, **p *<* 0.01 vs LPS group.

4. Discussion

The complexity of the herbal components that comprise XFBD complicate investigations into its active chemical components and their associated mechanisms of action. UPLC-Q/TOF-MS has the characteristics of high separation efficiency, fast scanning speed, high resolution, and high sensitivity and can rapidly characterize compounds in herbal medicines with accurate molecular mass and $MSⁿ$ multi-level mass spectrometry information ([Chang et al., 2021;](#page-12-0) [He et al., 2021](#page-12-0)). In this study, 113 chemical components of XFBD were analyzed using UPLC-Q/TOF-MS. Among them, there were 23 compounds from *Glycyrrhizae Radix et Rhizoma*, 20 from *Ephedrae Herba*, 16 from *Verbenae Herba*, 16 from *Polygoni Cuspidati Rhizoma et Radix*, 12 from *Coicis Semen*, 10 from *Citri Grandis Exocarpium*, 8 from *Pogostemonis Herba*, 7 from *Armeniacae Semen Amarum*, 6 from *Descurainiae Semen Lepidii Semen*, 5 from *Atractylodis Rhizoma*, 5 from *Artemisia Annua Herba*, and 4 from *Phragmitis Rhizoma*. Some active components of *Glycyrrhizae Radix et Rhizoma, Polygoni Cuspidati Rhizoma et Radix, Verbenae Herba,* and *Ephedrae Herba* have been found to exhibit anti-inflammatory properties. For example, ephedrine (7) from *Ephedrae Herba* contributes to immune homeostasis by balancing the production of inflammatory cytokines in TLR4 signaling ([Zheng et al., 2012](#page-13-0)). Naringin (59) is an active component of *Citri Grandis Exocarpium* that alleviates pathological lung damage and tissue edema in ALI mice ([Liu et al., 2011](#page-12-0)). Glycyrrhizic acid (99) is the main active ingredient of *Glycyrrhizae Radix et Rhizoma*, which can reduce lung inflammation by inhibiting the NF-κB protein ([Liu et al., 2021\)](#page-12-0). Amygdalin (19), an active component of *Armeniacae Semen Amarum* can reduce ALI damage in mice by inhibiting NF-κB and NLRP3 inflammatory bodies ([Zhang et al., 2017](#page-13-0)). Treatment with polydatin (41), a primary active component of *Polygoni Cuspidati Rhizoma et Radix*, can reduce total cell number in BALF and improves cell permeability [\(Q. Jiang et al., 2015](#page-12-0)). In particular, polydatin exerts an anti-inflammatory effect on ALI by inhibiting the TLR4/MyD88/NF-κB p65 pathway ([Zou et al., 2020](#page-13-0)). Verbenalin (26), bioactive compound identified in *Verbenae Herba*, also show notable anti-inflammatory effects in ALI [\(Yuan et al., 2018\)](#page-13-0). Among the 113 compounds identified, 46 have been reported to possess anti-inflammatory activity.

Network pharmacology predictions were made based on the analysis of 113 components obtained from XFBD. The results revealed that 314 genes were mainly enriched in disease and biological pathway, such as those in cancers, hepatitis, and toxoplasmosis and the NF-κB, AGE-RAGE, and p53 signaling pathways, respectively. GO analysis revealed that the effects of XFBD may involve many biological processes, including protein kinase activity, leukocyte differentiation, cytokine

Fig. 9. XFBD alleviates ALI by inhibiting the NF-κB pathway.

receptor combination, and transcription factor binding, with many of these affecting inflammations. PPI network analysis revealed that RELA, the nuclear transcription factor p65 regulatory gene, has a high degree of value, and controls the expression of NF-κB p65 protein ([Wang et al.,](#page-13-0) [2021;](#page-13-0) [X. Jiang et al., 2015\)](#page-12-0). After integrating these results, we identified RELA, NFKBIA, TNF and IL6 as highly relevant targets in inflammation pathways.

Network pharmacology predicts methods were employed to predict and validate the mechanism of action and relevant pathways associated with XFBD for treating ALI both in vivo and *in vitro*. XFBD markedly improved lung morphology, inhibited pulmonary edema formation, and prevented inflammatory cells filtration into the lung tissue, which also significantly inhibited MPO, COX-2, and MCP-1 production in the lung tissue induced by LPS and reduced the inflammatory factor content in BALF. In addition, we found that XFBD treatment effectively inhibited the LPS-stimulated activation of p-IKK, p–NF–κB p65, and COX-2. NF-κB is a well-known transcription factor related to inflammation, oxidative stress, and apoptosis. As a family of transcription factor proteins, NF-κB comprises 5 subunits: Rel, p65, RelB, p50, and p52 [\(Luan et al., 2016](#page-12-0)). It usually combines with its inhibitor IκB in the form of dimeric subunits (p65 and p50) to form a trimer. When cells are stimulated by inflammation, I_KB kinase changes from an inactive state to an active state, catalyzing the phosphorylation of IκB protein and releasing the NF-κB

protein ([Jing et al., 2015](#page-12-0)). NF-κB enters the nucleus, thereby initiating downstream IL-6, TNF-α, COX-2, and other inflammatory factors ([Zhang](#page-13-0) [et al., 2017](#page-13-0)) (Fig. 9). In our study, we predicted that XFBD could inhibit the NF-κB pathway to alleviate lung injury. We also demonstrated that XFBD can inhibit the activity of κB kinase and reduce the release of NF-κB protein from IκB protein, thereby inhibiting the function of NF-κB protein and reducing inflammatory damage.

Although some of the 113 components analyzed have been confirmed to exhibit pharmacological properties such as antiinflammatory and anti-fibrosis effects, this study did not independently verify the efficacy of the chemical components of XFBD for treating ALI. In the future, we will verify the efficacy of specific chemical components and explore their mechanisms of action. We will also evaluate the efficacy of pairing of different components to verify efficiency and efficacy of the formulation.

5. Conclusion

In this study, 113 chemical components were identified from XuanfeiBaidu Prescription, and the NF-κB signaling pathway was predicted by network pharmacology analysis of chemical components to be an effective way for XFBD to treat acute lung injury. Animal experiments and cell experiments confirmed that XFBD can reduce the lung injury caused by ALI by inhibiting the NF-κB pathway.

Ethics approval and consent to participate

All experimental procedures were approved by the Animal Care and Use Committee of Tianjin University of Traditional Chinese Medicine (authorization number: TCM-LAEC2021186).

Consent for publication

All authors agree to publish this article.

Availability of data and materials

The data analyzed in this study can be obtained from the corresponding author upon reasonable request.

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CRediT authorship contribution statement

Yanru Zhu: Formal analysis, conducted the experiments and analyses, drafted the manuscript, All authors approved the final manuscript. **Lifei Luo:** Formal analysis, and, Data curation, contributed to formal analysis and data curation, All authors approved the final manuscript. **Meng Zhang:** Formal analysis, and, Data curation, contributed to formal analysis and data curation, All authors approved the final manuscript. **Xinbo Song:** provided the experimental platform, All authors approved the final manuscript. **Ping Wang:** provided the experimental platform, All authors approved the final manuscript. **Han Zhang:** provided the experimental platform, All authors approved the final manuscript. **Jingze Zhang:** designed this study, revised the manuscript. All authors approved the final manuscript. **Dailin Liu:** designed this study, revised the manuscript, All authors approved the final manuscript.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

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Abbreviations

IL-10 interleukin-10 **iNOS** inducible nitric oxide synthase **KEGG** Kyoto Encyclopedia of Genes and Genomes **LPS** Lipopolysaccharide **MCP-1** monocyte chemotactic protein 1 **MPO** myeloperoxidase **NF-κB** nuclear factor kappaB **NO** nitric oxide **PPI protein-protein interaction TCM** traditional Chinese medicine **TNF-α** tumor necrosis factor-α **UPLC-Q/TOF-MS** ultra-performance liquid chromatography-tandem quadrupole time-of-flight mass spectrometry **XFBD** Xuanfei Baidu Formula

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