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IFP35 aggravates *Staphylococcus aureus* infection by promoting Nrf2-regulated ferroptosis



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HIGHLIGHTS

- Interferon-induced protein 35 (IFP35) levels increased significantly after staphylococcus aureus (SA) infection.
 IFP35 deficiency protected against SA-induced lung damage in mice.
- Ferroptosis occurred and led to lung injury after SA infection, which was ameliorated by IFP35 deletion.
- IFP35 aggravated SA-induced ferroptosis and tissue injury by enhancing K48-linked ubiquitination and degradation of Nrf2.

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GRAPHICAL ABSTRACT



ABSTRACT

Introduction: Serious *Staphylococcus aureus* (SA) infection is one of the most life-threatening diseases. Interferon-induced protein 35 (IFP35) is a pleiotropic factor that participates in multiple biological functions, however, its biological role in SA infection is not fully understood. Ferroptosis is a new type of regulated cell death driven by the accretion of free iron and toxic lipid peroxides and plays critical roles in tissue damage. Whether ferroptosis is involved in SA-induced immunopathology and its regulatory mechanisms remain unknown.

Objectives: We aimed to determine the role and underlying mechanisms of IFP35 in SA-induced lung infections.

Methods: SA infection models were established using wild-type (WT) and IFP35 knockout (*Ifp35^{-/-}*) mice or macrophages. Histological analysis was performed to assess lung injury. Quantitative real-time PCR, western blotting, flow cytometry, and confocal microscopy were performed to detect ferroptosis. Co-IP and immunofluorescence were used to elucidate the molecular regulatory mechanisms.

Results: We found that IFP35 levels increased in the macrophages and lung tissue of SA-infected mice.

Abbreviations: IFP35, interferon-induced protein 35; SA, staphylococcus aureus; WT, wild-type; ALI, acute lung injury; NMI, N-myc and STAT-interacting protein; BMDMs, bone marrow-derived macrophages; Nrf2, nuclear factor E2 related factor 2; Gpx4, glutathione peroxidase 4; GSH, glutathione; DAMPs, damage associated molecular patterns; MOI, multiplicity of infection; IL-6, interleukin- 6; TNF- α , tumor necrosis factor α ; LDH, lactate dehydrogenase; Fer-1, ferrostatin-1; Ptgs2, prostaglandin-endoperoxide synthase 2; ROS, reactive oxygen species; PIH, pyridoxal isonicotinoyl hydrazine; MDA, malondialdehyde; SLC7A11, recombinant solute carrier family 7, Member 11; BALF, bronchoalveolar lavage fluid; CHX, cycloheximide; CHQ, chloroquine; Keap1, kelch-like ECH-associated protein 1; LPO, lipid peroxide; Ub, ubiquitin.

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IFP35 deficiency protected against SA-induced lung damage in mice. Moreover, ferroptosis occurred and contributed to lung injury after SA infection, which was ameliorated by IFP35 deficiency. Mechanically, IFP35 facilitated the ubiquitination and degradation of nuclear factor E2-related factor 2 (Nrf2), aggravating SA-induced ferroptosis and lung injury.

Conclusions: Our data demonstrate that IFP35 promotes ferroptosis by facilitating the ubiquitination and degradation of Nrf2 to exacerbate SA infection. Targeting IFP35 may be a promising approach for treating infectious diseases caused by SA.

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Introduction

Staphylococcus aureus (SA) is a gram-positive coccus that can cause life-threatening diseases, such as pneumonia and other infections. The invasion of the lungs by SA significantly contributes to acute lung injury (ALI) and acute respiratory distress syndrome [1]. Although antibiotics can alleviate SA infections, the emergence of new antibiotic-resistant bacterial strains has greatly increased the mortality rate associated with these infections [2]. Hence, besides the development of new antibiotics, alternative and/or adjunctive treatments are urgently needed.

Interferon-induced protein 35 (IFP35) family proteins, including N-myc and STAT-interacting protein (NMI), play vital roles in antivirus responses [3,4]. Moreover, IFP35 and NMI act as damageassociated molecular patterns (DAMPs) that play critical roles in amplifying inflammation. IFP35 deletion alleviated the inflammatory response and increased the survival rate in an LPS-induced sepsis shock mouse model [5]. Several studies have shown that IFP35 is also involved in multiple inflammatory diseases, including sepsis, liver injury, lupus nephritis, and multiple sclerosis [5–8]. A recent study identified IFP35 as a biomarker and therapeutic target in mice infected by SARS-CoV-2 or influenza virus. Neutralizing antibodies against IFP35 significantly reduced lung injury and mortality in infected mice [9]. Although the function of IFP35 in innate immunity is well known, its pathological roles and molecular regulatory mechanisms during bacterial infection, particularly SA infection, remain poorly understood.

Ferroptosis is a novel form of programmed cell death mediated by excessive levels of free iron and lipid peroxides [10]. Ferroptosis is involved in various diseases, including tumors, neurodegenerative diseases, ischemic reperfusion injury, and autoimmune diseases [11–14]. Ferroptotic cell death releases DAMPs and alarm molecules that further amplify the inflammatory response. Ferroptosis is highly immunogenic, thus the inhibition of ferroptosis has significant anti-inflammatory effects [15]. Ferroptosis is closely associated with bacterial infections. Mycobacterium tuberculosis can induce ferroptosis in macrophages, which promotes bacterial spread, and exacerbates tissue necrosis [16]. Pseuarachidonic domonas aeruginosa oxidizes acidphosphatidylethanolamine by secreting lipoxygenase to induce ferroptosis in human bronchial epithelial cells [17]. SA induces lipid peroxidation in the lung of cystic fibrosis mice model [18]. In addition, ferrous iron levels increase in SA-stimulated macrophages, which are effective in defending against SA invasion by inducing ferroptosis-like bacterial death [19]. However, whether SA-infected cells undergo ferroptosis is unclear, and if so, the contribution of SA-induced ferroptosis to tissue damage (particularly in lung tissue), remains largely unknown.

Nuclear factor erythroid 2-related factor 2 (Nrf2) is a transcription factor that plays a crucial role in the cellular defence against oxidative stress. Several studies have shown that Nrf2 can regulate ferroptosis in various ways. For example, Nrf2 binds to the antioxidant response element in promoter regions of target genes involved in antioxidant defence, including glutathione peroxidase 4 (GPX4), recombinant solute carrier family 7 member 11 (SLC7A11), heme oxygenase-1 and NAD(P)H quinone oxidoreductase 1. These genes encode proteins that scavenge ROS and detoxify electrophiles [20]. Furthermore, Nrf2 reduces the iron uptake by downregulating the expression of transferrin receptor 1 and divalent metal transporter 1, both of which are involved in iron uptake [21]. Nrf2 activation also enhances glutathione synthesis (GSH) by upregulating the expression of glutamate-cysteine ligase, the ratelimiting enzyme in GSH biosynthesis [22]. Moreover, Nrf2 alleviates ferroptosis-associated ALI and diabetic nephropathy [23–25]. Although the roles of Nrf2 in ferroptosis-mediated pathophysiology have been extensively demonstrated, its roles in SAmediated immunopathology and the possible mechanisms governing Nrf2 are still largely unknown.

In this study, we found that IFP35 deletion ameliorated lung injury. Furthermore, ferroptosis was induced and contributed to lung injury in mice after SA infection, which was mitigated by IFP35 deficiency. Mechanistically, IFP35 interacted with Nrf2 to promote its ubiquitination and degradation, facilitating SAinduced ferroptosis and lung injury. Our data reveal that IFP35 promotes SA-induced immunopathology in a ferroptosis-related manner, indicating that new treatments for targeting IFP35 or ferroptosis are promising candidates for SA infection.

Materials and methods

Cell culture

Bone marrow-derived macrophages (BMDMs) were established as previously described [26]. BMDMs were cultured in RPMI 1640 medium (Biological Industries) containing 10 % FBS (Biological Industries), 100 U/mL of penicillin, 100 µg/mL of streptomycin and 20 ng/ml of mouse M-CSF at 37 °C with 5 % CO₂ for 5 days. CD11b⁺F4/80⁺ cells were identified as macrophages. Flow cytometry confirmed that the macrophage purity reached over 90 %. HEK293T cells were originally obtained from American Type Culture Collection. The cells were cultured in DMEM media containing 10 % FBS, 100U/mL of penicillin and 100 µg/mL of streptomycin at 37 °C with 5 % CO₂.

Bacterial culture

SA was cultured aerobically in Tryptic Soy Broth (TSB) medium at 37 °C on a shaking incubator for 14–16 h. Bacteria in logarithmic growth phase were harvested, and washed twice with sterilized PBS by centrifugation at 3000 g for 10 min and finally resuspended in PBS. Growth curves were established by measuring OD600. Bacterial numbers were quantified according to the growth curve and verified with colony-forming unit (CFU) assays.

Quantitative real-time PCR

Total RNA was extracted from cells with an RNA-Quick Purification Kit (ES Science). Then, approximately 200 ng of total mRNA was reverse-transcribed into complementary DNA (cDNA) using PrimeScriptTM RT Master Mix (Takara). qRT-PCR was carried out with TB Green[®] Premix Ex TaqTM (TaKaRa) in the CFX96 Touch Real-Time PCR Detection System (Bio-Rad). After normalizing to internal control (GAPDH) expression, data were determined by the comparative Ct method ($2^{-\Delta\Delta Ct}$). Primer sequences used for qPCR were shown in Supplementary Table 1.

Intracellular ROS, lipid peroxidation and Fe²⁺ detection

 5×10^5 BMDMs were plated in a 12-well plate and pretreated with or without the indicated inhibitors, then cells were stimulated with SA at a multiplicity of infection (MOI) of 200 for 3 h. After treatment, cells were incubated with 10 µM of 2', 7'-dichloro fluorescein-diacetate (DCFH-DA) (Beyotime), 10 µM of LiperFlou (Dojingo) and 1 µM of Ferro orange (Dojingo) for different times according to manuscript instructions respectively. Olympus FV3000 confocal microscope was used to observe and record the results. The excitation and emission wavelengths of DCF (oxidized DCFH-DA by intracellular ROS), oxidized Liperfluo and FerroOrange were 488 and 510 nm, 488 and 510 nm, 561 and 572 nm, respectively.

Ethics statement

All animal experiments were approved by the Animal Care and Use Committee of the Second Affiliated Hospital, Zhejiang University School of Medicine (Approval No. AIRB-2022–091).

Animal experimental design

lfp35^{-/-} mice (C57BL/6 background) were kindly provided by Dr Ying-Fang Liu (Sun Yat-sen University School of Medicine). *Nrf2^{-/-}* mice were obtained from the ShanghaiModel Organisms and agematched wild-type C57BL/6 mice were purchased from the Animal Center of Slaccas (Shanghai, China). Female mice were used in experiments. Mice were intraperitoneally injected with ferrostatin-1 (Fer-1) (12.5 µmol/kg) or DMSO solvent control with the same volume and concentration for 1 h prior to infection. Then the mice were anaesthetized by inhalation with 2 % isoflurane and infected intratracheally with SA (1 × 10⁸ CFU) to establish the murine lung infection model. In addition, control ones were administered at equal PBS volume. 24 h later, mice were sacrificed, and samples including bronchoalveolar lavage fluid (BALF) and lung tissue were taken for analysis. For survival study, mice were treated intratracheally with a lethal dose of SA (4 × 10⁸ CFU).

Iron, GSH/GSSG and malondialdehyde (MDA) assays

Lung tissues were washed in cold PBS and homogenized on ice using a Dounce homogenizer, centrifuged at 12000 rpm for 10 min. The supernatants were collected for analysis. Intracellular ferrous iron, GSH/GSSG and MDA were determined using the iron assay kit (Abcam), GSH and GSSG assay kit (Beyotime) and MDA assay kit (Beyotime), respectively. The absorbance at 593, 532 and 412 nm corresponding to iron, GSH/GSSG and MDA levels were determined using a microplate reader (SpectraMax 5).

Histological analysis

The entire lungs of the mice were fixed with 4 % polyformaldehyde overnight at room temperature. Then tissues were embedded in paraffin, cut into 4 μ m sections and subjected to hematoxylin and eosin staining. Images were observed using an Olympus BX53 inverted microscope.

Plasmid transfections, immunoblot and immunoprecipitation (IP)

Plasmid transfection was performed using Lipofectamine 3000 (Invitrogen). For some experiments, cells were treated with proteasome inhibitor MG132 (MedChemExpress), protein synthesis inhibitor cycloheximide (CHX) (MedChemExpress) or lysosome inhibitor chloroquine (CHO) (MedChemExpress) 24–36 h after transfection. Total cell lysates were obtained using WB and IP lysis buffer (Beyotime) supplemented with 1 mM PMSF (Sigma-Aldrich). Immunoblot analysis was performed with indicated antibodies as previously described [27]. For IP, extracts were incubated at 4 °C overnight with anti-Flag M2 magnetic beads or anti-HA magnetic beads. Beads were washed with 1 %-Triton buffer, eluted with $1 \times SDS$ loading buffer, and then operated as immunoblot analysis. The following antibodies were used: GPX4 (Abcam, ab125066), SLC7A11 (Abcam, ab175186), IFP35 (Abnova, H00003430-D01P), Nrf2 (Proteintech, 16396-1-AP), anti-Flag antibody (Beyotime, AF5051), anti-HA antibody (Beyotime, AF2305), anti-Myc antibody (Beyotime, AF2864).

Statistical analysis

Prism 8.0 software (GraphPad, La Jolla, CA, USA) was used for analyzing. Quantitative data were expressed as the means \pm SEM. Unpaired student's *t*-test was used for two group comparisons and one-way ANOVA was used for multiple group comparisons. Survival curve analysis was performed using the log rank test. *p* < 0.05 was defined as significant.

Results

IFP35 expression is elevated and its deficiency alleviates lung injury after SA infection

To investigate the potential molecular mechanisms underlying SA infection, we performed a microarray analysis of human monocyte-derived macrophages infected with SA using microarray data from the Gene Expression Omnibus (GEO). We found that the mRNA expression of IFP35 was significantly increased in SAinfected macrophages (GEO dataset, GDS4931) (Fig. 1a). Furthermore, we observed increased IFP35 staining intensity levels in lung tissue of SA-infected mice (Fig. 1b). Upregulated IFP35 mRNA and protein levels were also confirmed in BMDMs infected with SA (Fig. 1c-d). To clarify the role of IFP35 in SA infection, WT and Ifp35^{-/-} mice were intratracheally injected with a lethal dose of SA, and the *Ifp* $35^{-/-}$ mice showed a higher survival rate (Fig. 1e). Moreover, a lower expression of interleukin-6 (IL-6) and tumor necrosis factor α (TNF- α) in the BALF and a lower bacterial load in lung tissue of *Ifp* $35^{-/-}$ mice were observed (Fig. 1f-h). Similarly, significant attenuation of lung injury was observed in *Ifp*35^{-/-} mice compared to that in WT mice after SA infection, according to the histological analysis (Fig. 1i). These results suggested that IFP35 aggravated SA infection in vivo.

Ferroptosis occurred in vivo and in vitro after SA infection

Recent studies have found that ferroptosis has a significant effect on bacterial infection. Upon infection with SA, ferrous iron and lipid peroxidation levels increase in macrophages, suggesting the possible occurrence of ferroptosis [18,19]. Therefore, we infected mice and BMDMs with SA and performed a series of



Fig 1. IFP35 expression is elevated and its deficiency alleviates lung injury after SA infection. (a) Expression of IFP35 in monocyte-derived human macrophages that phagocytosed SA *in vitro* was analyzed. The raw data (GDS4931) derived from Gene Expression Omnibus datasets. (b) Mice were *i.t.* with a sublethal dose $(1 \times 10^8 \text{ CFU}, n = 3 \text{ mice/group})$ of SA for 24 h. IFP35 staining intensity levels in lung tissue were assessed. (c-d) BMDMs were infected with SA (MOI = 200) for 4 h, the gene and protein levels of IFP35 were detected. (e) WT and *lfp35^{-/-}* mice were *i.t.* with a lethal dose $(4 \times 10^8 \text{ CFU}, n = 10 \text{ mice/group})$ of SA for 5 days, mice survival rate was observed. (f-i) WT and *lfp35^{-/-}* mice were *i.t.* uith a lethal dose $(4 \times 10^8 \text{ CFU}, n = 10 \text{ mice/group})$ of SA for 5 days, mice survival rate was observed. (f-i) WT and *lfp35^{-/-}* mice were *i.t.* with a sublethal dose $(1 \times 10^8 \text{ CFU}, n = 4-6 \text{ mice/group})$ of SA for 24 h. (f-g) Concentrations of IL-6 and TNF- α levels in the BALF were measured. (h) Pulmoary bacterial load in lung tissue was determined. (i) Representative H&E staining images of merged lung sections were observed. (scale bars, 200 µm). Data in bar graphs and scattered dot plots are presented as mean \pm SEM, **p* < 0.05; ***p* < 0.001; ****p* < 0.0001.

experiments to evaluate ferroptosis at organ and cellular levels. As expected, higher iron levels were detected in lung tissue of infected mice than in those of uninfected mice (Fig. 2a). The changes in the redox status and in the levels of malondialdehyde (MDA), a major lipid peroxidation product, were assessed. Decreased GSH/GSSG ratios (Fig. 2b) and increased MDA levels (Fig. 2c) were observed in lung tissue after SA infection. Furthermore, the protein levels of ferroptosis-related molecules, including GPX4 and SLC7A11, were decreased (Fig. 2d) in lung tissue of infected mice. Notably, these ferroptosis-related changes in infected mice were significantly inhibited by ferostatin-1 (Fer-1), a well-characterized ferroptosis inhibitor, suggesting that ferroptosis is involved in SA-induced pulmonary infections. Monocytes/macrophages and neutrophils are vital inflammatory cells in the alveoli after SA infection, where ferroptosis may occur and affect pathogenesis. We found that SA infection triggered an increase in both the levels of



Fig 2. Ferroptosis occurred in lung tissues of SA-infected mice. WT mice were *i.p.* with the same volume of Fer-1 or DMSO at the same concentration (12.5 μ mol/kg), and 1 h later, *i.t.* with a sublethal dose (1 × 10⁸ CFU, n = 3-5 mice/group) of SA. Lung tissues were harvested at 24 h post-infection. (a-c) Concentrations of iron, GSH/GSSG, and MDA were detected. (d) GPX4 and SLC7A11 proteins levels were determined. (e) The numbers of CD45⁺CD11b⁺Ly6C⁺Ly6G⁻ monocytes/macrophages were counted. (f) LPO levels in CD45⁺CD11b⁺Ly6C⁺Ly6G⁺ monocytes/macrophages were analyzed. (g) The numbers of CD45⁺CD11b⁺Ly6C⁺Ly6G⁺ neutrophils were counted. (h) LPO levels in CD45⁺CD11b⁺Ly6C⁺Ly6G⁺ neutrophil subsets were analyzed. (i) The mitochondrial morphology of mouse lung tissue was observed. (scale bars, 0.5 μ m). Data in scattered dot plots are presented as mean ± SEM, **p* < 0.001; ****p* < 0.001.

CD11b⁺Ly6C⁺Ly6C⁻ monocytes/macrophages and CD11b⁺Ly6C⁺-Ly6G⁺ neutrophils, as well as in their lipid peroxidation levels. These alterations were suppressed by pretreating the infected mice with Fer-1 (Fig. 2e-h). Finally, fewer mitochondrial cristae were observed in lung tissue after SA infection, which represents a remarkable morphological change occurring during ferroptosis (Fig. 2i). These results suggested that SA induced ferroptosis in lung tissue of mice.

Next, we examined the *in vitro* SA-induced cell death by infecting BMDMs with SA at different MOIs. Cell death was assessed by detecting the release of lactate dehydrogenase (LDH) into the cell supernatants. The cell death of the BMDMs infected with SA increased in an MOI-dependent manner (Fig. S1a). To investigate whether SA induced cell death via ferroptosis, the cells were pretreated with different concentrations of Fer-1. Fer-1 could partially inhibit cell death at a concentration of 10 μ M (Fig. S1b). A remarkable decrease in *Gpx4*expression and an increase in prostaglandinendoperoxide synthase (*Ptgs2*) expression were observed in BMDMs infected with SA (Fig. S1c-d). In addition, the levels of ferroptosis hallmarks, including ROS, lipid peroxide, and free iron, increased after SA infection, as shown by the intracellular staining results (Fig. S1e). Notably, these ferroptosis-related changes were partially abrogated by the pretreatment of BMDMs with Fer-1 (Fig. S1c-e). Transmission electron microscopy results revealed that the mitochondria in SA-infected BMDMs showed key ferroptosis features, including shrunken mitochondria, an increased membrane density, and reduced or even lost mitochondrial cristae. As expected, pretreatment with Fer-1 significantly reduced mitochondrial damage in SA-infected BMDMs (Fig. S1f). To determine whether SA-induced cell death was iron-dependent, we pretreated the BMDMs with pyridoxal isonicotinoyl hydrazone (PIH), an iron chelator, which resulted in reduced cell death (Fig. S1g) and *Ptgs2* expression (Fig. S1h). Collectively, these observations suggested that SA triggers ferroptosis in macrophages.

Inhibition of ferroptosis reduces the bacterial load and alleviates pulmonary pathological changes in SA-infected mice

Ferroptosis is a form of programmed cell death with strong immunogenicity and is considered as a target for therapeutic intervention in several inflammatory diseases [28]. Next, we determined the effect of ferroptosis inhibition on SA-induced lung inflammation and injury. The mice were intraperitoneally administered with Fer-1 (12.5 µmol/kg) 1 h before SA infection. Our data showed that the survival rate of the mice pretreated with Fer-1 increased (Fig. 3a). Pretreatment with Fer-1 also reduced the levels of pro-inflammatory cytokines, including IL-6 and TNF-a, in the BALF of SA-infected mice (Fig. 3b-c). Furthermore, ferroptosis inhibition decreased the bacterial load in SA-infected lung tissues (Fig. 3d). Pulmonary histopathological examination confirmed that pretreatment with Fer-1 relieved SA-induced lung injury, including interstitial congestion and edema, alveolar septal thickening, and infiltration of inflammatory cells into lung parenchyma and alveolar spaces (Fig. 3e).

Effect of IFP35 deletion on SA-induced ferroptosis in vivo and in vitro

As shown above, SA induced cell death and pulmonary immunopathology through ferroptosis. We questioned whether the protective effects of IFP35 deficiency on SA infection could be attributed to reduced ferroptosis. We challenged *Ifp*35^{-/-} and WT mice with SA. As expected, *Ifp*35^{-/-} mice showed lower iron levels (Fig. 4a), higher GSH/GSSG ratios (Fig. 4b), and lower MDA levels (Fig. 4c) in lung tissue compared with WT mice. Moreover, pulmonary GPX4 and SLC7A11 protein levels were significantly higher in *Ifp*35^{-/-} mice after SA infection (Fig. 4d). In addition, the number of CD11b⁺Ly6C⁺Ly6G⁻ monocytes/macrophages and CD11b⁺Ly6C⁺-Ly6G⁺ neutrophils decreased, as did their lipid peroxidation levels, in SA-infected *Ifp*35^{-/-} mice (Fig. 4e-h). These data favored a protective role for IFP35 deletion against SA-induced ferroptosis in lung tissue.

Next, we assessed the effect of IFP35 deficiency on SA-induced ferroptosis *in vitro*. WT and IFP35-knockout BMDMs were infected with bacteria at different MOIs. Data showed that cell death of IFP35-knockout cells at an MOI of 100 or 200 was lower than that of WT cells (Fig. 4i). In addition, increased *Gpx4* expression and decreased *Ptgs2* expression were observed in IFP35-deficient BMDMs (Fig. 4j-k). Intracellular staining showed that IFP35 deficiency reduced levels of key ferroptosis-related markers, including intracellular ROS, lipid peroxides, and iron, after SA infection (Fig. 4l). Collectively, these data demonstrated that IFP35 deficiency ameliorated SA-induced ferroptosis in macrophages.

IFP35 deficiency inhibits ferroptosis through an Nrf2-dependent mechanism

Next, we explored the molecular mechanism by which IFP35 knockout reduced SA-mediated ferroptosis. As shown above, IFP35 deletion enhanced GPX4 and SLC7A11 expression and reduced ROS, lipid peroxides, and iron levels in SA-infected BMDMs. Given the different ways in which Nrf2 regulates ferroptosis, we questioned whether IFP35 regulates SA-mediated ferropto-

sis via Nrf2. IFP35-knockout and WT cells were infected with SA, and we found that the Nrf2 mRNA levels of IFP35-knockout and WT BMDMs did not differ (Fig. 5a); however, the protein levels of IFP35-knockout BMDMs were higher than those of WT BMDMs after SA stimulation (Fig. 5b). To investigate the role of Nrf2 in SAinduced ferroptosis, we treated the BMDMs from WT and Nrf2^{-/-} mice with SA at various MOIs. As expected, the cell death of Nrf2-knockout BMDMs was higher when the cells were infected at an MOI of 100 and 200. This was completely reversed by Fer-1 pretreatment (Fig. 5c). Gpx4 expression decreased and Ptgs2 expression increased in Nrf2-deficient cells following SA infection (Fig. 5d-e). In addition, increased intracellular ROS, lipid peroxides, and iron levels, were observed in SA-treated Nrf2-deficient cells using a confocal microscope (Fig. 5f). The changes in all these ferroptosis-related indicators were also significantly reversed via Fer-1 pretreatment. These findings demonstrated that Nrf2 played an important role in resistance to SA-induced ferroptosis in macrophages. To further clarify whether IFP35 deficiency ameliorates ferroptosis by upregulating Nrf2, we pretreated IFP35-knockout cells with brusatol, a Nrf2-specific inhibitor. Nrf2 inhibition significantly increased cell death and Ptgs2 expression in IFP35-knockout BMDMs, to levels even higher than those of WT cells (Fig. 5gh). Confocal microscopy revealed that Nrf2 suppression significantly increased ROS, lipid peroxides, and iron levels of IFP35knockout cells (Fig. 5i). Taken together, these data indicated that IFP35 deficiency ameliorated ferroptosis by upregulating Nrf2 expression.

IFP35 promotes Nrf2 degradation via K48-linked ubiquitination

Under homeostatic conditions, Nrf2 is rapidly ubiquitinated and degraded by binding to Kelch-like ECH-associated protein 1 (Keap1) in the cytoplasm. Upon exposure to oxidative stress, Nrf2 is activated and separated from Keap1. Activated Nrf2 translocates to the nucleus to promote transcription of antioxidant genes [29]. Considering that IFP35 decreased Nrf2 protein expression but had no effect on the mRNA level, we hypothesized that IFP35 enhanced the degradation of Nrf2. To test this hypothesis, we examined the interaction between IFP35 and Nrf2 in cells. Under confocal microscopy, an enhanced co-localization of IFP35 and Nrf2 was found in SA-infected BMDMs and 293 T cells compared to that of uninfected cells (Fig. 6a-b). The interaction between IFP35 and Nrf2 was also confirmed by co-immunoprecipitation and immunoblot analyses of transfected 293 T cells (Fig. 6c-d). Next, we investigated whether IFP35 promoted Nrf2 degradation by treating cells with a protein synthesis inhibitor (cycloheximide, (CHX)) at different time points. Immunoblot analysis showed that IFP35 enhanced Nrf2 degradation in a time and dose-dependent manner (Fig. 6e-f), and this effect was reversed by treatment with the proteasome inhibitor MG132 rather than with the lysosome inhibitor (chloroquine, (CHQ)) (Fig. 6g). These results suggested that IFP35 promoted Nrf2 degradation through the ubiquitin-proteasome pathway. Ubiquitination is an important step in the proteasome-mediated protein degradation [30]. We examined the effect of IFP35 on Nrf2 ubiquitination and found that IFP35 overexpression increased Nrf2 ubiquitination (Fig. 6h). Lysine 48 (-K48)-linked ubiquitination is required for proteasomal degradation. Thus, we tested the effect of IFP35 on the K48-linked ubiquitination of Nrf2, and observed that IFP35 overexpression increased this parameter (Fig. 6i). Considering the critical role of Keap1 in Nrf2 degradation, we investigated the effect of IFP35 on Keap1 level. Interestingly, IFP35 also interacted with Keap1 in 293 T cells and that IFP35 overexpression increased Keap1 protein levels (Fig. 6j-l), indicating that IFP35 can also promote Nrf2 degradation by regulating the Keap1 level. Collectively, these data demonstrated that IFP35 interacted with Nrf2 and Keap1 and pro-



Fig 3. Ferroptosis inhibition reduces the bacterial load and alleviates pulmonary pathological changes in SA-infected mice. (a) WT mice were *i.t.* with a lethal dose $(4 \times 10^8 \text{ CFU}, n = 6-8 \text{ mice/group})$ of SA for 5 days after being *i.p.* with the same volume of Fer-1 or DMSO at the same concentration (12.5 µmol/kg), 1 h earlier, mice survival rate was observed. (b-e) WT mice were *i.t.* with a sublethal dose $(1 \times 10^8 \text{ CFU}, n = 5-6 \text{ mice/group})$ of SA for 24 h after being *i.p.* with Fer-1 or DMSO (12.5 µmol/kg), 1 h earlier, (b-c) Concentrations of IL-6 and TNF- α levels in the BALF were detected. (d) Pulmonary bacterial loads were measured. (e) Representative H&E staining images of the merged lung sections were observed. (scale bars, 200 µm). Data in scattered dot plots are presented as mean ± SEM, **p* < 0.05; ***p* < 0.01; *****p* < 0.0001.

moted K48-linked ubiquitination and degradation of Nrf2 via the proteasome pathway.

Discussion

Our major findings demonstrated that IFP35 aggravated SA induced lung injury. Ferroptosis occurred and contributed to SAinduced tissue damage. IFP35 promoted SA-induced ferroptosis by modulating Nrf2 stability to facilitate the pathological processes. The serum IFP35 concentration is highly correlated with COVID-19 severity. Additionally, the administration of an anti-IFP35 neutralizing antibody significantly reduced lung injury and mortality in SARS-COVID-2- and influenza-infected mice [9]. Here, we showed for the first time that IFP35 expression increased significantly after SA infection. Our results suggested that *Ifp*35^{-/-} mice exhibited increased survival, reduced bacterial load, and less lung injury, supporting the essential role of IFP35 deficiency in alleviating inflammation and lung injury. IFP35 can promote apoptosis and ROS production to inhibit tumorigenesis [31]. Furthermore, IFP35 promotes tumour growth and lung metastasis during renal cancer progression by inhibiting autophagy induction [32]. Here, IFP35 was functionally significant in executing SA-induced ferroptosis, as IFP35 deficiency ameliorated SA-induced ROS production,

lipid peroxidation, and iron accumulation. These findings confirm the crucial role of IFP35 in facilitating SA-induced lung injury by promoting ferroptosis.

Ferroptosis is a form of programmed cell death that is triggered by iron-dependent lipid peroxidation, resulting in plasma membrane damage. In recent years, emerging reports have suggested that ferroptosis is activated during bacterial infection-related injury in host tissues [33]. In this study, we experimentally demonstrated that ferroptosis was activated after SA infection. Elevated levels of ROS, lipid peroxides, and free iron were detected in SAinfected cells and lung tissues, whereas these effects of SA infection were abrogated by Fer-1. In addition, the lethality, inflammatory response, and lung injury were partially reversed by Fer-1 pretreatment in SA-infected mice. These results indicate that ferroptosis is a potential therapeutic intervention target. Nevertheless, considering that ferroptosis inhibition did not completely block SA-mediated cell death effects, our findings cannot formally exclude intersections with other cell death pathways, such as pyroptosis and necroptosis [34,35].

Nrf2 is a critical cytoprotective factor that regulates antioxidant responses by controlling the expression of genes that eliminate oxidative and electrophilic stresses [36]. It is well established that Nrf2 plays a positive role in reducing iron and ROS levels. Nrf2 tar-



Fig 4. Effect of IFP35 deletion on SA-induced ferroptosisin vivo and in vitro. WT and $lfp35^{-/-}$ mice were *i.t.* with a sublethal dose (1 × 10⁸ CFU, n = 4-5 mice/group) of SA. Lung tissues were harvested at 24 h post-infection. (a-c) Concentration of iron, GSH/GSSG, and MDA were detected. (d) Levels of GPX4 and SLC7A11 proteins were determined. (e) The numbers of CD45⁺CD11b⁺Ly6C⁺Ly6G⁻ monocytes/macrophages were counted. (f) LPO levels in CD45⁺CD11b⁺Ly6C⁺Ly6G⁻ monocytes/macrophages were analyzed. (g) The numbers of CD45⁺CD11b⁺Ly6C⁺Ly6G⁻ neutrophils were counted. (h) LPO levels in CD45⁺CD11b⁺Ly6C⁺Ly6G⁻ monocytes/macrophages were analyzed. (g) The numbers of CD45⁺CD11b⁺Ly6C⁺Ly6G⁻ neutrophils were counted. (h) LPO levels in CD45⁺CD11b⁺Ly6C⁺Ly6G⁻ monocytes/macrophages were analyzed. (g) The numbers of CD45⁺CD11b⁺Ly6C⁺Ly6G⁻ neutrophils were counted. (h) LPO levels in CD45⁺CD11b⁺Ly6C⁺Ly6G⁻ monocytes/macrophages were analyzed. (g) The numbers of CD45⁺CD11b⁺Ly6C⁺Ly6G⁻ neutrophils were counted. (h) LPO levels in CD45⁺CD11b⁺Ly6C⁺Ly6G⁻ monocytes/macrophages were analyzed. (i) WT and IFP35-deficient BMDMs were infected with SA at different MOIs, cytotoxicity was assessed. (j-k) WT and IFP35-deficient BMDMs were infected with SA (MOI = 200) for 4 h, *Gpx4* and *Ptgs2* mRNA expression levels were detected. (l) WT and IFP35-deficient BMDMs were infected with SA (MOI = 200) for 3 h, representative fluorescence images showed the production of ROS, LPO, and Fe²⁺. DCFH-DA staining represented intracellular ROS, Liperfluo staining represented LPO, and FerroOrange staining represented intracellular Re²⁺. (scale bars, 50 µm). Data in bar graphs and scattered dot plots are presented as mean ± SEM, *p < 0.001; ***p < 0.001; ****p < 0.001.



Fig 5. IFP35 deficiency inhibits ferroptosis through an Nrf2-dependent mechanism. (a-b) WT and IFP35-deficient BMDMs were infected with SA (MOI = 200) at different time points, Nrf2 mRNA and protein levels were detected. (c) WT and Nrf2-deficient BMDMs were pretreated with Fer-1 or not and infected with SA (MOI = 200) for 4 h, *Gpx4* and *Ptgs2* mRNA expression levels were detected. (f) WT and Nrf2-deficient BMDMs were pretreated with Fer-1 or not and infected with SA (MOI = 200) for 3 h, representative fluorescence images showed the production of ROS, LPO, and Fe²⁺. DCFH-DA staining represented intracellular ROS, Liperfluo staining represented LPO, and FerroOrange staining represented intracellular Fe²⁺. (scale bars, 50 μ m). (g-h) WT and IFP35-deficient BMDMs were infected with SA (MOI = 200) for 4 h after pretreatment with or without brusatol (40 nM) 1 h earlier, representative fluorescence images showed the production of ROS, LPO, and Fe²⁺. DCFH-DA staining represented in the production of ROS, LPO, and Fe²⁺. DCFH-DA staining represented with SA (MOI = 200) for 4 h after pretreatment with or without brusatol (40 nM) 1 h earlier, (g) Cytotoxicity was determined. (h) *Ptgs2* mRNA expression levels were measured. (i) WT and IFP35-deficient BMDMs were infected with SA (MOI = 200) for 3 h. GNOI = 200) for 4 h after pretreatment with or without brusatol (40 nM) 1 h earlier, representative fluorescence images showed the production of ROS, LPO, and Fe²⁺. DCFH-DA staining represented intracellular ROS, Liperfluo staining represented LPO, and FerroOrange staining represented intracellular Fe²⁺. (scale bars, 50 μ m). Data in bar graphs are presented as mean ± SEM, *p < 0.05; **p < 0.01; ****p < 0.001.



gets several genes that mitigate lipid peroxide formation and ferroptotic cascade [37]. Here, we showed that Nrf2-deficient cells exhibited increased ferroptotic cell death. We also found an increased Nrf2 protein level in IFP35-knockout cells. Nrf2 inhibition significantly enhanced ferroptosis and Ptgs2 expression in IFP35-knockout cells. Our data demonstrated that IFP35-deficient cells inhibited ferroptosis by upregulating Nrf2. Under unstressed conditions, Keap1 binds to Nrf2 in the cytoplasm and promotes its proteasomal degradation [29]. E3 ubiquitin ligase complexes control ubiquitination and proteasomal degradation of Nrf2 [38]. Intracellular IFP35 mediates the ubiquitination of RIG-I, which is involved in innate immunity [39]. Our data showed that IFP35 interacted with Nrf2 and Keap1, promoting the K48-linked ubiquitination and degradation of Nrf2 through the proteasome pathway. Given the numerous ways in which Nrf2 promotes cell survival, it is not surprising that blocking Nrf2 or its downstream targets can reduce the ability of cells to respond to stress and lead to increased cell death, such as pyroptosis and ferroptosis. Although our study focused on the involvement of Nrf2 in SA-induced ferroptosis, we need to further explore the possibility that pyroptosis is involved in this process.

Conclusion

In summary, our study suggested the deleterious effects of IFP35 on immunopathology evoked by SA infection. Ferroptosis was involved in SA-induced pathological processes, and IFP35 deletion reduced SA-mediated ferroptosis. Mechanistic investigations indicated that IFP35 deficiency upregulated Nrf2 by inhibiting its ubiquitination and degradation to reduce the ferroptosis induced by SA. Our study provides novel insights into the pathogenesis of SA infections. The specific targeting of IFP35, or ferroptosis, is a promising strategy for the treatment of diseases associated with SA.

Compliance with Ethics Requirements

All Institutional and National Guidelines for the care and use of animals (fisheries) were followed.

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.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jare.2023.09.042.

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Fig 6. IFP35 promotes Nrf2 degradation by enhancing K48-linked ubiquitination. (a) BMDMs were infected with SA (MOI = 200) for 3 h, and then were fixed and immunostained with Nrf2 and IFP35 antibodies. (b) HEK293T cells were transiently transfected with HA-IFP35 and Flag-Nrf2 for 24 h and then were infected with SA (MOI = 30) for 3 h. Cells were fixed and immunostained with anti-Flag and anti-HA antibodies. (c-d) HEK293T cells were transiently transfected with HA-IFP35 and Flag-Nrf2 or the control plasmid, as indicated. Cell lysates were subjected to IP with anti-HA (c) or anti-Flag (d) antibody, followed by IB analysis with anti-HA or anti-Flag antibody. Proteins in whole cell lysates were used as positive control (input). (e) HEK293T cells were transiently transfected with an HA-IFP35 plasmid or a control plasmid, together with a flag-Nrf2 plasmid for 24 h and then treated with 10 μM CHX for various times. IB images of Nrf2 in cell lysates were shown. (f) HEK293T cells were transfected with a Flag-Nrf2 plasmid together with an increasing number of HA-IFP35 plasmids (0, 0.5, 1, or 2 μg), and then treated with MG132 (10 μM) for 3 h, IB analysis of the cell lysates was shown. (g) HEK293T cells transfected with a Flag-Nrf2 plasmid and an HA-IFP35 plasmid and then treated with MG132 (10 μM) or chloroquine (100 μM) for 3 h, IB analysis of cell lysates from cell lysates was shown. (h-i) HEK293T cells were transiently co-transfected with Myc-ubiquitin (Ub) (h) or Myc-K48 (i), together with HA-IFP35, as indicated. Cell lysates were subjected to IP with an anti-Flag antibody. (j-k) HEK293T cells were transiently co-transfected with Flag-Atter (k) antibody, followed by IB analysis with anti-Flag antibody. (j-k) HEK293T cells were transiently co-transfected with Ha-IFP35, as indicated. Cell lysates were subjected to IP with an anti-Flag antibody. (j-k) HEK293T cells were transiently co-transfected with Flag-Atter (k) antibody, followed by IB analysis with anti-Flag antibody. Proteins in whole cell lysates were used as

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