DR7dA, a novel antioxidant peptide analog, demonstrates antifibrotic activity in pulmonary fibrosis in vivo and in vitro

Lu Cheng¹,², Dan Wang¹,², Bochuan Deng¹, Jieru Li¹, Jiao Zhang¹, Xiaomin Guo¹, Tiantian Yan¹, Xin Yue¹, Yingying An¹, Bangzhi Zhang¹,* Junqiu Xie¹,*

¹Key Laboratory of Preclinical Study for New Drugs of Gansu Province, School of Basic Medical Sciences & Research Unit of Peptide Science, Chinese Academy of Medical Science, 2019RU066, Lanzhou University, Lanzhou 730000, China

²School of Life Sciences, Lanzhou University, Lanzhou 730000, China
a) Running title: DR7dA alleviated PF in vivo and in vitro

b) Corresponding author:

Bangzhi Zhang; Junqiu Xie

Address: School of Basic Medical Sciences, Lanzhou University, 199 Dong Gang West Road, Lanzhou 730000, China

Tel: +86 931 8915522

Fax: +86 931 8911255

E-mail: zhangbz@lzu.edu.cn; xiejq@lzu.edu.cn

c) Number of text pages: 41

Number of Tables: 2

Number of Figures: Main figures -8, Supplementary figures -2

Number of References: 65

Number of words in Abstract: 249

Number of words in Introduction: 528

Number of words in Discussion: 1473

d) Abbreviations

AEC - alveolar epithelial cell

BLM - bleomycin

CAT - catalase

DCFH-DA - 2',7'-dichlorodihydrofluorescein diacetate

ECM - extracellular matrix

FBS - fetal bovine serum
Fmoc - 9-fluorenlymethyloxycarbonyl

GAPDH - glyceraldehyde-3-phosphate dehydrogenase

GSH - glutathione

IL - interleukin

MDA - malondialdehyde

MMP2 - matrix metalloproteinase 2

NAC - N-acetyl-L-cysteine

NOX - NADPH oxidase

OS - oxidative stress

PF - pulmonary fibrosis

ROS - reactive oxygen species

SOD - superoxide dismutase

TGF-β1 - transforming growth factor-β1

TNF - tumor necrosis factor

α-SMA - α-smooth muscle actin

e) Recommended section: 1) Cellular and Molecular

2) Gastrointestinal, Hepatic, Pulmonary, and Renal

3) Drug Discovery and Translation Medicine
Abstract

Pulmonary fibrosis (PF), which is characterized by enhanced extracellular matrix (ECM) deposition, is an interstitial lung disease that lacks an ideal clinical treatment strategy. It has an extremely poor prognosis, with an average survival of 3-5 years after diagnosis. Our previous studies have shown that the antioxidant peptide DR8 (DHNNPQIR-NH₂), which is extracted and purified from rapeseed, can alleviate PF and renal fibrosis. However, natural peptides are easily degraded by proteases in vivo, which limits their potency. We have since synthesized a series of DR8 analogs based on amino acid scanning substitution. DR7dA (DHNNPQ (D-alanine) R-NH₂) is an analog of DR8 in which L-isoleucine (L-Ile) is replaced with D-alanine (D-Ala), and its half-life is better than that of DR8. In the current study, we verified that DR7dA ameliorated TGF-β1-induced fibrogenesis and bleomycin-induced PF. The results indicated that DR7dA reduced the protein and mRNA levels of TGF-β1-target genes in TGF-β1-induced models. Surprisingly, DR7dA blocked fibrosis in a lower concentration range than DR8 in cells. In addition, DR7dA ameliorated tissue pathological changes and ECM accumulation in mice. BLM caused severe oxidative damage, but administration of DR7dA reduced oxidative stress and restored antioxidant defense. Mechanistic studies suggested that DR7dA inhibits ERK, P38 and JNK phosphorylation in vivo and in vitro. All results indicated that DR7dA attenuated PF by inhibiting ECM deposition and oxidative stress via blockade of the MAPK pathway. Hence, compared with its parent peptide, DR7dA has higher druggability and could be a candidate compound for PF treatment in the future.
**Significance statement**

In order to improve druggability of DR8, we investigated the structure-activity relationship of it and replaced the L-Ile with D-Ala. We found that the stability and antifibrotic activity of DR7dA were significantly improved than DR8, as well as DR7dA significantly attenuated TGF-β1-induced fibrogenesis and ameliorated BLM-induced fibrosis by inhibiting ECM deposition and oxidative stress via blockade of the MAPK pathway, suggesting DR7dA may be a promising candidate compound for the treatment of PF.
Introduction

Pulmonary fibrosis (PF) is a chronic disease characterized by interstitial inflammation and fibrosis. In PF, abnormal fibroblast and myofibroblast differentiation results in α-smooth muscle actin (α-SMA) expression and extracellular matrix (ECM) deposition. Increased ECM results in loss of lung compliance and damage to alveolar structure, eventually leading to respiratory failure and death. In recent years, the incidence and mortality of PF have been increasing gradually; thus, PF is an important human health issue (Distler et al., 2019; Thannickal et al., 2004; Wynn, 2008). At present, pirfenidone and nintedanib are approved for clinical use in delaying the progression of PF, but they cannot reverse the fibrosis process. In addition, pirfenidone can cause some side effects, such as photosensitivity, rashes, and gastrointestinal discomfort (Galli et al., 2017). Lung transplantation is the most effective way to prolong patient survival. However, the widespread application of lung transplantation is limited by the high difficulty and cost of surgery, the lack of lung resources and the occurrence of immune rejection (George et al., 2019). Therefore, it is necessary to find an effective medicine to alleviate PF.

Transforming growth factor-β1 (TGF-β1) is a main profibrotic cytokine involved in the inflammatory response, oxidative stress (OS), myofibroblast differentiation and ECM deposition (Saito et al., 2018). OS involves an imbalance of antioxidant and prooxidant processes, including reactive oxygen species (ROS) production and/or antioxidant defense impairment. OS is implicated as an important factor in the pathogenesis of PF, which involves alveolar epithelial cell (AEC) injury and apoptosis.
and fibroblast proliferation and differentiation (Kliment and Oury, 2010). In view of the role of OS in the occurrence and development of PF, we believe that antioxidants may play an antifibrotic role in PF. In our previous studies, we reported that the rapeseed \((Brassica campestris\) L.)-derived antioxidant peptide DR8 (DHNNPQIR-NH₂) can block the progression of PF and renal fibrosis (Deng et al., 2020; Wang et al., 2019).

Peptide drugs typically have the advantages of high efficiency and low toxicity, so research on new peptide drugs has increased in recent years. However, natural active peptides are easily degraded by endogenous proteases, and their poor stability and short half-lives \((t_{1/2} \text{ values})\) have limited their applications in medicine (Fosgerau and Hoffmann, 2015). Chemical modification strategies, including the introduction of nonnatural amino acids, cyclization, skeleton modification and side chain modification, are commonly used to improve the stability of natural peptides (Erak et al., 2018; Werle and Bernkop-Schnurch, 2006). Among these approaches, the introduction of D-type amino acids into the peptide sequence is the most common, simple, and effective strategy to prevent degradation. In our previous studies on alanine and D-amino acid scanning analogs of DR8, we found that the activity was retained after replacement of Ile with Ala but lost after replacement with D-Ile (Wang et al., 2021). Since replacing L-amino acids with nonnatural D-amino acids can improve stability and since D-Ala is readily available, we chose to replace the Ile of DR8 with D-Ala. To investigate whether the modified peptide has greater stability in serum and retains the antifibrotic activity of the parent peptide, a TGF-β1-induced cell
model and a bleomycin (BLM)-induced mouse model were used to validate the new analog in the current study.
Materials and Methods

Peptide synthesis

DR7dA was prepared with the 9-fluorenylmethyloxycarbonyl (Fmoc) solid-phase method (Blanco-Canosa and Dawson, 2008; Chandrudu et al., 2013). The peptide was purified and verified by reverse-phase HPLC (Waters, Milford, USA) to >95% homogeneity with acetonitrile (5-95% in 30 min). Mass spectrometry (MaXis 4G, Bruker, USA) was used to confirm the chemical identity of the peptide.

Serum stability study

Serum stability has been widely used in many reports (Hong et al., 1999; Jenssen and Aspmo, 2008; Kim et al., 2010; Noto et al., 2008), and we verified this assay. This experiment was performed as described in a previous study (Wang et al., 2021). The peptide (56 µL of 10 mM) was added to normal mouse serum (224 µL) and incubated at 37°C. An aliquot of 40 µL was taken at 0, 15, 30, 60, 120 and 240 min, and an equal volume of acetonitrile was added to precipitate serum proteins. The mixture was incubated on ice (10 min). After centrifugation (13,000×g, 15 min), the supernatant was stored at -80°C. Samples (20 µL) were analyzed by reverse-phase HPLC to determine the t1/2. The enzymatic hydrolysis processes of the peptide conformed to the first-order kinetic equation: \( A_t = A_0e^{-Kt} \), when \( A_t/A_0 = 0.5 \), \( t_{1/2} = \ln 2/K \).

Cell culture and treatment

A549 cells were grown in 1640 (Gibco, Carlsbad, USA), and NIH3T3 cells were grown in DMEM (Gibco) with 10% fetal bovine serum (FBS, BI, Beit HaEmek, Israel) at 37°C in 5% CO₂. Through the retrieval of relevant literature, it is not difficult to
find that 1-10 ng/mL TGF-β1 was used to induce cell models, and many results show that 5 ng/mL TGF-β1 can be successfully used to construct cell models (Ji et al., 2018; Wang et al., 2016). Similarly, 1-10 ng/mL TGF-β1 was selected to treat cells in previous studies, and the results showed that 5 ng/mL TGF-β1 can stably and effectively induce cell fibrogenesis, such as cell proliferation, EMT, morphologic changes, and high expression of fibrosis-related genes and proteins (Deng et al., 2020; Wang et al., 2021; Wang et al., 2019). Therefore, 5 ng/mL TGF-β1 was used in this study. Cells in complete medium were seeded in 6-well plates for 24 h at 37°C. After 12 h of serum starvation, the cells were treated with 5 ng/mL TGF-β1 (HEK293 derived, PeproTech, Rocky Hill, USA) with or without DR7dA for 1 h or 48 h.

**MTT assay**

Cells in complete medium were seeded in 96-well plates for 24 h and treated with DR7dA (0, 10, 20, 40, 80, 160 μM) without FBS for 24 h. MTT (5 mg/mL, Sigma, St. Louis, USA) was added to each well, and the cells were incubated for 4 h at 37°C. Then, the original medium was removed, and 150 μL of DMSO was added to each well. After gentle shaking, the absorbance was measured at 570 nm. The percent survival is shown as the percentage relative to the control.

**ROS generation assay**

As previous research (Wang et al., 2019), cells in complete medium were seeded in glass-bottom cell culture dishes for 24 h at 37°C. After 12 h of serum starvation, the cells were cultured with 5 ng/mL TGF-β1 alone or with DR7dA for 12 h. Furthermore, they were incubated in medium containing 2',7'-dichlorodihydrofluorescein diacetate
(DCFH-DA, 10 μM, Sigma-Aldrich) for 30 min. The ROS signal was captured by confocal microscopy.

**Immunofluorescence**

Cells in dishes were fixed for 15 min at room temperature. The cells were incubated with primary antibodies (in Table 1) overnight at 4°C after being blocked with 10% bovine serum albumin for 1 h at 37°C. Secondary antibodies were added to label the target proteins, and the cells were incubated for 1 h at room temperature. The nuclei were stained with DAPI. Images were acquired with a confocal microscope.

**Animals and treatments**

Mice were considered the first-line animal model for preclinical testing (Jenkins et al., 2017) and C57BL/6 mice were consistently prone to BLM-induced PF. Most studies were performed in mice 6-8 weeks old (~20 years old in humans) (Jenkins et al., 2017; O'Dwyer and Moore, 2018) because aging may directly lead to many age-related respiratory diseases, the most common of which is PF (Birch et al., 2018; Schafer et al., 2017; Selman and Pardo, 2014). Meanwhile, male sex hormones exacerbate PF (Voltz et al., 2008). Therefore, specific pathogen free female C57BL/6 mice (8-week-old, 18-22 g) were purchased from the Laboratory Animal Center of Lanzhou University (SCXK(Gan)2018-0002). All animals underwent 1 week of adaptive feeding before the experiments at 22 ± 2°C.

The BLM-induced PF model is the most commonly utilized preclinical model in vivo because pathological changes are most similar to human PF (Chua et al., 2005). The BLM-induced animal model is widely used in the assessment of potential antifibrotic
agents, and a large number of compounds have been shown to prevent fibrotic progression (Kolb et al., 2020). It has also been reported that intratracheal instillation of 2-5 mg/kg BLM alone can induce PF in C57BL/6 mice (Li et al., 2021). As reported in previous studies, 5 mg/kg BLM can effectively and significantly induce PF, and subcutaneous injection of DR8 and DR8 analogs (0.5 mg/kg/d) showed good antifibrotic activity, low toxicity and few effects at this dose (Deng et al., 2020; Wang et al., 2021; Wang et al., 2019). Therefore, the same experimental scheme was performed, and 0.5 and 2.5 mg/kg/d were determined as the dosage regimen of DR7dA in this experiment.

Wei et al. believed that the basic number of small animal experiments should be ≥ 10 in the Methodology of Pharmacological Experiment (Wei et al., 2010). To avoid < 10 samples caused by death during the process, ≥ 11 mice were randomly divided into each group. The mice were randomly divided into 6 groups: the normal group (n=11), saline group (n=11), BLM group (n=12), DR7dA groups (0.5 and 2.5 mg/kg, n=11) and N-acetyl-L-cysteine (NAC) group (600 mg/kg, n=11) (Li et al., 2020). Except in the normal group, saline with 5 mg/kg BLM (Nippon Kayaku, Tokyo, Japan) or saline was injected intratracheally into the mice. The DR7dA groups were subcutaneously injected with 0.5 or 2.5 mg/kg/d, and the NAC group was given 600 mg/kg/d by gavage. An equal amount of saline was subcutaneously injected into the mice in the normal group and the saline group for 21 consecutive days. All mice were euthanized (sodium pentobarbital, 50 mg/kg, intraperitoneal injection), 0.8-1 mL of blood was collected from the orbit, and approximately 0.2 mL of serum was collected after
centrifugation (5000 rpm, 30 min). The whole lung tissues were washed with cold PBS to remove the residual blood. Some of the lung was fixed in 10% formalin solution for 48 h before paraffin embedding and sectioning, and the remaining tissue was stored at -80°C.

Mouse experiments were approved by the Animal Experiments Committee of the Lanzhou University (SYXK(Gan)2018-0002). All operations were performed under anesthesia (sodium pentobarbital, 50 mg/kg, intraperitoneal injection), and all efforts were made to minimize suffering.

**Tissue histology and immunohistochemistry**

Hematoxylin and eosin (H&E) and Masson’s trichrome staining were performed on 4 μm sections. The lung sections were deparaffinized and rehydrated. Immunohistochemistry was performed with an SP kit (ZSGB-Bio, Beijing, China). Endogenous peroxidase was blocked after antigen retrieval. After blocking, the sections were incubated with primary antibodies (in Table 1) overnight at 4°C. Incubation with a secondary antibody (ZSGB-Bio, Beijing, China) was performed at room temperature, and the sections were visualized with DAB and hematoxylin. The staining intensity was observed using an optical microscope and analyzed by ImageJ.

**Serum biochemical measurements**

The levels of superoxide dismutase (SOD), malondialdehyde (MDA) and catalase (CAT) in serum were detected using commercial kits according to the instructions (Nanjing Jiancheng Bioengineering Institute, Nanjing, China).

**Western blot analysis**
Proteins were obtained from cells and tissue using RIPA buffer (Beyotime, Shanghai, China). The proteins were separated via 10% SDS-PAGE after detecting the protein concentrations with a BCA protein assay kit (Thermo, Rockford, USA) and then transferred to a PVDF membrane (Millipore, Bedford, USA). The membrane was blocked with 6% nonfat dry milk for 1 h and then incubated with primary antibodies at 4°C overnight. After the bands were incubated with HRP-conjugated secondary antibodies for 1 h, the proteins were visualized with an enhanced chemiluminescence (ECL) kit (Yeasen Biotech, Shanghai, China). The signals were measured using Evolution Capt software (Vlber Lourmat, Marne la Vallée, France), and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was used as an internal control. The antibodies are listed in Table 1.

**Real-time quantitative PCR (RT-qPCR)**

TRIzol (Takara, Kusatsu, Japan) was used to extract RNA from cells and tissue. The RNA was reverse transcribed after quantification. RT-qPCR was used on an ABI System. The $2^{-\Delta\Delta Ct}$ method with GAPDH as the internal reference was used to quantify the target genes. The sequences are shown in Table 2.

**Statistical analysis**

The statistical analyses were performed using GraphPad Prism 8.3.0 (San Diego, California, USA). Each experiment was performed more than three times, and all data are expressed as the mean ± SD. One-way ANOVA followed by Tukey’s post-hoc test was used for analyses among groups. $P < 0.05$ was considered to indicate statistical significance.
Results

DR7dA inhibits TGF-β1-induced PF in vitro

After purification by RP-HPLC and characterization by mass spectrometry (Supp. Fig 1), DR7dA with a purity of 100% (Supp. Fig 2) was used in the following experiments. The structure of DR7dA is shown in Figure 1A; the red part is D-Ala. Then, we compared the stability of DR7dA with that of DR8 (70.19 ± 6.83 min) (Wang et al., 2021) in vitro and found that the stability of DR7dA (201.08 ± 58.86 min) was greatly improved in serum. Then, we explored the activity of DR7dA. In PF, both epithelial cells and fibroblasts are involved in the fibrotic process, so A549 and NIH3T3 cells were selected to study the activity of DR7dA in vitro. First, to evaluate the cell safety of DR7dA, we used MTT assay to evaluate the toxicity of DR7dA in cells. We used five concentrations of DR7dA ranging from 10 to 160 μM. Unsurprisingly, compared with the control, DR7dA did not show a cytotoxic effect at 160 μM (Fig. 1B and C). Subsequently, we performed a preliminary study on the activity of DR7dA in two cell lines. TGF-β1 can induce cell proliferation and activation in vitro; thus, it is commonly used to establish fibrosis models. Transformation of fibroblasts into myofibroblasts is associated with an increase in ECM products, and α-SMA can serve as an indicator of PF. Therefore, TGF-β1-induced cell models were selected in our study, and α-SMA was used for testing in a preliminary study. As expected, α-SMA expression increased in NIH3T3 and A549 cells incubated with TGF-β1. DR7dA suppressed α-SMA in a dose-dependent manner, and a significant reduction was observed at 10 μM in
NIH3T3 cells (Fig. 1D and F) and A549 cells (Fig. 1E and H). Therefore, we used several concentrations lower than 10 μM and found that the lowest effective concentration of DR7dA was 1 μM in NIH3T3 cells (Fig. 1D and G) and 5 μM in A549 cells (Fig. 1E and I). Compared with that of DR8, the effective concentration of DR7dA was lower in both cell lines. Later, 2.5 μM and 10 μM were chosen for NIH3T3 cells and 5 μM and 10 μM were chosen for A549 cells to further analyze the TGF-β1-induced model in vitro. Further results in NIH3T3 (Fig. 2A and B) and A549 (Fig. 2A and C) cells showed that DR7dA inhibited the expression of fibrosis-related proteins whose expression was induced by TGF-β1 at selected concentrations, including α-SMA, Fibronectin, Collagen I, and Vimentin. In addition, we examined the effect of DR7dA on fibrogenesis at genetic level. The results showed that DR7dA inhibited the mRNA expression of Acta2, Fn1, Coll1a1, Vim and Mmp2 in NIH3T3 cells (Fig. 2D) and ACTA2, FN1, COL1A1, VIM and MMP2 in A549 cells (Fig. 2E) after exposure to TGF-β1. Moreover, immunofluorescence showed that TGF-β1 increased Collagen I levels, but this effect was suppressed by DR7dA in A549 cells (Fig. 2F). Compared with DR8, DR7dA not only exhibited better stability but also retained its antifibrotic activity at a lower effective concentration in vitro. All results indicated that DR7dA exhibited ideal antifibrotic activity against TGF-β1-induced fibrogenesis by inhibiting cell activation and ECM accumulation.

**DR7dA decreases TGF-β1-induced oxidative damage in vitro**

OS is an important pathogenic mechanism of PF, and TGF-β1 can induce oxidative damage and antioxidant deficiency in cells. To verify whether DR7dA, like DR8, can
inhibit OS caused by TGF-β1-induced ROS production, we used DCFH-DA to examine intracellular ROS levels. DCFH-DA is an oxidation-sensitive probe that can enter cells and eventually interact with intracellular endogenous ROS to generate fluorescence, so ROS levels were detected by measuring fluorescence intensity. The results showed that TGF-β1 treatment elevated ROS levels, but this effect was attenuated by DR7dA (Fig. 3A) in NIH3T3 and A549 cells. In addition, TGF-β1-induced upregulation of NADPH oxidase 4 (NOX4) expression can produce ROS and cause DNA damage and mitochondrial dysfunction, so we also detected the effect of DR7dA on NOX4 expression. As expected, Western blot and RT-qPCR analyses indicated that DR7dA decreased the protein and mRNA levels of NOX4 in NIH3T3 (Fig. 3B-D) and A549 cells (Fig. 3G-I). TGF-β1 not only leads to ROS production but also suppresses antioxidant system components, such as SODs and CAT. As shown in Fig. 3E, the mRNA levels of Sod1, Sod2, and Cat were decreased in the TGF-β1 group but increased after treatment with DR7dA in NIH3T3 cells. Moreover, immunofluorescence also showed that DR7dA decreased NOX4 levels in A549 cells (Fig. 3F). The results showed that DR7dA can reduce TGF-β1-induced oxidative damage and restore the antioxidant system, suggesting that DR7dA may block the PF process by inhibiting OS.

**DR7dA blocks the TGF-β1-induced MAPK signaling pathway in vitro**

Once TGF-β1 binds with receptors, it can activate the typical Smad pathway and other atypical pathways. The MAPK pathway is involved in the fibrotic process, cell proliferation and cell differentiation. To determine the signaling pathway involved in
the inhibitory effect of DR7dA *in vitro*, the levels of phosphorylated MAPK were analyzed. The results showed that the phosphorylation levels of ERK, P38 and JNK were higher after TGF-β1 exposure than the levels in the control group. A significant decrease in the phosphorylation level was observed after treatment with DR7dA for 1 h in NIH3T3 (Fig. 4A and B) and A549 cells (Fig. 4C and D), but there was no difference between the two concentrations. All data showed that DR7dA slowed PF *in vitro* by suppressing the TGF-β1-induced MAPK pathway.

**DR7dA ameliorates BLM-induced PF *in vivo***

Subsequently, a BLM-induced PF model was used to verify the effect of DR7dA *in vivo*. NAC, a precursor of glutathione (GSH) that acts as a ROS scavenger, is extensively used as a positive control in animal PF models (Chen et al., 2013; Hamdy et al., 2012; Li et al., 2020; Mizuguchi et al., 2006), so we used NAC as a positive control in mice. In mouse experiments, the doses of DR7dA were 0.5 and 2.5 mg/kg, and the dose of NAC was 600 mg/kg (Li et al., 2020). As shown in Fig. 5A and B, we observed continued weight gain of the mice in the normal group and initial weight loss followed by weight gain in the remaining groups. The results of H&E staining suggested that the normal lung structure was severely destroyed, the alveolar wall was thickened and inflammatory cells were accumulated after BLM stimulation (Fig. 5C). These changes were reversed by DR7dA and NAC. In PF, high expression of α-SMA results in tissue contraction and decreased lung compliance, and matrix metalloproteinase 2 (MMP2) can activate TGF-β1 to accelerate fibrosis. The α-SMA expression induced by BLM was reversed by DR7dA, as indicated by
immunohistochemical staining (Fig. 5C and D). The assay indicated that the expression of α-SMA, Fibronectin and MMP2 was notably increased in the BLM group but suppressed by DR7dA and NAC (Fig. 5E and F). In addition, as shown in Fig. 5G-I, we observed similar results with regard to the effect of DR7dA on the mRNA expression of Acta2, Fn1 and Mmp2 after BLM treatment. These data suggested that DR7dA attenuated the development of fibrosis in a dose-dependent manner. Notably, the effect of DR7dA was equivalent to that of NAC at a dose less than one hundredth of the NAC dose.

**DR7dA alleviates BLM-induced collagen deposition* in vivo**

Overexpression and deposition of collagen are pathological features of PF. The results of Masson’s trichrome staining showed increased amounts of collagen fibers in the BLM treatment group but decreased amounts in the DR7dA and NAC groups (Fig. 6A and B). In addition, the level of Collagen I was measured by immunohistochemistry (Fig. 6A and C) and Western blot analysis (Fig. 6E and F). As expected, the levels of Collagen I were significantly increased in the BLM-treated group but reduced by DR7dA and NAC treatment. The Col1a1 levels also showed the same result (Fig. 6D) in mice. These results confirmed that DR7dA was able to reduce collagen accumulation induced by BLM in mice.

**DR7dA modulates BLM-induced OS and inflammation**

To verify the impact of DR7dA on BLM-induced oxidative damage, the levels of MDA were measured as indicators of oxidative damage, and the activity of SOD and CAT was determined to evaluate antioxidants in serum. As shown in Fig. 7A-C, after
stimulation with BLM, the MDA content markedly increased, and SOD and CAT activity was inhibited. In contrast, administration of DR7dA decreased the MDA content and enhanced SOD and CAT activity. After exposure to BLM, the mRNA levels of Sod1, Sod2 and Cat were markedly lower than those in the control group, but DR7dA recovered the expression of these mRNAs related to antioxidant enzymes (Fig. 7D). Moreover, the changes in NOX4 were measured by RT-qPCR (Fig. 7E) and immunohistochemistry (Fig. 7F and G). Surprisingly, DR7dA significantly inhibited the BLM-induced increase in NOX4, and the RT-qPCR results showed the same tendency as the immunohistochemistry results regarding the mRNA expression of Nox4. Furthermore, tumor necrosis factor (TNF)-α, interleukin (IL)-1β and IL-6 were elevated in BLM-induced PF and participated in the development of PF. The results showed that the mRNA levels of these inflammatory factors were also reduced by DR7dA (Fig. 7H). These data indicated that DR7dA alleviated PF by restoring the oxidation/antioxidant balance and regulating the inflammatory response in mice in a concentration-dependent manner.

**DR7dA suppresses TGF-β1/MAPK signaling in BLM-induced PF**

TGF-β1, a major fibrotic cytokine, is considered to regulate various fibrotic processes and is involved in BLM-induced PF. Unsurprisingly, BLM administration increased TGF-β1 protein and mRNA levels, while DR7dA apparently reduced TGF-β1 expression (Fig. 8A-C). In *in vitro* studies, we found that DR7dA exerted antifibrotic activity by reducing the TGF-β1-induced phosphorylation of MAPK. We also detected the effect of DR7dA on the MAPK pathway *in vivo*. DR7dA significantly
inhibited the BLM-induced increases in the levels of phosphorylated ERK, P38 and JNK (Fig. 8A and D). These data indicated that DR7dA alleviated BLM-induced PF by regulating the MAPK signaling pathway.
Discussion

Because the lungs are directly connected to the external environment, they are susceptible to the environmental influence. PF is caused by a variety of types of injury to the lung, including poisoning and autoimmune, drug-induced, infectious, and traumatic injuries (Thannickal et al., 2004). Repetitive injury of epithelial cells initiates PF, and AECs also secrete a variety of profibrotic mediators that induce fibroblast differentiation into myofibroblasts (Sakai and Tager, 2013). Then, fibroblasts proliferate and differentiate into myofibroblasts, producing ECM. ECM deposition results in alveolar collapse and breathing restriction and eventually leads to respiratory failure and death (Distler et al., 2019; Wynn, 2011). In this study, we found that DR7dA alleviated BLM-induced PF in mice and TGF-β1-induced fibrogenesis in cells. Our results showed that DR7dA inhibited ECM deposition and fibrotic progression in vitro and in vivo. DR7dA inhibited the differentiation of epithelial and fibroblast cells into myofibroblasts in vitro and reduced collagen deposition and pathological changes in vivo.

MMPs can degrade ECM components, but their activity is blocked by tissue inhibitors of MMPs. Many MMPs are involved in fibrosis, such as MMP2, MMP7, MMP9, and MMP28 (Roque et al., 2020). MMP2 is mainly expressed in alveolar epithelial cells in PF, which may be related to basement membrane rupture (Dancer et al., 2011). In our results, DR7dA inhibited BLM-induced elevations in MMP2 protein and mRNA levels in vivo and inhibited TGF-β1-induced increases in MMP2 mRNA levels in vitro. On the one hand, DR7dA may reduce the damage caused by MMP2 to the basement
membrane, which may reduce the invasion of fibroblasts into the alveolar cavity. On the other hand, DR7dA may indirectly inhibit TGF-β1 activation through MMP2, meaning that the activation of TGF-β1-induced downstream signaling is reduced.

After repeated injury, epithelial cells release inflammatory cytokines that recruit inflammatory cells to the site of injury (Wynn, 2011). Innate and adaptive immunity are involved in fibrosis. Neutrophils migrate to damaged tissue under the action of several chemokines and ILs, and macrophages produce TNF-α, IL-1, and IL-6, which maintain tissue inflammation. TNF-α, IL-1 and IL-6 can promote fibrosis in the lungs (Mack, 2018). We found that the increases in Tnf, Il1b and Il6 mRNA levels after BLM stimulation were inhibited by DR7dA, suggesting that DR7dA may inhibit PF through inhibition of inflammation.

Compared with other organs, the lungs are particularly sensitive to OS because they contact higher oxygen levels. At low levels, ROS can mediate normal cellular activities as second messengers. Antioxidants, including CAT, GSH, SOD and ascorbic acid, exist to clear or remove ROS and prevent OS. When the lungs are damaged, excessive ROS can lead to OS, which in turn leads to further ROS production and fibrosis (Kinnula and Crapo, 2003; Kliment and Oury, 2010; van der Vliet et al., 2018). Increases in ROS levels eventually lead to damage to biomolecules, such as proteins, lipids, and DNA, inducing tissue damage and inflammation (Sies and Jones, 2020). In our results, we found that the levels of the lipid peroxidation product MDA were increased, while those of the antioxidant enzymes SOD and CAT were decreased, after BLM induction, indicating the generation of OS. The NOX
family is a ROS-generating enzymatic system that plays a role in PF. It has been reported that NOX4 is the cause of ROS accumulation in PF and that NOX4 is upregulated in human and mouse PF models (Crestani et al., 2011). NOX4 has been studied more than other NOXs in PF, and unlike other NOXs, NOX4 activity is mainly regulated by gene expression levels (Crestani et al., 2011; Hecker et al., 2012; Hecker et al., 2009). NOX4 is associated with cell proliferation (Chan et al., 2009) and mediates fibroblast differentiation and proliferation (Amara et al., 2010). Elevated NOX4 expression was also observed in the in vivo and in vitro models, as has been reported previously. The above phenomena were improved after administration of DR7dA to the models, indicating that DR7dA can partially restore TGF-β1-induced and BLM-induced deficiencies in antioxidant defense.

TGF-β is a powerful profibrotic factor, and its expression is increased during the development of fibrosis in many organs. Mammals expressing three subtypes of TGF-β (TGF-β1-3) also express latent associated protein. PF mainly results from TGF-β1 stimulation (Ask et al., 2008). TGF-β1 is involved in epithelial cell apoptosis, EMT, epithelial cell migration, fibroblast proliferation and differentiation, and myofibroblast activation (Saito et al., 2018). In our studies, TGF-β1 was overexpressed after BLM induction, but this overexpression was reversed after DR7dA treatment in vivo.

Activated TGF-β1 binds with receptors to activate the typical Smad pathway. In addition, TGF-β1 signaling is transmitted through other atypical pathways, and the MAPK pathway and phosphatidylinositol-3-kinase pathway take part in the fibrotic
process (Derynck and Zhang, 2003). Our results showed that DR7dA improved PF through the MAPK signaling pathway. MAPK signaling is involved in cell proliferation, cell metabolism, cell migration and cell differentiation (Lavoie et al., 2020; Newton and Holden, 2006; Shaul and Seger, 2007; Weston and Davis, 2002). Many kinases of MAPK include a redox-sensitive site and are very sensitive to ROS inactivation. Apoptosis signal-regulating kinase-1 is an oxidation-sensitive protein that can activate the JNK and P38 pathways (Tobiume et al., 2001). A vicious cycle exists in which ROS activate JNK and mitochondrial outer membrane protein-dependent ROS production, resulting in increased ROS production and sustained JNK activation (Blaser et al., 2016; Chambers and LoGrasso, 2011; Win et al., 2014). In our work, DR7dA reduced ROS and NOX4 production, possibly through the JNK and P38 pathways. In addition, P38 plays a major role in adjusting inflammatory expression (Newton and Holden, 2006). Therefore, the inhibitory effect of DR7dA on the inflammatory response may occur through the P38 signaling pathway. However, PF involves complex signaling pathways, and TGF-β1 binds to receptors to activate a variety of pathways; hence, DR7dA may also act through other pathways.

NAC, a precursor of GSH that acts as a ROS scavenger, can effectively reduce BLM-induced PF in mice (Hagiwara et al., 2000). However, in clinical trials, NAC has not been shown to have a beneficial effect on forced vital capacity or mortality (Martinez et al., 2014). On the one hand, blindly eliminating ROS may hinder normal ROS signal transduction, which may aggravate PF. On the other hand, NAC cannot
block the source of ROS and may therefore have a limited effect (Gonzalez-Gonzalez et al., 2017; Kato and Hecker, 2020). Therefore, NAC is not recommended for the treatment of PF in clinical practice (even in combination with other drugs) (Cameli et al., 2020). However, since DR8 is an antioxidant peptide, we used NAC as a positive control in our work, and the results showed that NAC can reduce PF, as previously reported. The antioxidative, anti-inflammatory and antifibrotic effects of DR7dA on PF were equal to or better than those of NAC at a dose of less than one hundredth that of NAC. The administration methods of DR7dA and NAC are different and have also been reported in other literature (Corboz et al., 2018; Guan et al., 2018; Li et al., 2020).

Peptides have the advantages of high activity, low toxicity and strong specificity, and more peptide drugs are being used in the prevention, diagnosis and treatment of diseases (Fosgerau and Hoffmann, 2015). However, natural peptides are easily degraded by enzymes in vivo, resulting in poor stability and short t1/2 values. Long-acting strategies for peptides can extend the t1/2 (Erak et al., 2018). Our previous studies have shown that DR8 can reduce BLM-induced PF and unilateral ureteral obstruction-induced renal fibrosis in mice. In this work, the results showed that the serum stability of DR7dA was improved after replacing the Ile of DR8 with D-Ala. DR7dA also showed good antifibrotic activity at a lower effective concentration than DR8. Therefore, the introduction of D-Ala at appropriate sites is a method to optimize active peptides. There is still much work to be done on DR7dA in further studies, such as investigation of the antifibrotic activity of DR7dA in other animal models and
evaluation of safety. In addition, different dosing routes and dosages should be tested in animal experiments to determine the best method, and the pharmacokinetics of analogs in vivo should be determined to compare the t_{1/2} values in vivo.

In summary, after studying the structure-activity relationship through amino acid scanning, we improved the degradation of the natural peptide DR8 in vivo by replacing Ile with D-Ala. Compared with DR8, DR7dA not only exhibited better stability but also retained antifibrotic activity in TGF-β1-induced and BLM-induced models. Moreover, we found that the effective concentration of DR7dA in vitro was significantly lower than that of DR8. In addition, DR7dA decreased oxidative damage involved in the occurrence and development of PF by inhibiting ROS and NOX4. We have demonstrated that DR7dA ameliorates PF via the ROS/TGF-β1/MAPK signaling pathway in vitro and in vivo. Therefore, DR7dA may be a promising candidate compound for the treatment of PF.
Acknowledgement

We gratefully thank Dr. Wangsheng Sun for providing method of peptide modification, and Dr. Feiyun Gao for providing result of mass spectrometry.
Author contributions

Participated in research design: Cheng, Wang, Deng, B.Z. Zhang, Xie

Conducted experiments: Cheng, Wang, Deng, Li, J. Zhang

Performed data analysis: Cheng, Guo, Yan, Yue, An

Wrote or contributed to the writing of the manuscript: Cheng, Wang, Deng, Xie
References


Martinez FJ, Andrade JD, Anstrom KJ, King TE, Raghu G (2014) Randomized trial of


Footnotes

This work was supported by the CAMS Innovation Fund for Medical Sciences (CIFMS) (No. 2019-I2M-5-074, No. 2021-I2M-1-026, No. 2021-I2M-3-001), the Program for the Ministry of Education “Peptide Drugs” Innovation Team (No. IRT 15R27), the Gansu Science and Technology Program (No. 18JR2RA031), the Lanzhou Science and Technology Bureau (No. 2019-4-4), and the Fundamental Research Funds for the Central Universities (No. lzujbky-2021-it17).

No author has an actual or perceived conflict of interest with the contents of this article.
Figure legends

**Figure 1.** DR7dA inhibits TGF-β1-induced α-SMA expression *in vitro.* (A) Structure of DR7dA. (B and C) Cytotoxicity of DR7dA in NIH3T3 and A549 cells. Expression of α-SMA with different concentrations of DR7dA in NIH3T3 (D, F and G) and A549 (E, H and I) cells. *p < 0.05, **p < 0.01 vs. control; #p < 0.05, ##p < 0.01 vs. TGF-β1.

**Figure 2.** DR7dA inhibits TGF-β1-induced fibrogenesis *in vitro.* (A) Western blot of α-SMA, Fibronectin, Collagen I, and Vimentin in NIH3T3 and A549 cells. (B) Band quantitative analysis of α-SMA, Fibronectin, Collagen I, and Vimentin in NIH3T3 cells. (C) Band quantitative analysis of α-SMA, Fibronectin, Collagen I, and Vimentin in A549 cells. (D) mRNA levels of Acta2, Fn1, Collal, Vim and Mmp2 in NIH3T3 cells. (E) mRNA levels of ACTA2, FN1, COL1A1, VIM and MMP2 in A549 cells. (F) Immunofluorescence of Collagen I in A549 cells (original magnification, 400×). Scale bars, 100 μm. *p < 0.05, **p < 0.01 vs. control; #p < 0.05, ##p < 0.01 vs. TGF-β1.

**Figure 3.** DR7dA decreases TGF-β1-induced oxidative damage *in vitro.* (A) ROS levels measured with DCFH-DA in NIH3T3 and A549 cells (original magnification, 400×). Scale bars, 100 μm. (B and C) Expression of NOX4 in NIH3T3 cells. (D) Nox4 mRNA levels in NIH3T3 cells. (E) Sod1, Sod2 and Cat mRNA levels in NIH3T3 cells. (F) Immunofluorescence staining of NOX4 in A549 cells (original magnification, 400×). Scale bars, 100 μm. (G and H) Level of NOX4 in A549 cells. (I) mRNA expression of NOX4 in A549 cells. *p < 0.05, **p < 0.01 vs. control; #p < 0.05, ##p < 0.01 vs. TGF-β1.

**Figure 4.** DR7dA blocks TGF-β1-induced MAPK signaling *in vitro.* (A and B) Levels
of ERK, P38 and JNK phosphorylation in NIH3T3 cells. (C and D) Expression of phosphorylated MAPK in A549 cells. *p < 0.05, **p < 0.01 vs. control; #p < 0.05, ##p < 0.01 vs. TGF-β1.

**Figure 5.** DR7dA ameliorates BLM-induced PF in vivo. (A) Weight changes. (B) survival. (C) Photos of the lungs, H&E staining and immunohistochemical staining of α-SMA (original magnification, 100×). Scale bars, 100 μm. (D) Statistical results of immunohistochemical staining. (E and F) Western blot analysis of α-SMA, Fibronectin and MMP2. (G-I) mRNA levels of Acta2, Fn1 and Mmp2. *p < 0.05, **p < 0.01 vs. the normal group; #p < 0.05, ##p < 0.01 vs. the BLM group.

**Figure 6.** DR7dA alleviates BLM-induced collagen deposition. (A) Masson’s trichrome staining and immunohistochemical staining of Collagen I (original magnification, 100×). Scale bars, 100 μm. (B) Quantitative analysis of Masson’s trichrome staining. (C) Quantitative analysis of Collagen I. (D) Colla1 mRNA level analyses with RT-qPCR. (E-F) Expression of Collagen I as determined by Western blot analysis. *p < 0.05, **p < 0.01 vs. the normal group; #p < 0.05, ##p < 0.01 vs. the BLM group.

**Figure 7.** DR7dA modulates BLM-induced OS and inflammation. (A) MDA content. (B and C) SOD and CAT activity in serum. (D) mRNA expression of Sod1, Sod2, and Cat in mice. (E) RT-qPCR results for Nox4. (F) Immunohistochemical staining of NOX4 (original magnification, 100×). Scale bars, 100 μm. (G) Positive staining areas for NOX4. (H) Tnf, Il1b and Il6 mRNA levels measured with RT-qPCR. *p < 0.05, **p < 0.01 vs. the normal group; #p < 0.05, ##p < 0.01 vs. the BLM group.
Figure 8. DR7dA suppresses BLM-induced PF via the TGF-β1/MAPK signaling pathway. (A) Western blot assay of the levels of TGF-β1 and the phosphorylation levels of ERK, P38, and JNK. (B) Statistical result of TGF-β1. (C) The level of Tgfb1 was measured by RT-qPCR. (D) Band quantitative analysis of the phosphorylation levels of ERK, P38, and JNK. *p < 0.05, **p < 0.01 vs. the normal group; #p < 0.05, ##p < 0.01 vs. the BLM group.
**Table 1.** Antibody used for Western blot, immunohistochemistry and immunofluorescence.

<table>
<thead>
<tr>
<th>Antibodies</th>
<th>Species</th>
<th>WB</th>
<th>IHC</th>
<th>IF</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>α-SMA</td>
<td>Rabbit</td>
<td>1:500</td>
<td>1:200</td>
<td></td>
<td>Abcam</td>
</tr>
<tr>
<td>Fibronectin</td>
<td>Rabbit</td>
<td>1:1000</td>
<td></td>
<td></td>
<td>Abcam</td>
</tr>
<tr>
<td>Collagen I</td>
<td>Rabbit</td>
<td>1:1000</td>
<td>1:500</td>
<td>1:100</td>
<td>Servicebio</td>
</tr>
<tr>
<td>MMP2</td>
<td>Rabbit</td>
<td>1:500</td>
<td></td>
<td></td>
<td>Servicebio</td>
</tr>
<tr>
<td>Vimentin</td>
<td>Rabbit</td>
<td>1:1000</td>
<td></td>
<td></td>
<td>Cell Signaling Technology</td>
</tr>
<tr>
<td>NOX4</td>
<td>Rabbit</td>
<td>1:200</td>
<td>1:200</td>
<td>1:100</td>
<td>Boster</td>
</tr>
<tr>
<td>TGF-β1</td>
<td>Rabbit</td>
<td>1:1000</td>
<td></td>
<td></td>
<td>Abcam</td>
</tr>
<tr>
<td>p-ERK</td>
<td>Rabbit</td>
<td>1:1000</td>
<td></td>
<td></td>
<td>Cell Signaling Technology</td>
</tr>
<tr>
<td>p-P38</td>
<td>Rabbit</td>
<td>1:1000</td>
<td></td>
<td></td>
<td>Cell Signaling Technology</td>
</tr>
<tr>
<td>p-JNK</td>
<td>Rabbit</td>
<td>1:1000</td>
<td></td>
<td></td>
<td>Cell Signaling Technology</td>
</tr>
<tr>
<td>ERK</td>
<td>Rabbit</td>
<td>1:1000</td>
<td></td>
<td></td>
<td>Beyotime</td>
</tr>
<tr>
<td>P38</td>
<td>Rabbit</td>
<td>1:1000</td>
<td></td>
<td></td>
<td>Cell Signaling Technology</td>
</tr>
<tr>
<td>JNK</td>
<td>Rabbit</td>
<td>1:1000</td>
<td></td>
<td></td>
<td>Beyotime</td>
</tr>
<tr>
<td>GAPDH</td>
<td>Rabbit</td>
<td>1:5000</td>
<td></td>
<td></td>
<td>Proteintech</td>
</tr>
<tr>
<td>HRP-conjugated IgG</td>
<td>Goat</td>
<td>1:10000</td>
<td></td>
<td></td>
<td>ImmunoWay</td>
</tr>
<tr>
<td>CoraLite594-conjugated</td>
<td>Goat</td>
<td></td>
<td></td>
<td>1:200</td>
<td>Proteintech</td>
</tr>
</tbody>
</table>
**Table 2. Primer pairs used for RT-qPCR.**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Forward primer (5′- 3′)</th>
<th>Reverse primer (5′- 3′)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Human</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ACTA2</td>
<td>ACTGCCTTGGTGTGAGACAA</td>
<td>CACCATCACCCCCCTGATGTC</td>
</tr>
<tr>
<td>FN1</td>
<td>ACAACACCGAGGAGTCTAGAGAC</td>
<td>GGACCAACAGGATGCTTCCCTGAG</td>
</tr>
<tr>
<td>COL1A1</td>
<td>GTGCCGATGACGTGATCTGTGA</td>
<td>CGGTGTTTCTTGGTCCGGT</td>
</tr>
<tr>
<td>VIM</td>
<td>AGGCAAGCAAGGAGTCCACTGA</td>
<td>ATCTGGCGTCCAGGGACTCAT</td>
</tr>
<tr>
<td>MMP2</td>
<td>GATACCCCTTTAGCGTAAAGGA</td>
<td>CCTTCTCCCAAGGATCCATAGC</td>
</tr>
<tr>
<td>NOX4</td>
<td>CTTCCGTGGTTTGCAGATT</td>
<td>TGGGTCCACAACAGAAAAACA</td>
</tr>
<tr>
<td>GAPDH</td>
<td>GTCTCTCTCTGACTTCAACACAGCG</td>
<td>ACCACCTCTGTGCTGAGCCA</td>
</tr>
<tr>
<td>Mouse</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Acta2</td>
<td>ACTGGGACGACATGGAAAAG</td>
<td>CATCTCCAGAGTCCAGCACA</td>
</tr>
<tr>
<td>Fn1</td>
<td>ATGTGGACCCCTCTCTAGATGT</td>
<td>GCCCCAGTGATTCCAGAAAAAGG</td>
</tr>
<tr>
<td>Col1a1</td>
<td>GCTCCTCTCTAGGGGCCACT</td>
<td>CCACGTCTCAACCATTGGG</td>
</tr>
<tr>
<td>Vim</td>
<td>CGTCCACAGCGACCTACAG</td>
<td>GGGGGATAGGAAATAGAGGGT</td>
</tr>
<tr>
<td>Mmp2</td>
<td>CAAGTTCCCCGGCGATGTC</td>
<td>TTCTGGTCAGGTCACCTGTC</td>
</tr>
<tr>
<td>Nox4</td>
<td>GAAGGGGTTAAACACCTCTGC</td>
<td>ATGCTCTGCTTAAACACAAATCT</td>
</tr>
<tr>
<td>Sod1</td>
<td>AACCAGTTGTGGTGTGAGGAC</td>
<td>CCACATGTGTTTCTTAGAGTTGAGG</td>
</tr>
<tr>
<td>Sod2</td>
<td>CAGACCTGCTTACGACTATGG</td>
<td>CTCGGGCTAGTTGAGATTGT</td>
</tr>
<tr>
<td>Cat</td>
<td>AGCGACCAGATGAAGCTAGT</td>
<td>TCCGCTCTGCTGCAAGAGTG</td>
</tr>
<tr>
<td>Tnf</td>
<td>CCCTCACACTCAATCATCTTCTT</td>
<td>GCTACGACGTGGGCTACAG</td>
</tr>
<tr>
<td>Il1b</td>
<td>CTGCAGCTTGGAGATGTTG</td>
<td>GGGGAACCTCTCGAGACTCAA</td>
</tr>
<tr>
<td>Gene</td>
<td>Forward Primer</td>
<td>Reverse Primer</td>
</tr>
<tr>
<td>------</td>
<td>----------------</td>
<td>----------------</td>
</tr>
<tr>
<td>Il-6</td>
<td>AGTTGCCTTTCTGGGACTGA</td>
<td>TCCACGATTCCCAGAGAAC</td>
</tr>
<tr>
<td>Tgfb1</td>
<td>ATGGTGGACCGCAACAAC</td>
<td>CCAAGGTAACGCCAGGAA</td>
</tr>
<tr>
<td>Gapdh</td>
<td>AGGAGTAAGAAACCCTGGAC</td>
<td>CTGGGATGGAATTGTGAG</td>
</tr>
</tbody>
</table>
Fig 3

A

NH3T3
Control | TGF-β1 | DR7dA (2.5 μM) | DR7dA (10 μM)

A549
Control | TGF-β1 | DR7dA (5 μM) | DR7dA (10 μM)

F

Control | TGF-β1 | DR7dA (5 μM) | DR7dA (10 μM)

G

NOX4
Control | TGF-β1 | DR7dA (5 μM) | DR7dA (10 μM)

DAP1
Control | TGF-β1 | DR7dA (5 μM) | DR7dA (10 μM)

Merge

B

NH3T3

GAPDH

TGF-β1 - + + +
DR7dA - - 2.5 10 μM

NOX4

GAPDH

TGF-β1 - + + +
DR7dA - - 2.5 10 μM

C

NOX4/GAPDH band intensity

TGF-β1 - + + +
DR7dA - - 2.5 10 μM

mRNA (fold change)

Sod1 Sod2 Cag

D

Ratio (NovoGlo)

TGF-β1 - + + +
DR7dA - - 2.5 10 μM

E

G

NOX4

GAPDH

TGF-β1 - + + +
DR7dA - - 5 10 μM

H

NOX4/GAPDH band intensity

TGF-β1 - + + +
DR7dA - - 5 10 μM

I

Ratio (NovoGlo)
Fig 4

A

N1H3T3

p-ERK

45 KD

ERK

45 KD

p-P38

45 KD

P38

45 KD

p-JNK

45 KD

JNK

45 KD

GAPDH

35 KD

TGF-β1

- + + + +

5 ng/mL

DR7dA

- - 2.5 10 μM

C

A549

p-ERK

45 KD

ERK

45 KD

p-P38

45 KD

P38

45 KD

p-JNK

45 KD

JNK

45 KD

GAPDH

35 KD

TGF-β1

- + + + +

5 ng/mL

DR7dA

- - 5 10 μM

B

Band intensity (% of Control)

p-ERK

p-P38

p-JNK

**

**

##

##

##

##

D

Band intensity (% of Control)

p-ERK

p-P38

p-JNK

**

##

##

#
Fig 5

(B) Survival rates were measured for each group over time. The results showed that DR7dA at doses of 0.5 mg/kg and 2.5 mg/kg significantly improved survival compared to saline and BLM-treated groups.

(D) Area of α-SMA in lung sections was quantified. DR7dA at 0.5 mg/kg and 2.5 mg/kg significantly reduced the area of α-SMA compared to saline and BLM-treated groups.

(E) Western blot analysis for α-SMA, Fibronectin, MMP2, and GAPDH. BLM treatment significantly increased the expression of α-SMA and Fibronectin, while DR7dA and NAC treatment reduced the expression of these proteins.

(F) Band intensity of α-SMA, Fibronectin, and MMP2 was measured. DR7dA at 0.5 mg/kg and 2.5 mg/kg significantly reduced the band intensity of these proteins compared to saline and BLM-treated groups.

(G) The ratio of α-SMA to GAPDH was calculated. DR7dA at 0.5 mg/kg and 2.5 mg/kg significantly reduced the ratio compared to saline and BLM-treated groups.

(H) The ratio of MMP2 to GAPDH was calculated. DR7dA at 0.5 mg/kg and 2.5 mg/kg significantly reduced the ratio compared to saline and BLM-treated groups.

(I) The ratio of Fibronectin to GAPDH was calculated. DR7dA at 0.5 mg/kg and 2.5 mg/kg significantly reduced the ratio compared to saline and BLM-treated groups.
DR7dA, a novel antioxidant peptide analog, demonstrates antifibrotic activity in pulmonary fibrosis in vivo and in vitro

Lu Cheng¹·², Dan Wang¹·², Bochuan Deng¹, Jieru Li¹, Jiao Zhang¹, Xiaomin Guo¹,
Tiantian Yan¹, Xin Yue¹, Yingying An¹, Bangzhi Zhang¹·*, Junqiu Xie¹·*
Supplementary Materials

Supplementary Figure 1. Identification of DR7dA with mass spectrometry.

Supplementary Figure 2. Purification of DR7dA with reverse phase HPLC.