

# The PPAR- $\gamma$ agonist pioglitazone alleviates bleomycin-induced lung fibrosis in male BALB/c mice

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## ABSTRACT

**Background:** Many transcription factors may be involved in the pathogenesis of pulmonary fibrosis (PF). One such factor is PPAR $\gamma$ . The PPAR $\gamma$  agonist, pioglitazone (PG), has demonstrated general lung protective activity in animal models and is considered a promising therapeutic agent for fibrotic intervention. This study aimed to investigate the effect of PG on the expression of connective tissue remodeling genes in the lungs using bleomycin (BLM)-induced lung fibrosis (BIF).

**Methods:** The study was conducted on male BALB/c mice. PF was induced by pretreatment with bleomycin sulfate and cyclophosphamide. The mice were randomly divided into 3 groups: the first group was administered BLM at a dose of 0.15 U/kg in 50  $\mu$ l of sterile saline (0.9% NaCl), and the second group was administered 50  $\mu$ l of saline. The third group was not induced with pulmonary fibrosis and served as a control group. On the 4<sup>th</sup> day of the experiment, animals from the first and second groups were randomly divided into animals that received PG orally at a dose of 20 mg/kg or saline (40  $\mu$ l) for 14 days. 4-hydroxyproline was determined in right lung tissue samples. Gene expression was determined using real-time PCR.

**Results:** PG administration to BIF mice resulted in a significant reduction and normalization of the total number of BAL cells, fibrosis score, mRNA expression of genes associated with connective tissue – *Col1a1* (P=0.0466), *Col3a1* (P=0.0053), *Mmp2* (P=0.0006), *Tgfb2* (P=0.0459), and *Tgfb3* (P=0.0017), as well as mRNA of genes regulating lung connective tissue inflammation and fibrosis – *Mrc1* (P=0.0263), *Edn1* (P=0.0012), *Pparg* (P=0.0044), *Nr1d1* (P=0.0053) and *Fn1* (P=0.0125).

**Conclusions:** PPAR $\gamma$  activation by PG alleviates BIF by decreasing collagen deposition, *Col1a1* and *Col3a1* mRNA expression, remodeling of lung tissue (decreasing *Mmp2*, *Edn1*, and *Fn1* mRNA), and M2-specific profibrotic macrophage *Mrc1* mRNA.

**Key words:** pulmonary fibrosis, inflammation, bleomycin, pioglitazone, PPAR $\gamma$ .

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**Ethics approval and consent to participate:** This study was performed in line with the principles of the Declaration of Helsinki. Ethical approval and consent to participate in the study were obtained from the Committee on Bioethics and Ethical Issues of Poltava State Medical University (Minutes No. 207 as of 23.08.2022).

**Consent for publication:** Not applicable.

**Availability of data and material:** The data that support the findings of this study are available from the corresponding author upon reasonable request.

**Conflict of interest:** The authors declare no conflicts of interest.

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## Introduction

Pulmonary fibrosis (PF) is a common complication of various lung diseases, including chronic obstructive pulmonary disease [1], bronchial asthma [2], COVID-19 infection [3], idiopathic PF [4], etc., and inhalation of aggressive substances such as silica [5], CO, NO<sub>2</sub>, O<sub>3</sub>, SO<sub>2</sub> [6], and tobacco smoking [7], etc. Severe PF may require lung or lung cell transplantation [8, 9].

The key factors of lung fibrosis are increased endothelial cell activation, dysfunctional vascular barrier integrity [10], excessive fibrillar collagen deposition in the interstitial extracellular matrix [11], impaired macrophage-fibroblast crosstalk [12], extracellular matrix dysregulation [13], and immune inflammation [14]. Many transcriptional factors might be involved in the promotion of lung fibrosis, such as Nf-κB [15], AP-1 [16], STAT3, FOXP1, JUNB, ATF3, FosL2, BATF, and Fra2 [17]. Other transcriptional factors, such as PPAR [18], Kruppel-like factor 2, CEBPA [19], NRF2F2 [20], etc., inhibited lung tissue fibrosis, counteracting profibrogenic factors.

PPARG investigations provided promising results to attenuate PF [21-24] using a PPARG agonist. One of the PPARG agonists, PG, demonstrated common lung protective activity in animal models of acute lung injury [25], pulmonary hypertension, right heart failure [26], hyperoxia-induced lung injury [27], sepsis-induced acute lung injury [28], and alcohol-induced alveolar macrophage phagocytic dysfunction [29], etc. Recently, it was shown that PG might be a potential therapeutic agent for fibrotic intervention [30].

This study assessed the effects of PG on the expression of connective tissue remodeling genes in murine lungs using BIF.

## Material and Methods

### *Animals and experimental protocol*

Four- to 8-week-old BALB/c male mice (n=56) were used throughout the study. Mice were kept at an ambient temperature 20±2°C under a 12h normal phase light-dark cycle and fed a standard diet. Drinking water and food were freely available.

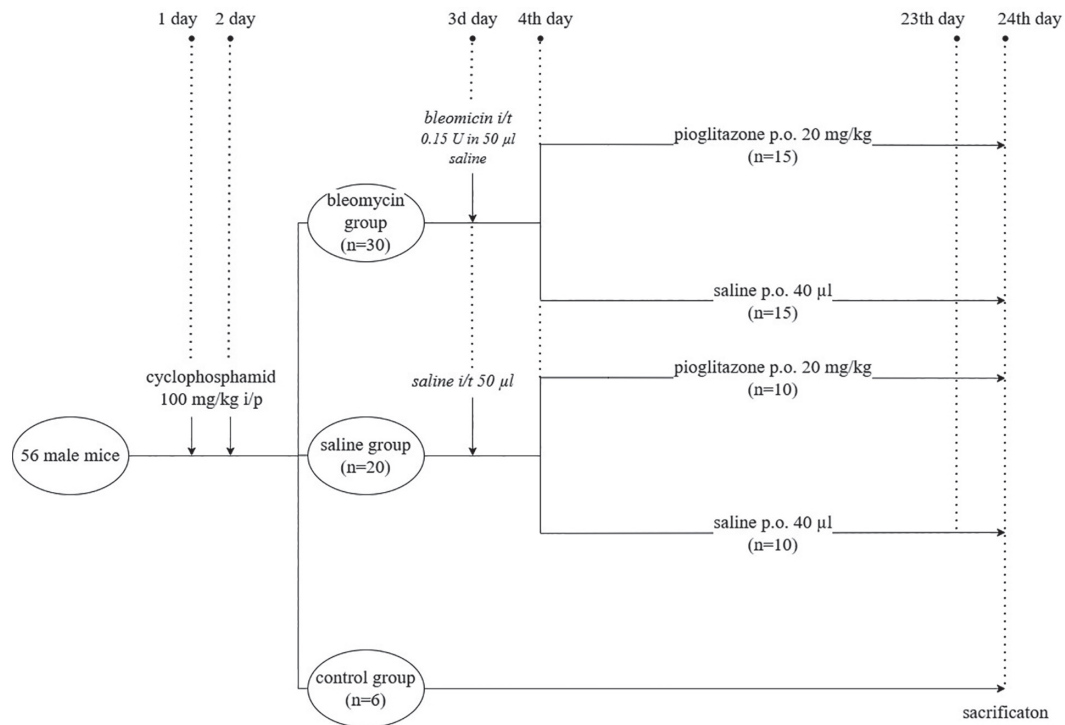
The animal experiment was approved by the Commission on Bioethics and Ethical Issues of Poltava State Medical University (Protocol No. 207 of 23.08.2022).

In the study model, pulmonary fibrosis was induced with bleomycin sulfate in male BALB/c mice with pretreatment with cyclophosphamide to increase the fibrotic response by suppressing T-suppressor T cells, which modulate pulmonary fibrosis *in vivo* in BALB/c mice. For this purpose, 56 male mice were intraperitoneally injected with cyclophosphamide (Endoxan) (Baxter Oncology GmbH, Germany) at a dose of 100 mg/kg two days before BLM instillation. After treatment with cyclophosphamide, mice were randomly divided into 3 groups: the first group (BLM) (n=30) was administered BLM (Sigma-Aldrich, USA, Cat. No. 971) at a dose of 0.15 U/kg in 50 µl of sterile saline (0.9% NaCl) by oropharyngeal aspiration (OA) [31, 32]. The second group of animals (Saline) (n=20) received OA saline 50 µl. Before OA, as described previously, animals were lightly anesthetized with sodium thiopental (50 mg/kg) administered intraperitoneally [33]. The third group (n=6) was not exposed to the induction of pulmonary fibrosis and served as a control group.

After a single OA administration of BLM and saline, on day 4 of the experiment, animals of the first and second groups were randomly divided into animals receiving oral PG at a dose of 20 mg/kg, which was dissolved in sterile saline immediately before administration (40 µl) [34] or saline (40 µL) for n=15 and n=10 animals, respectively, for the first and second groups (hereinafter referred to as BLM + PG, BLM + Saline, and Saline + PG, Saline + Saline, respectively) for 14 days (Figure 1). On day 24 of the experiment, the animals were euthanized by intraperitoneal injection of sodium thiopental at a dose of 250 mg/kg, and the lungs were removed for further biochemical, histopathological, and molecular biological analyses.

### *Determination of 4-hydroxyproline in lung tissue samples*

The right lung lobe samples were weighed, dried in an oven at 90°C, and the weight was recorded again. The weight loss coefficient in mice during the study period was calculated as the ratio of the initial weight



**Figure 1.** Research design.

of the mouse to its final weight. Dry tissues were placed in glass ampoules containing 0.5 ml of 6M HCl (Sigma-Aldrich, USA, Cat. No. H1758) and soldered. Ampoules were boiled at 120°C for 8 hours. After cooling down and adding 5 µl of phenolphthalein (1%, Sigma-Aldrich, USA, Cat. No. 77098), the samples were neutralized with NaOH 10M (Sigma-Aldrich, USA, Cat.No. 1310732). Dark precipitate and brown color were removed by adding 100 µl of carbon suspension (10 mg/ml activated charcoal, Sigma-Aldrich, USA, Cat. No. 7440440) with further centrifugation. 5µl of standard or hydrolyzed sample were pipetted in duplicates onto 96 well plate, and 5 µl citrate acetate buffer (5% citric acid (Sigma-Aldrich, USA, Cat. No. 77929), 7.2% sodium acetate (Sigma-Aldrich, USA, Cat. No. 127093), 3.4% sodium hydroxide, 1.2% glacial acetic acid (Sigma-Aldrich, USA, Cat. No. 64197) was added to each well, as 100 µl of freshly prepared chloramine-T solution (14.1 mg Chloramine-T (Sigma-Aldrich, USA, Cat. No. 7080504), 100 µl n-propanol (Sigma-Aldrich, USA, Cat. No. 102603), 100 µl distilled water, 0.8 ml citrate acetate buffer).

The samples were incubated at room temperature for 20 minutes. After adding 100 µl of Ehrlich's reagent (2.5 g of 4-(dimethylamino)benzaldehyde (Sigma-Aldrich, USA, Cat. No. 102603), 9.3 ml of n-propanol, and 3.9 ml of 70% perchloric acid (Carl Roth, Germany, Cat. No. 7601903), the plate was incubated for 20 minutes at 65°C. After cooling down, the samples were measured at 492 nm on a LabLine-026 (Labline, Austria) photometer, and a standard curve from 0 to 3 mg/ml 4-hydroxyproline (Sigma-Aldrich, USA, Cat. No. 51354) was created. Data were expressed as µg/ right lung lobe [32].

#### *Bronchoalveolar lavage*

Bronchoalveolar lavage (BAL) was performed according to the basic method [35]. Mice were euthanized with thiopental sodium, after which their chest cavities were opened and their left lungs were cannulated through the trachea. The left lungs were washed *in situ* with three consecutive aliquots of sterile 1× PBS, depending on the size of the mouse. The

wash fluid from one mouse was then collected, centrifuged at 1500 rpm for 10 minutes, and the cell pellet was resuspended in phosphate-buffered saline (PBS). To count the total number of cells in BAL, a standard method was used involving the vital dye trypan blue and a hemocytometer [36].

#### *RNA preparation and quantitative reverse transcription PCR*

Mice from all experimental and control groups were used for RNA extraction. Samples were collected from the caudal part of the left lung. Total RNA was extracted from the lung using the RNeasy mini kit (QIAGEN, Germany, Cat. No. 74104). To generate single-stranded DNAs, total RNA ( $\approx 1 \mu\text{g}$ , MaestroNano Spectrophotometer MN-913, Taiwan) was reverse transcribed using QuantiTect<sup>®</sup> Reverse Transcription Kit (QIAGEN, Germany, Cat. No. 205313). For SYBR Green-based analysis, the cDNA equivalent of 50 ng of total RNA from each sample was amplified in the CFX96TM Real-Time PCR Detection system (Bio-Rad, USA) using a QuantiTect<sup>®</sup> SYBR-green PCR Kit (QIAGEN, Germany, Cat. No. 204143).

The gene expressions were detectable as  $2^{-\Delta\text{Ct}}$ . All values were normalized to the expression of the house-keeping gene S2 [37].

The sequences of specific primers used for real-time PCR are provided in Table 1. All oligonucleotides were obtained from Metabion International AG (Germany).

All pairs of primers were checked for specificity by Primer-BLAST software (<https://www.ncbi.nlm.nih.gov/tools/primer-blast/index.cgi>), and PCR products were verified by the automatic capillary electrophoresis system QIAxcel Advanced (QIAGEN, Germany).

#### *Histological analysis*

For histopathological analysis, the middle 1/3 of the left lobe of each animal's lung was excised and inflated with 10% neutral buffered formalin immediately after sacrifice. Tissue samples were paraffin-embedded, and 3  $\mu\text{m}$ -thick sections were stained with Mallory's trichrome (Abcam, Cat. No. 150686), which highlights collagen fibers in varying intensities of blue.

Digital images were acquired using an Axiocam 105 Color camera mounted on an Axio Lab.A1 light microscope (Carl Zeiss, Göttingen, Germany) and processed using ZEN 2.5 Lite software (Blue edition, version V1.0 ru 04/2018 103).

An experienced pathologist, familiar with the study groups, assessed the level of fibrosis, defined as the presence of collagen structures, in all lung sections using a semiquantitative approach. Five areas of view were evaluated per tissue section using pixel-by-pixel analysis (pixel size:  $2.2 \times 2.2 \mu\text{m}$ ), followed by the calculation of the ratio of the collagen-stained area to the total lung tissue area, referred to as the quantitative fibrosis coefficient. Image analysis was conducted using ImageJ open-source software. Staining vectors for collagen-rich areas were determined manually based on color information and the spatial localization of tissue structures.

To assess the reproducibility of collagen quantification, 12 measurements were conducted on 6 pairs of consecutive lung tissue sections stained using Mallory's trichrome method across different staining batches, following the protocol outlined by Masugi et al. [43].

#### *Statistical analysis*

Descriptive statistics was applied to the data using the GrafPad Prism version 8.0.1 for Windows statistical software package (GraphPad Prism Software, USA). Determination of the correspondence of quantitative indicators of the Gaussian distribution in groups was carried out using the D'Agostino-Pearson normality test. In the case of a normal distribution, the parametric statistics one-way ANOVA was used for multiple comparisons with subsequent testing of statistical hypotheses for pairwise comparisons using the Tukey test. If it was impossible to determine the normality of the distribution due to the small size of the group, calculations were performed using the non-parametric statistics Kruskal-Wallis test. The data on the graphs were presented as scatter plots of individual values, boxes with lines of the mean and standard deviation ( $M \pm SD$ ) and violin plot for each of the studied groups. The study was based on the null hypothesis that administration of BLM, PG, or saline solution does not lead to changes in lung fibrosis or mRNA

**Table 1.** Primer sequences for mRNA measurement.

Gene	Primer sequences	Oligo ID	References
<i>Mrc1</i>	Forward: GTGGAGTGATGGAACCCAG	230111B085A01 1/52	[38]
	Reverse: CTGTCCGCCAGTATCCATC	230111B085B01 2/52	
<i>Col1a1</i>	Forward: CTGACGCATGGCCAAGAAGA	230111B085A02 9/52	[39]
	Reverse: ATACCTCGGGTTTCCACGTC	230111B085B02 10/52	
<i>Col3a1</i>	Forward: GGTGGTTTTTCAGTTCAGCTATGG	230111B085C02 11/52	
	Reverse: CTGGAAAGAAGTCTGAGGAATG	230111B085D02 12/52	
<i>Edn1</i>	Forward: CCACAGACCAGGCAGTTAGAT	230111B085E02 13/52	
	Reverse: TGAATGGTACTTTGGGCCCTGA	230111B085F02 14/52	
<i>Fn1</i>	Forward: TCCAGCCCCACCCTACAAGT	230111B085A03 17/52	
	Reverse: CCAGACCAAACCATAAGAAC	230111B085B03 18/52	
<i>Mmp2</i>	Forward: TCAACGGTCGGGAATACAGC	230111B085E01 5/52	[40]
	Reverse: AGCTGTTGTAGGAGGTGCCCT	230111B085F01 6/52	
<i>Mmp9</i>	Forward: AAGGGTACAGCCTGTTCCCTGGT	230111B085G01 7/52	
	Reverse: CTGGATGCCGTCTATGTCGTCT	230111B085H01 8/52	
<i>Pparg</i>	Forward: CCAGAGCATGGTGCCTTCGCT	211116B056G04 31/87	[41]
	Reverse: CAGCAACCATTTGGGTCAGCTC	211116B056H04 32/87	
<i>Tgfb2</i>	Forward: CAGGAGTGGCTTACCACAAAG	230111B085E03 21/52	[37]
	Reverse: TGGCATATGTAGAGGTGCCATCA	230111B085F03 22/52	
<i>Tgfb3</i>	Forward: TCGACATGATCCAGGGACTG	230111B085G03 23/52	
	Reverse: CCACTGAGGACACATTGAAACG	230111B085H03 24/52	
<i>Nr1d1</i>	Forward: CGTTTCGCATCAATCGCAACC	191115B025G10 164/193	[42]
	Reverse: GATGTGGAGTAGGTGAGGTC	191115B025G06 132/193	
S2	Forward: TGCCAGTGCAGAAGCAGACT	230111B085A04 25/52	[37]
	Reverse: CACCAAGACCAACGTGACCA	230111B085B04 26/52	

expression in mouse lung tissue. P-values of  $<0.05$  were considered statistically significant.

## Results

### *Changes in 4-Hydroxyprolin and BAL Cellularity After BIF and PG Treatment in the Mouse Lung*

We did not find any statistically significant differences in 4-Hydroxyprolin concentration in lung tissue, either after BIF or PG treatment (Figure 2A). We observed a significant increase in the total cell count in BAL in mice after BLM oropharyngeal instillation ( $P=0.0061$ ). PG treatment of mice with BIF led to a significant decrease and normalization of the total cell count in BAL ( $P=0.0196$ ) (Figure 2B). We have noted statistically significant differences in mice weight loss ratio after BLM oropharyngeal instillation ( $P=0.0029$ ) (Figure 2C).

### *The changes in mouse lung morphology after BIF and PG treatment*

The BIF development induced a significant increase in the fibrosis coefficient in the lung compared with control ( $P=0.0033$ ), Saline + Saline ( $P=0.006$ ), and Saline + PG ( $P=0.0001$ ) groups (Figure 3A). PG treatment significantly decreased the fibrosis coefficient in comparison with BIF mice ( $P=0.0041$ ).

Pathohistological scores in the main experimental group (BLM + PG) showed significant alleviation of BIF (Figure 3). In this group, the level of fibrosis did not significantly differ from that of the comparison groups: Saline + PG, Saline + Saline, or control.

In the BLM + Saline group, fibrosis scores reached the highest levels compared with all other groups, confirming the development of bleomycin-induced lung pathology.

The control and comparison groups – comprising mice treated with saline alone, saline administered twice, or PG combined with saline – showed no statistically significant differences in collagen deposition. All groups demonstrated normal lung architecture across all examined sections.

### *Changes in Col1a1, Col3a1, Mmp2, Mmp9, Tgfb2, and Tgfb3 mRNA after BIF and PG Treatment in the Mouse Lung*

The levels of connective tissue-related genes' mRNA during BIF and after PG administration are shown in Figure 4. Treatment of control mice with oropharyngeal or oral saline and PG did not induce any significant changes in the mRNA expression of all investigation genes. The development of BIF significantly increased mRNA of *Col1a1* in comparison with control mice ( $P=0.0052$ ); *Col3a1* – with control and saline-treated mice ( $P=0.0015$ ,  $P=0.0030$ , respectively); *Mmp2* – with saline-treated mice ( $P=0.0373$ ). At the same time, we observed a statistically insignificant increase in the mRNA expression of *Mmp9*, *Tgfb2*, and *Tgfb3* genes. PG treatment of BIF mice significantly decreased the mRNA expression of *Col1a1* ( $P=0.0466$ ), *Col3a1* ( $P=0.0053$ ), *Mmp2* ( $P=0.0006$ ), *Tgfb2* ( $P=0.0459$ ), *Tgfb3* ( $P=0.0017$ ), and insignificantly decreased *Mmp9*.

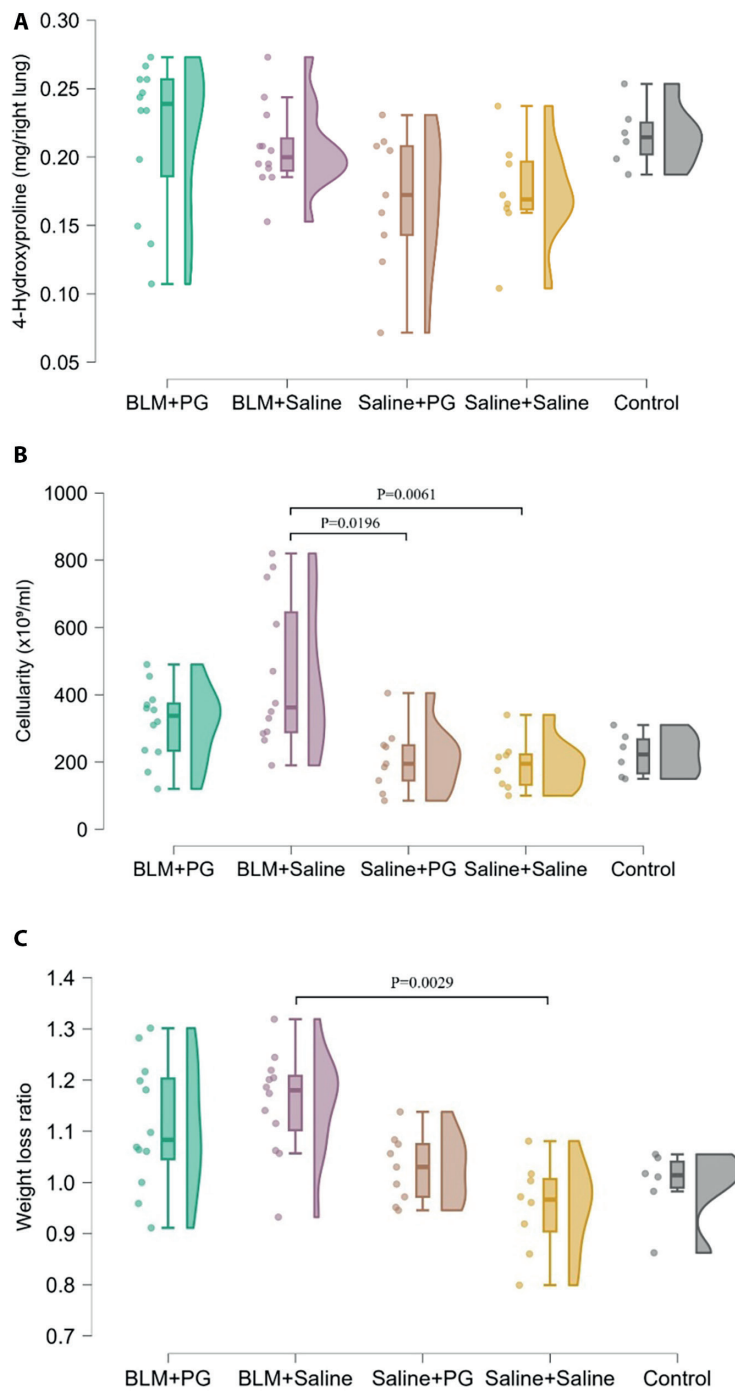
### *Changes in Mrc1, Edn1, Pparg, Nr1d1, and Fn1 mRNA after BIF and PG treatment in the mouse lung*

Figure 5 shows the mRNA expression of some genes that can regulate connective tissue inflammation and fibrosis in lung tissue. Control mice treated with oropharyngeal or oral saline and PG did not exhibit significant changes in the mRNA levels of the investigated genes. Fibrosis induced by BLM led to an increase in mRNA expression for *Mrc1* compared with control ( $P=0.0007$ ) and saline-treated ( $P=0.0166$ ) mice; *Edn1* compared with saline-treated mice ( $P=0.0458$ ); and *Fn1* compared with control mice ( $P=0.0205$ ). *Pparg* and *Nr1d1* showed an insignificant increase in mRNA levels.

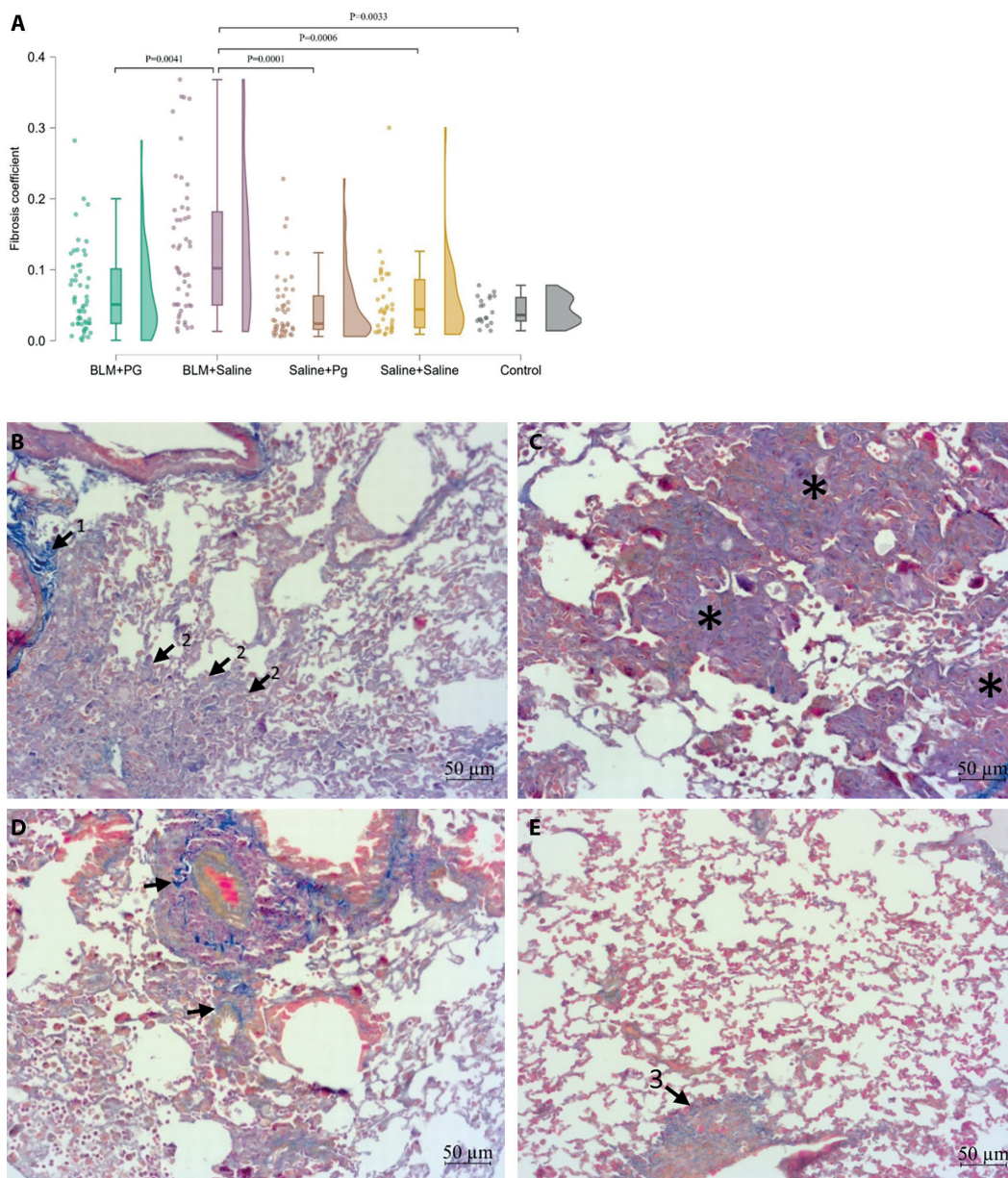
PG administration to BIF mice revealed a statistically significant decrease in *Mrc1* ( $P=0.0263$ ), *Edn1* ( $P=0.0012$ ), *Pparg* ( $P=0.0044$ ), *Nr1d1* ( $P=0.0053$ ), and *Fn1* ( $P=0.0125$ ) mRNA.

## Discussion

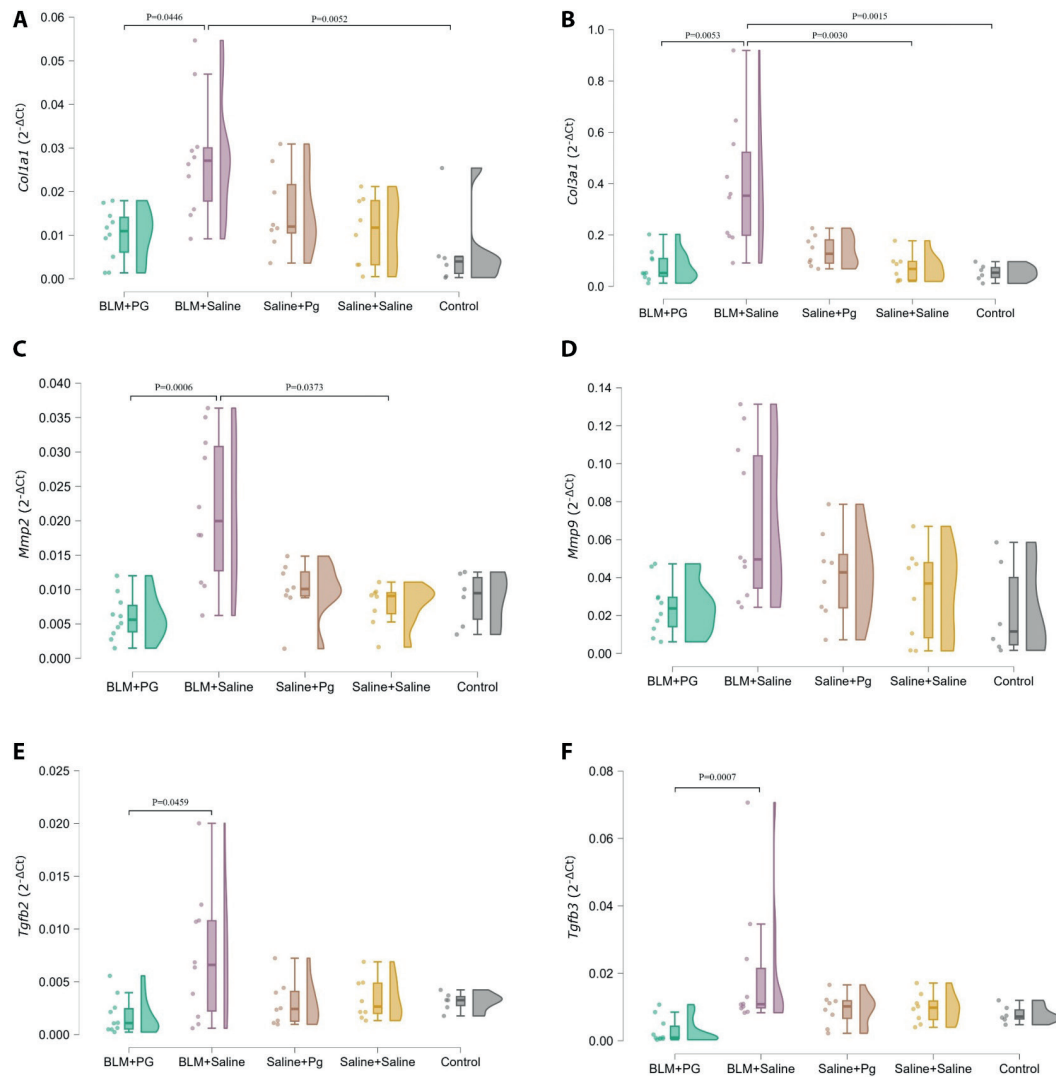
For the study of PG antifibrotic activity in the mouse lung, the model of BIF was used, following the



**Figure 2.** Changes in oxyproline content morphometric parameters in mouse lung tissue after the administration of pioglitazone during experimental inflammatory pulmonary fibrosis: A) 4-hydroxyproline/right lung; B) cellularity of bronchoalveolar lavage; C) weight loss ratio. Between-group differences were determined by one-way ANOVA with Tukey's *post hoc* test. The Kruskal-Wallis test was used to compare the Control group with all others. Exact P-values are given.



**Figure 3.** Lung tissue changes after the administration of PG during experimental PF (Mallory's trichrome staining). Scale bars 50  $\mu\text{m}$ . A) changes of fibrosis coefficient in the lung of investigated groups. Representative histological section demonstrating collagen depositions in mouse lungs: B) decreased fibrosis persisting along the bronchovascular bundles following PG administration (1 – physiological collagen deposition; 2 – area of fibrotic changes in lung tissue (BLM + PG group); C) increased fibrosis spread from the bronchovascular bundles. Asterisks indicate areas of fibrotic changes in the lung tissue (BLM + Saline group); D) collagen structures of the lung appear normal along the bronchovascular bundles (arrows) in Saline + PG (comparison group); E) area of potential lung tissue fibrosis (Saline + Saline group). Between-group comparisons were performed using one-way ANOVA with Tukey's *post hoc* test. Exact P-values are given.

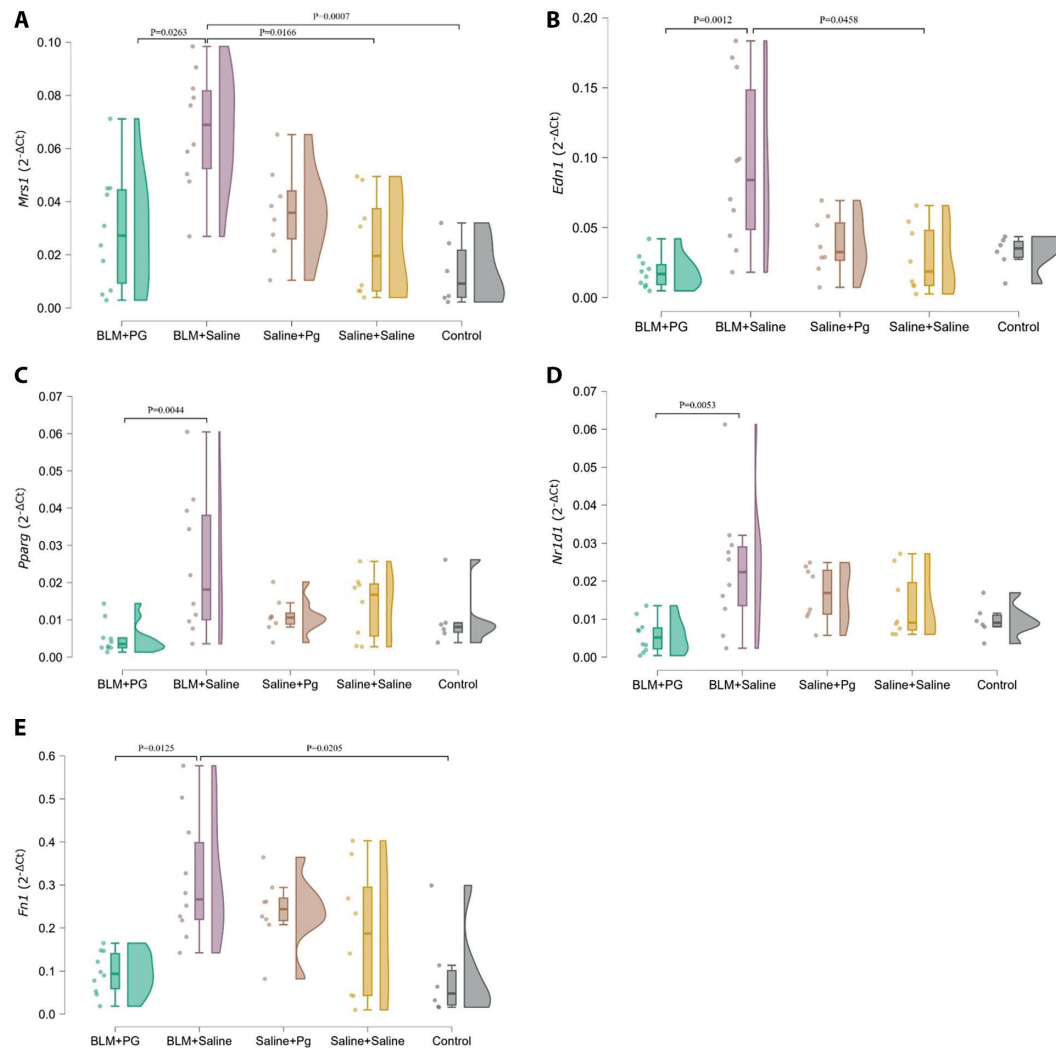


**Figure 4.** Changes in gene expression levels: A) *Col1a1*; B) *Col3a1*; C) *Mmp2*; D) *Mmp9*; E) *Tgfb2*; F) *Tgfb3*. Between-group differences were determined by one-way ANOVA with Tukey's *post hoc* test. The Kruskal-Wallis test was used to compare the Control group with all others. Exact P-values are given.

inhibition of cyclophosphamide-sensitive T cells [31]. This model produced the highest collagen synthesis in the lung 21 days after BLM administration. PG was administered for 20 days after BLM installation, and this time course was optimal for the investigation of its antifibrotic activity [44, 45].

Induction of BIF led to the increase of BAL total cellularity and lung hydration. At the same time, during the pathomorphological examination, fibrosis coefficient increased significantly. These data were accompanied by an increase in *Col1a1* and *Col3a1* genes expression, and *Mmp2* gene expression.

COL1A1, a member of the collagen family involved in epithelial-mesenchymal transition [46], might serve as a fibrotic progression marker [47]. Similar properties were described for COL3A1 [48], and this protein might act synergistically with COL1A1 [49]. These findings suggest the development of lung fibrosis and collagen over-deposition. Although collagen over-deposition is a hallmark of lung fibrosis, current research mostly focuses on the cellular aspect, leaving collagen, particularly its dynamic remodeling (degradation and turnover), largely unexplored [50]. We did not observe statistically significant



**Figure 5.** Changes in gene expression levels: A) *Mrc1*; B) *Edn1*; C) *Pparg*; D) *Nr1d1*; E) *Fn1*. Between-group differences were determined by one-way ANOVA with Tukey's *post hoc* test. The Kruskal-Wallis test was used to compare the Control group with all others. Exact P-values are given.

differences in 4-hydroxyproline concentration. This result reminds us to be cautious when using the 4-hydroxyproline content assay to evaluate the severity of lung fibrosis [51].

At the same time, we observed an increase in *Tgfb2* mRNA expression and *Tgfb3* mRNA expression (statistically insignificant). These TGF-beta isoforms drive the pathogenesis of fibrotic diseases, including lung fibrosis [52, 53].

Induction of BIF showed an increase in lung *Mrc1* mRNA expression. The *Mrc1* gene encodes the synthesis of macrophage scavenger receptor 1 (CD206). CD206-expressing M2 macrophages are involved in

lung fibrosis progression [54]. Also, in lung fibrosis, the endothelin-1 played an important role in derived fibroblast activation, proliferation, as well as differentiation into myofibroblasts – processes that lead to excessive collagen deposition [55]. We also observed the increase of *Edn1* mRNA in mice lungs. Another potential contributor to lung fibrosis is fibronectin 1 (Fn1) [56], which might be involved together with collagen type 1 in airway remodeling [57]. In murine BIF, there was an increase in *Fn1* mRNA.

In our study, we estimated the mRNA expression of two important nuclear receptors, NR1D1 (Rev-Erb alpha) and PPAR-gamma, which have a wide range

of downstream target genes that are involved in many physiopathological processes, such as immunity, inflammation, autophagy, metabolism, etc. [24, 58]. After the BIF induction, a statistically insignificant increase in *Pparg* and *Nr1d1* mRNA was observed. This insignificance can be explained by the high individual variation of gene expression. We hypothesize that this slight increase of *Pparg* and *Nr1d1* mRNA might display the beginning of restorative processes in lung tissue on the 20<sup>th</sup> day after BIF induction. This suggestion goes in parallel with the observation of the importance of *Pparg* in the pathogenesis of lung fibrosis in other models [59] as well as *Nr1d1* [60]. It was shown that Rev-Erb alpha reduced PF by suppressing fibroblast differentiation [61]. Moreover, the absence of PPARG-associated ligands may have led to a compensatory increase in expression of their receptors [62].

Thus, the development of the BIF model led to an increase in collagen deposition, *Col1a1* and *Col3a1* mRNA expression with complicated lung tissue remodeling (*Mmp2*, *Edn1*, and *Fn1* mRNA overexpression), and *Mrc1* (CD206) mRNA expression (characterizing profibrotic M2 macrophages).

Administration of the PPARG agonist PG decreased collagen deposition, *Col1a1*, and *Col3a1* mRNA expression. At the same time, we observed the decreasing of *Tgfb2* and *Tgfb3* mRNA expression. *Mmp2* mRNA expression, as well as *Mrc1*, *Edn1*, and *Fn1*, were decreased after PG treatment. In addition, PG administration statistically significantly decreases the *Pparg* and *Nr1d1* mRNA expression up to the normal level. This observation needs further discussion. In the basal state, the PPAR-RXR complex is bound to corepressor and is transcriptionally inactive. The binding of different ligands promotes a conformational change, which results in the release of corepressors, allowing the recruitment of – and the interaction with coactivators [63]. It was shown that after PPARG stimulation, PPAR-RXR complex interacts with target genes and cell-type-specific coregulators, and this led to the decrease of *Pparg* expression [64, 65]. On the other hand, NR1D1 (Rev-Erb alpha) is an orphan nuclear receptor and is induced by PPARG activation [66]. These data support the idea of coordinated expression of *Pparg* and *Nr1d1* genes.

PG didn't have a statistical significant effect after saline exposure on the mRNA expression of *Col1a1*, *Col3a1*, *Mmp2*, *Mmp9*, *Tgfb2*, *Tgfb3* as well as *Mrc1*, *Edn1*, *Pparg*, *Nr1d1*, *Fn1* in healthy animals. These data go in parallel with observations that PG primarily acts to normalize increased tissue expression of profibrotic factors, rather than decrease basal (normal) expression in healthy tissues [67–71].

Thus, PG treatment alleviates the development of BIF through the activation of PPARG with consequent depression of TGF-beta/Smad pathways [72–74], which had an important role for procollagen 1A1, 3A1, and fibronectin synthesis [75]. In addition, PG prevented endothelin-1 mRNA expression during lung fibrosis. The endothelin-1 promotor recruits AP-1, HIF-1, and GATA2 [76], which counteract PPARG [77–79].

Our study has several limitations: 1) significant individual variability in the mRNA expression together with the limited number of animals per group may reduce the sensitivity of the study; 2) the future investigations on protein level are needed to prove antifibrotic and immunomodulative activity of PG, including cytokines and PPARG cofactors.

## Conclusion

Activation of PPARG by PG alleviates BIF, decreasing collagen deposition, *Col1a1* and *Col3a1* mRNA expression, remodeling of lung tissue (decreasing *Mmp2*, *Edn1*, and *Fn1* mRNA), and M2-specific profibrotic macrophage *Mrc1* mRNA.

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