Pirfenidone Is Renoprotective in Diabetic Kidney Disease

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ABSTRACT

Although several interventions slow the progression of diabetic nephropathy, current therapies do not halt progression completely. Recent preclinical studies suggested that pirfenidone (PFD) prevents fibrosis in various diseases, but the mechanisms underlying its antifibrotic action are incompletely understood. Here, we evaluated the role of PFD in regulation of the extracellular matrix. In mouse mesangial cells, PFD decreased TGF-β promoter activity, reduced TGF-β protein secretion, and inhibited TGF-β–induced Smad2-phosphorylation, 3TP-lux promoter activity, and generation of reactive oxygen species. To explore the therapeutic potential of PFD, we administered PFD to 17-wk-old db/db mice for 4 wk. PFD treatment significantly reduced mesangial matrix expansion and expression of renal matrix genes but did not affect albuminuria. Using liquid chromatography with subsequent electrospray ionization tandem mass spectrometry, we identified 21 proteins unique to PFD-treated diabetic kidneys. Analysis of gene ontology and protein–protein interactions of these proteins suggested that PFD may regulate RNA processing. Immunoblotting demonstrated that PFD promotes dosage-dependent dephosphorylation of eukaryotic initiation factor, potentially inhibiting translation of mRNA. In conclusion, PFD is renoprotective in diabetic kidney disease and may exert its antifibrotic effects, in part, via inhibiting RNA processing.


Diabetic nephropathy (DN) is the single major cause of the emerging epidemic of ESRD in the United States,1 accounting for nearly 50% of all new cases.2 Characteristic morphologic lesions of DN include glomerular hypertrophy, thickening of the basement membrane, and mesangial expansion.3 Several interventions, such as tight glycemic control and antihypertensive therapy, especially angiotensin-converting enzyme inhibitors (ACEIs) and angiotensin II receptor blockers,4–9 have been shown to slow the progression of established disease. Nevertheless, DN remains a major long-term complication of both types 1 and 2 diabetes,10,11 because treatment commenced after the manifestation of overt clinical nephropathy often does not arrest progression to ESRD.11 The annual medical cost for treatment of patients with diabetes ESRD is expected to be $18 to 30 billion (US) during the next decade.12–15 It is therefore imperative to identify...
novel drug-therapeutic regimens that can ideally arrest further progression of the disease after manifestation of nephropathy.

Pirfenidone (PFD; 5-methyl-1-phenyl-2-(1H)-pyridone) is a low molecular weight synthetic molecule that exerts dramatic antifibrotic properties in cell culture and various animal models of fibrosis.16,17 PFD has emerged as a promising oral treatment with few adverse effects in open-label clinical studies. A study of hemodialysis patients with a history of sclerosing peritonitis demonstrated that it may not be necessary to adjust dosages of PFD for renal impairment and that the drug is well tolerated even in ESRD.18 In an open-label study wherein PFD dosages of PFD for renal impairment and that the drug is well tolerated even in ESRD,18 In an open-label study wherein PFD was administered to patients with advanced refractory focal sclerosis, there was a good safety profile in patients with impaired renal function and heavy proteinuria, and PFD slowed the rate of decline of renal function by 25%.19 In a Phase III trial for patients with idiopathic pulmonary fibrosis in Japan, PFD was reported to promote stabilization and improvement of lung function.20 Of note, there have been no reports that PFD may worsen renal blood flow, lower BP, affect glycemic parameters, or cause hyperkalemia, thereby making this treatment approach truly unique as compared with presently available renin-angiotensin-aldosterone antagonists. Thus, the combined experience with PFD in patients and in animal models of progressive kidney disease suggests that the compound is safe and may provide stabilization of renal function.

To determine whether PFD is potentially beneficial in diabetic kidney disease, we studied the effects of PFD in cell culture experiments and in the db/db mouse model of diabetic kidney disease. In cell culture studies, PFD inhibited TGF-β production and TGF-β signaling and reduced TGF-β-induced reactive oxygen species (ROS) production. In the db/db mouse, PFD promoted resolution of mesangial matrix when administered after the onset of nephropathy. For identification of novel pathways of PFD relevant to DN, proteomic studies of the whole kidneys followed by bioinformatic analyses revealed RNA processing as a novel mechanism of PFD action. In support of a role of PFD to affect mRNA translation, PFD was found to regulate the activity of eukaryotic initiation factor (eIF4E), a key mRNA cap-structure binding protein, in mesangial cells in culture.

RESULTS

Pirfenidone Reduces TGF-β Production and Inhibits TGF-β Signaling

To determine whether PFD regulates TGF-β production in murine mesangial cell (MMC) line, we performed studies to evaluate the effect of PFD on the glucose-responsive TGF-β1 promoter (pA835)21 and on TGF-β1 protein secreted in the conditioned media (Figure 1). PFD was able to reduce both the TGF-β1 promoter activity and TGF-β1 protein secretion but at different dosages. The promoter activity was significantly inhibited at 500-µg/ml concentrations, whereas PFD inhibited secreted TGF-β protein at 100 µg/ml (Figure 1). Thus, in relation to the TGF-β system, PFD seems to be more sensitive to inhibit protein production as compared with gene transcription.

To evaluate effects of PFD on TGF-β signaling, we assessed Smad2 phosphorylation and 3TP-Lux activity. PFD inhibited TGF-β1-induced Smad2 phosphorylation (Figure 2A) at all dosages of 100 to 1000 µg/ml. Surprisingly, there was also an effect of PFD to reduce total Smad2/3 protein. PFD also inhibited TGF-β1–induced 3TP-Lux activity as shown in Figure 2B, but the inhibition reached significance only at a concentration of 1000 µg/ml.

Pirfenidone Reduces TGF-β–Induced Mesangial Cell ROS Generation

We recently demonstrated that TGF-β stimulates ROS production via an NADPH oxidase pathway and with a time course that is likely independent of Smads.22 Because PFD has been postulated to inhibit NADPH oxidase in other cell types,23 we determined whether there was a similar effect of PFD to block TGF-β–induced ROS in mesangial cells. As shown in Figure 3, PFD blocked the TGF-β–induced increase in the ROS production in mesangial cells (100 to 1000 µg/ml, in a dosage-dependent manner).
PFD Inhibits TGF-β1-Induced Matrix Gene Expression in Mesangial Cells

Mesangial cells exposed to TGF-β1 (10 ng/ml) for 24 h exhibit a stimulation of α1(I) collagen and α1(IV) collagen mRNA levels (Figure 4). Pretreatment with PFD (added 30 min before TGF-β1 addition) reduced TGF-β-stimulated type I collagen (Figure 4A) and type IV collagen (Figure 4B).
Table 1. Clinical parameters of mice at the beginning and the end of study

<table>
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<tr>
<th>Mice</th>
<th>Body Weight (g)</th>
<th>Urinary Albumin:Creatinine (µg/mg)</th>
<th>Blood Glucose (mg/dl)</th>
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<td>Db/m</td>
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<td></td>
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<tr>
<td>baseline</td>
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<td>36.42 ± 45.00</td>
<td>216.90 ± 43.00</td>
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<tr>
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<tr>
<td>Db/db</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>baseline</td>
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<td>670.90 ± 334.50</td>
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<tr>
<td>end of study</td>
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<td>427.00 ± 249.00</td>
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<tr>
<td>Db/db + PFD</td>
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<td>baseline</td>
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<td>443.00 ± 391.00</td>
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<td>42.00 ± 2.95</td>
<td>779.00 ± 561.00</td>
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</tbody>
</table>

aData are means ± SEM.

b\(P < 0.05\) versus db/m at baseline.

c\(P < 0.05\) versus db/m at end of study.

PFD Treatment Alters Protein Expression in the Kidney

To identify potential new pathways by which PFD may be beneficial in diabetic kidney disease, we carried out proteomics of kidneys from the nondiabetic, diabetic, and diabetic mice treated with PFD. Proteomics were performed on kidney lysate by liquid chromatography with subsequent tandem mass spectrometry (LC-MS/MS), and the results are summarized in the Venn diagram shown in Figure 6. Twenty-one proteins were uniquely found in PFD-treated diabetic kidneys (Table 3). Several of these proteins were involved in calcium signaling, RNA translation, nucleotide-binding proteins, and nuclear translocation.

Network-Based Analysis Reveals a Possible New Mechanism of PFD Action in Diabetic Kidney Disease

To gather more insight into the PFD-activated pathways in the diabetic kidney, we explored the 21 newly identified PFD-unique proteins (Table 3) with respect to their physical interactions in a protein–protein interaction network (PPI). Due to the paucity of murine PPI data, we assembled a corresponding human PPI network, comprising 57,235 interactions among 11,203 proteins, integrated from yeast two-hybrid experiments, predicted interactions via orthology, and curation of the literature. Of the 21 PFD-unique mouse proteins, 14 have clear human orthologs (Table 4) and 11 were able to be mapped onto the PPI network (Figure 7). Aiming to construct a PFD-centered network, we then pulled out the first interacting neighbors of the 11 PFD-unique proteins, resulting in a network comprising 518 proteins and 655 interactions. Interestingly, there was only one interaction between two PFD-unique proteins: The splicing factor arginine/serine-rich involved in premRNA splicing (SFRS4) and the heterogeneous nuclear ribonucleoprotein H (hnRNPH2; Figure 7). Gene ontology and pathways enrichment analysis revealed that the majority of the significantly enriched biologic functions are related to posttranscriptional or posttranslational regulation pathways such as ubiquitin cycle, control of protein translation, and mRNA processing. Of particular interest is the interplay between hnRNPH2 and SFRS4. Both of these proteins not only physically interact with each other but also share 90 interacting proteins with members of the heterogeneous nuclear ribonucleoproteins, splicing factors, and mRNA polymerase protein families. These proteins are central to pathways involved with pre-mRNA processing, splicing, and localization (Figure 7).

PFD Treatment Regulates elf4E Phosphorylation

Several studies have shown that increased phosphorylation of elf4E stimulates initiation of mRNA translation. elf4E phosphorylation increases binding to capped mRNA in vitro, thereby modulating mRNA translation initiation in cells.
Smad phosphorylation and TGF-β relevant to the proteomic approach, we identified novel pathways that may be protective after the onset of diabetic kidney disease. Using a microvascular approach, we demonstrate that PFD can block TGF-β transduction, and inhibit TGF-β-induced matrix stimulation in mesangial cells. In the db/db mouse, PFD provides histologic protection after the onset of diabetic kidney disease. Using a proteomic approach, we identified novel pathways that may be relevant to the in vivo effects of PFD in diabetic kidney disease.

The inhibition of the glucose-responsive promoter of TGF-β suggests that PFD would have effects on the regulation of signaling pathways and transcription factors involved in high-glucose stimulation of the TGF-β1 gene. The signaling pathways stimulated by high glucose to regulate TGF-β include protein kinase C, extracellular signal–regulated kinase, p38, and ROS production. Which of these pathways may be involved to inhibit high-glucose stimulation is unclear.

PFD seems to have several effects in the Smad pathway. Our data demonstrate that PFD inhibits Smad2 phosphorylation. PFD is able to inhibit the stimulation of both type I collagen synthesis and type I collagen expression.

DISCUSSION

Novel treatments for DN are urgently required. Antifibrotic agents that are orally available and work via a nonhypoglycemic and nonhypertensive pathway would be especially attractive as disease-modifying therapies. In this study, we demonstrate the effects of PFD to inhibit numerous pathways in cell culture and in a mouse model of diabetic kidney disease. Although the exact mechanism of action remains unclear, we demonstrate that PFD can block TGF-β production at the transcriptional and protein levels, inhibit TGF-β-induced Smad phosphorylation and TGF-β–induced gene transcription, and inhibit TGF-β–induced matrix stimulation in mesangial cells. In the db/db mouse, PFD provides histologic protection after the onset of diabetic kidney disease. Using a proteomic approach, we identified novel pathways that may be relevant to the in vivo effects of PFD in diabetic kidney disease.

Table 2. PFD reduces glomerular mesangial matrix expansion

<table>
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<th>Parameter</th>
<th>% of Glomeruli Counted (Mean Grid No.)</th>
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</tr>
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<tr>
<td></td>
<td>Grade 1</td>
<td>Grade 2</td>
</tr>
<tr>
<td>Db/m</td>
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<td>22</td>
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<td>Db/db + PFD</td>
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*P < 0.05 versus db/m.

bP < 0.05 versus db/db.

Table 3. Proteins unique to db/db mouse kidneys treated with PFD

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<th>Name of Protein Identified</th>
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<td>Calbindin-28K [Mus musculus]</td>
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<td>Clathrin, light polypeptide (Lcb) [Mus musculus]</td>
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<td>Eukaryotic translation elongation factor 1 α 1 [Mus musculus]</td>
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<td>Eukaryotic translation elongation factor 1 α 2 [Mus musculus]</td>
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</tr>
<tr>
<td>Glutaminyl-prolyl-tRNA synthetase [Mus musculus]</td>
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</tr>
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<td>Glycine amidinotransferase (l-arginine:glycine amidinotransferase)</td>
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Figure 6. (A) Venn diagram depicting the distribution of proteins in normal db/m mouse kidney. (B) PFD-treated db/db diabetic mouse kidney. (C) db/db diabetic mouse kidney (n = 4).

PFD induced dephosphorylation of eIF4E in a dosage-dependent manner (Figure 8).
and α1(IV) collagen by TGF-β in mesangial cells. Our cell culture data demonstrate that PFD is able to inhibit both the stimulation of TGF-β and its downstream pathways to stimulate matrix gene expression.

Apart from effects of PFD on matrix regulation, there is a growing recognition that PFD has potent anti-inflammatory activities. Of interest is the potent effects of PFD to inhibit TGF-β–induced ROS production in mesangial cells (in this study), suggesting that PFD may be inhibiting NADPH oxidase. Indeed, PFD can inhibit NADPH oxidase, act as a scavenger of ROS and OH−, and inhibit lipid membrane peroxidation, suggesting that one effect of PFD may be via its antioxidant pathway.25,36,37

To determine whether PFD may be renoprotective after the onset of diabetic kidney disease, we chose the C57BLKS db/db mouse model. A major benefit of the model is the consistent temporal development of hyperglycemia (6 to 8 wk), albuminuria (10 to 12 wk), and mesangial matrix expansion (14 to 16 wk). Our treatment protocol therefore started with oral PFD at 17 wk, and the treatment was continued for 4 wk. Even with such a short treatment protocol, we found a significant reduction in the degree of diffuse glomerular mesangial matrix expansion and a reduction in renal gene expression of type IV collagen. The degree of glomerular mesangial matrix expansion and a reduction in renal gene expression of type IV collagen. The degree of resolution of both mesangial matrix expansion and a reduction in renal gene expression of type IV collagen. The degree of gramicidin matrix gene expression was similar to previous studies with intraperitoneally administered anti–TGF-β antibodies.38–40 The results of the preclinical studies in this accepted mouse model of diabetic kidney disease is strong evidence in support of potential renoprotective benefit of oral PFD in human DN.

Interestingly, we did not see a benefit of PFD to reduce albuminuria in the db/db mice. The results are again similar to the effect of anti–TGF-β antibodies in that there is a dissociation of renoprotective benefits and reduction of albuminuria. The data would support the concept that different pathways are involved in regulating albuminuria from mesangial matrix expansion and that renoprotection could occur in the face of persistent albuminuria. Previous reports of animal models of kidney disease demonstrated a consistent reduction of renal matrix accumulation with PFD but varying effects on proteinuria.41–43 These data are important in interpreting clinical data from antifibrotic approaches. It is clearly conceptually possible to have effects to reduce mesangial matrix expansion and by inference protect the GFR, without necessarily reducing albuminuria. Another important factor that seems to be refractive to PFD treatment is the BP. A BP-lowering effect as a result of PFD treatment cannot be ruled out in our studies; however, PFD was not found to lower BP in previous animal or human studies when BP was measured.44–46

Angiotensin receptor antagonists have been used in the db/db mouse model,47–53 and generally show DN to be delayed by the use of ACEIs.47 Although we have not performed comparative studies with blockers of renin–angiotensin system (RAS), we speculate that treatment with PFD will be additive to that of ACEIs and angiotensin antagonists. As PFD has no reported effect on BP or blocking of the RAS, the mechanism of renoprotection by PFD is likely distinct to blockers of the RAS. Of note, one clinical study with PFD in patients with FSGS did not find any reduction of BP.46

Thus far, the only clinical study reported to date for PFD in kidney disease is an open-label study of patients with advanced FSGS.19 This study demonstrated that patients with refractory FSGS, whose disease did not respond to steroids, may have a slower decline in the renal function with PFD. Interestingly, PFD was found to have a significant reduction in slowing the rate of progression without affecting albuminuria.19 However, the lack of effect on proteinuria raises the question of how to monitor patients with antifibrotic therapies to determine

Table 4. Human orthologs of PFD-unique mouse proteins

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<tr>
<th>Mouse Entrez Gene ID</th>
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and α1(IV) collagen by TGF-β in mesangial cells. Our cell culture data demonstrate that PFD is able to inhibit both the stimulation of TGF-β and its downstream pathways to stimulate matrix gene expression.
whether such an approach provides benefit in our animal study. It is also possible that the lack of rapid weight gain could potentially play a role in reducing the degree of progressive kidney disease; however, it is unlikely that this would be the major reason for the PFD-induced improvement, because the mice did continue to gain weight while on the drug. Clearly, for advancing the progress of testing novel clinical therapies, new biomarkers related to ongoing renal fibrosis and inflammation are urgently needed.

As an initial attempt to identify novel biomarkers that would be relevant to PFD treatment of diabetic kidney disease and to understand the potential mechanism of renoprotection, we performed a proteomic screen of the kidneys in our study with db/db mice. Identification of proteins uniquely present in the PFD-treated kidneys demonstrated that several were involved in mRNA translation. Gene ontology and interaction analyses of the human orthologs of PFD-unique mouse proteins revealed a network comprising 518 proteins and 655 interactions and an interplay between hnRNPH and SFRS4. hnRNPH2 binds heterogeneous nuclear RNA and has been shown to have either exon-enhancing or -silencing activity, depending on the context of the binding site. SRFS4 binds to pre-mRNA transcripts and components of the spliceosome and can either activate or repress splicing, depending on the location of the pre-mRNA binding site. Its ability to activate splicing is regulated by phosphorylation and interactions with other splicing factor–associated proteins (http://harvester.fzk.de/harvester/human).

Several studies have previously linked DN to dysregulation of mRNA translational processing, therefore we postulated that the effect of PFD on induction of mRNA processing pathways may underlie its beneficial effects in diabetic kidney disease. One of the key proteins involved in mRNA translation is eIF4E, which binds to the 5’ cap structure of mRNA. Phosphorylation increases the binding of eIF4E to capped mRNA in vitro and results in increased protein synthesis. In mesangial cells, PFD inhibited the eIF4E phosphorylation in a dosage-dependent manner. These data strongly suggest that PFD modulates mRNA/protein synthesis. Interestingly, eIF4E phosphorylation is stimulated by high glucose. The new data are the first evidence that PFD can potentially regulate mRNA translation of proteins, and the proteomic and network analysis suggests that this pathway may be of major significance in diabetic kidney disease.

In summary, PFD has beneficial effects in cell culture systems to reduce TGF-β production and activity. PFD also has potent anti-inflammatory effects as a result of its ability to block ROS production in mesangial cells. Administration of oral PFD led to a dramatic reduction of glomerular mesangial matrix with a short course of therapy after the onset of established disease in the db/db mouse model. As numerous candidate pathways are affected by PFD, further studies using unbiased approaches are necessary to establish the dominant pathways by which PFD may confer renoprotective benefits. These insights will be crucial to best determining the clinical monitoring of patients with progressive kidney disease and improve the likelihood of rapid

Figure 7. Protein–protein interaction network of PFD-unique db/db kidney proteome. The figure depicts the human protein–protein interaction network centered on 11 human proteins orthologous to the mouse proteins identified only in PFD-treated db/db kidneys. The network comprises 518 proteins and 655 interactions. The PFD-unique interacting proteins are grouped in the meta-nodes depicted by rectangular structures. The enriched gene ontology categories are reported for each meta-node with shades based on the enrichment P value. The total number of proteins in each meta-node is also featured.
advancement of novel clinical therapies focused on reducing inflammation and fibrosis.

CONCISE METHODS

Cell Culture and Transfection Studies

MMCs and HEK293 cells were used in cell culture studies. MMCs were originally isolated from kidneys of SJL/J(H-2) normal mice and transformed with non–capsid-forming SV-40 virus to establish a permanent cell line. MMCs were maintained at 37°C in a humidified incubator with 5% CO2/95% air and propagated in DMEM (Life Technologies BRL, Gaithersburg, MD) containing 10 mM d-glucose, 10% FCS, 100 U/ml penicillin, 100 mg/ml streptomycin, and 2 mM supplemental glutamine. HEK293 cells were obtained from American Type Culture Collection (ATCC) (Manassas, VA) and cultured in DMEMG450/10% FCS medium. For transient transfection studies, MMCs or HEK293 cells were transfected using Lipofectamine2000 (Invitrogen, Carlsbad, CA). Plasmids used included the glucose-responsive TGF-β1 promoter-reporter construct pA835-luciferase (pA835-luc), the 3TP-lux TGF-β-sensitive plasmid, and a plasmid for β-galactosidase (pLENXZ) to standardize for transfection efficiency. After transfection, cells were treated with varying dosages of PFD (100 to 1000 µg/ml) for up to 24 h. Cells were then harvested, and luciferase and β-galactosidase activity was measured, as described previously.

Western Blot Analysis

MMCs were grown in six-well plates with DMEM/10% FCS until 80% confluence. Cells were then serum-starved for 16 h and modulated with various dosages of PFD before TGF-β1 treatment. The total protein was isolated by cell lysis buffer (50 mM Tris [pH 7.2], 150 mM NaCl, 1% TritonX-100, 1 mM EDTA, and protease inhibitor cocktail). For phospho-Smad2 detection, 40 µg of total protein was electrophoresed on 10% SDS gel and transferred to the nitrocellulose membrane, blocked, and incubated with pSmad2 antibody at 1:500 dilution. Enhanced chemiluminescence by horseradish peroxidase–tagged secondary antibody enabled visualization of the protein band as described previously. The membranes were subsequently stripped and immunoblotted with total Smad2/3 (Santa Cruz Biotechnology, Santa Cruz, CA). Immunoblotting for phospho-eIF4E was carried out as already described, followed by total eIF4E immunoblotting (Cell Signaling Technology, Danvers, MA).

Intravenous Animal Studies

Five- to 6-wk-old male, homozygous, obese KSJ db/db mice (Lepr-db/db; Jackson Laboratories, Bar Harbor, ME) and the corresponding heterozygote lean controls (db/db) were obtained. Mice were housed four to five per cage in micro-isolators with bedding changes two or three times per week. Animal studies were approved by the institutional animal care and use committee at Thomas Jefferson University. At week 17, the db/db mice were randomly assigned to two test groups: db/db untreated and db/db treated with PFD. The db/db group that was randomized to PFD treatment had 0.5% PFD added to their food at this time, and the mice were individually caged. PFD was provided by Dr. Solomon Margolin (Marnac, Dallas, TX). Mice that were fed PFD took in approximately 25 mg/d PFD and were treated for 4 wk total from week 17 to week 21. At the end of 21 wk, mice underwent 24-h urine collections in metabolic cages and were killed. Urine albumin/creatinine was performed with ELISA specific for albumin (Exocel, Philadelphia, PA) and standardized by urine creatinine (Nova

Figure 8. (A) Effect of PFD dosage on phosphorylation of eIF4E protein. As shown in this Western blot, PFD decreased eIF4E phosphorylation in a dosage-dependent manner. (B) Quantification of P-eIF4E/total eIF4E from immunoblots in A (n = 4). Data are means ± SEM. *P < 0.05 PFD treatment versus control.
and 1/50th of trypsin (wt/wt), 10 μl of this peptide preparation was loaded onto a Thermo Hypersil-Keystone BioBasic C18 column (0.18 mm, 100 mm) that served as the Surveyor HPLC front end of a ThermoElectron ProteomeX Workstation. The peptides were separated at a flow rate of 100 nl/min, using a gradient with Buffer A (0.1% formic acid in water), Buffer B (0.1% formic acid in acetonitrile), and 18S as listed in the Supplemental Methods.

RNA Isolation and Analysis
Total RNA was extracted from mouse kidneys using the RNeasy Mini Kit (Qiagen, Valencia, CA) according the manufacturer’s instructions. Real-time PCR was performed as described previously64,65 using the primers for α1-type I collagen, α1-type IV collagen, fibronectin, and 18S as listed in the Supplemental Methods.

Histopathology
The right kidney was sliced sagittally and placed in buffered formalin. After paraffin embedding, 4-μ sections were stained with PAS. Fifty glomeruli were evaluated for each kidney. The histologic specimens from both treated and nontreated db/db mice as well as controls from db/m mice were scored using a semiquantification scale from 1 to 4 as previously reported.66 Morphometry of sections of kidneys from each of the db/m, db/db, and PFD-treated db/db mice was carried out as previously reported.67 Twenty-five randomly selected glomeruli in the outer cortex of each kidney section were evaluated in a blinded manner.

Proteomic Analyses of the db/m, db/db, and PFD-Treated db/db Mouse Kidney Proteins
In solution, trypsinization of the mouse kidney proteins was carried out as follows: 10 μg of kidney proteins was taken in a final reaction volume of 100 μl, reduced by addition of dithiothreitol in 10 mM ammonium bicarbonate to a final concentration of 20 mM dithiothreitol, incubated at 50°C for 1 h, and then alkylated with 20 mM iodoacetamide at room temperature in the dark for 1 h. Assuming 10 μg of protein per sample and 1/50th of trypsin (wt/wt), 10 μl of trypsin solution (concentration 10 ng/μl in 100 mM ammonium bicarbonate solution) was added to each protein tube and digested for 24 h at 37°C, and subsequently the pH was adjusted to approximately 2 to 3 with 5% formic acid. The reaction mixture resulting from in-solution trypsinization was solvent-evaporated to dryness. The dried down tryptic digests were resuspended in 15 μl of 1% formic acid. A total of 10 μl of this peptide preparation was loaded onto a Thermo Hypersil-Keystone BioBasic C18 column (0.18 X 100 mm) that served as the Surveyor HPLC front end of a ThermoElectron ProteomeX Workstation. The peptides were separated at a flow rate of 175 nl/min, using a gradient with Buffer A (0.1% formic acid in water), Buffer B (0.1% formic acid in acetonitrile), and a 2 to 50% gradient over 45 min. As peptides eluted from the column, they were subjected to ESI-MS/MS spectra analysis using a ThermoFinnigan LTQ-Orbitrap Elite mass spectrometer and the SEQUEST algorithm to determine the best protein matches. For obtaining reliable protein identification, Human Proteome Organization directives were used: (1) Only peptides with a ΔCn score of >0.1 were qualified; (2) the cross-correlation scores of single, double, and triple charged peptides had to be greater than 1.9, 2.2, and 3.75, respectively; and (3) rank of preliminary scoring value had to be ≤4.

In addition, a peptide had to be a tryptic cleavage to be accepted, and, as modifications, the oxidation of methionine and carbamidomethylation of cysteine were permitted.

Statistical Analysis
For continuous variables, a two-tailed ANOVA was used to test means. Histogram of mesangial matrix and arteriolar hyalinosis was evaluated using frequencies in a two-tailed Fisher exact test. For proteomics data analyses, total protein from three different mouse kidneys from each of the three populations (1, db/m control; 2, db/db without treatment; and 3, db/db treated with PFD) were separately analyzed by LC/MS/MS as described, and only the statistically significant identifications common to all mice (P < 0.05) from any single group were qualified for subsequent analysis.

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DISCLOSURES
None.

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