Overexpression of upstream stimulatory factor 2 accelerates diabetic kidney injury

Shu Liu, Lihua Shi, and Shuxia Wang

Graduate Center for Nutritional Sciences, University of Kentucky, Lexington, Kentucky

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Liu S, Shi L, Wang S. Overexpression of upstream stimulatory factor 2 accelerates diabetic kidney injury. Am J Physiol Renal Physiol 293: F1727–F1735, 2007.—Diabetic nephropathy is the most common cause of end-stage renal failure in the United States. Hyperglycemia is an important factor in the pathogenesis of diabetic nephropathy. Hyperglycemia upregulates the expression of transforming growth factor-β (TGF-β), which stimulates extracellular matrix deposition in the kidney, contributing to the development of diabetic nephropathy. Our previous studies demonstrated that the transcription factor, upstream stimulatory factor 2 (USF2), was upregulated by high glucose, which bound to an 18-bp sequence in the thrombospondin 1 (TSP1) gene promoter and regulated high glucose-induced TSP1 expression and TGF-β activity in mesangial cells, suggesting that USF2 might play a role in the development of diabetic nephropathy. In the present studies, we examined the effect of overexpression of USF2 on the development of diabetic nephropathy. Type 1 diabetes was induced in USF2 transgenic mice [USF2 (Tg)] and their wild-type littermates (WT) by injection of streptozotocin. Four groups of mice were studied: control WT, control USF2 (Tg), diabetic WT, and diabetic USF2 (Tg). Mice were killed after 15 wk of diabetes onset. At the end of studies, control USF2 (Tg) mice (6 mo old) exhibited increased urinary albumin excretion. These mice also exhibited glomerular hypertrophy, accompanied by increased TSP1, active TGF-β, fibronectin accumulation in the glomeruli compared with control WT littermates. Type 1 diabetes onset further augmented the urinary albumin excretion and glomerular hypertrophy in the USF2 (Tg) mice. These findings suggest that overexpression of USF2 accelerates the development of diabetic nephropathy.

TGF-β

DIABETIC NEPHROPATHY is the most common cause of end-stage renal failure in the United States. About 20–30% of type 1 and type 2 diabetic patients develop diabetic nephropathy (5). Diabetic nephropathy is characterized by both glomerulosclerosis with thickening of the glomerular basement membrane and mesangial matrix expansion, and tubulointerstitial fibrosis (11). Hyperglycemia is an important factor in the pathogenesis of diabetic nephropathy (32). Hyperglycemia upregulates the expression of a fibrogenic growth factor, transforming growth factor-β (TGF-β), contributing to the development of diabetic nephropathy (29). The importance of TGF-β in the development of diabetic nephropathy is well-established. TGF-β is involved in both the early and later stages of diabetic nephropathy (3, 20, 27). Moreover, studies have shown that anti-TGF-β antibodies prevent the development of diabetic nephropathy (2, 28), providing a direct evidence for the involvement of TGF-β in the pathogenesis of diabetic nephropathy. The fibrogenic effects of TGF-β are due to its upregulation of extracellular matrix components, including collagen, fibronectin, osteopontin, and the downregulation of matrix-degrading enzymes (12, 40).

Studies demonstrated that the matricellular protein, thrombospondin 1 (TSP1), is a major regulator of TGF-β activation and extracellular matrix protein expression by renal mesangial cells under high-glucose conditions (21, 35, 38). However, the mechanisms by which high glucose upregulates TSP1-dependent TGF-β activity are not well-understood. Previously, we demonstrated that the transcription factor, upstream stimulatory factor 2 (USF2), was upregulated by high glucose, which bound to an 18-bp sequence in the TSP1 gene promoter and regulated high glucose-induced TSP1 expression and TGF-β activity in mesangial cells (36). Overexpression of USF2 stimulated TSP1 expression and TGF-β activity in mesangial cells. Taken together, these studies suggest that USF2 might play a role in the development of diabetic nephropathy.

To test whether USF2 plays a role in the development of diabetic nephropathy in vivo, we generated global transgenic mice with overexpression of mouse USF2. The rationale for making USF2 transgenic mice is because USF2-deficient mice have high rates of prenatal mortality and a short life span (2.5–4 mo in males, 10 mo in females) (30). Studies examining these mice following diabetes onset, which may further shorten their life span, may preclude the ability to study the progressive development of diabetic nephropathy. In addition, heterozygous USF2+/− mice do not have altered expression levels of USF2 in the kidney and would thus not be appropriate for our in vivo studies. Moreover, lack of mesangial cell-specific promoters rule out the possibility of generation of a kidney-specific USF2-deficient mouse model. Based on the above considerations, we made global transgenic mice with overexpression of mouse USF2 driven by a human cytomegalovirus immediate-early enhancer linked to the chicken β-actin promoter. The current studies explored the role of USF2 in short-term diabetic nephropathy to test our hypothesis that USF2 transgenic mice would develop more severe renal injury than wild-type (WT) littermates. Type 1 diabetes was induced in USF2 transgenic mice and their WT littermates. The development of diabetic nephropathy in these mice was determined by analyzing the renal functional (urinary albumin excretion) and structural changes (glomerular hypertrophy and mesangial matrix expansion).

MATERIALS AND METHODS

Generation of Mice With Overexpression of USF2

For construction of transgenic mice, a mouse USF2 transgene was cloned into pCAGGS plasmid (provided by Dr. B. Spear at University of Kentucky) as shown in Fig. 1A. The transgenic mice were gener-
characterization of the expression of transgene in kidney from transgenic mice and WT littermates. To characterize the expression of transgene in kidneys, transgene-negative and transgene-positive mice as identified by PCR were killed. Kidneys were collected. Left kidneys were used for extraction of total RNA and making kidney homogenates. Right kidneys were fixed with 4% paraformaldehyde. Total RNA was extracted from the kidney using TRIzol (Invitrogen) and Northern blot analysis was performed to examine the overexpressed mRNA levels of USF2 in transgenic mice. For Northern blot analysis, equal amounts of total RNA (10 μg) were denatured, electrophoresed, and transferred to nylon membranes. RNA was fixed by UV cross-linking. The USF2 probe (mouse USF2 cDNA, generously provided by Dr. Sawa- dogo at the University of Texas MD Anderson Cancer Center) was radioabeled by random prime DNA-labeling kit (Roche Molecular Biochemicals) with [α-32P] dCTP. The membrane was prehybridized in ExpressHyb hybridization solution (Clontech, Palo Alto, CA) for 30 min at 68°C, and hybridization was carried out at 68°C for 1 h in fresh hybridization solution with denatured probe. The membrane was washed three times with 2× SSC (1× SSC = 0.15 M NaCl and 0.015 M sodium citrate), 0.05% SDS for 15 min at room temperature, and then twice with 0.2× SSC, 0.1% SDS at 50°C for 20 min. Blots were developed, and films were scanned. The absorbance units were corrected for the β-actin levels. In addition, USF2 protein levels in kidney homogenates were determined by Western blotting as described previously (36). Finally, fixed kidneys were embedded in paraffin, and 5-μm sections were stained with anti-USF2 antibody (Santa Cruz Biotechnology, Santa Cruz, CA) using Vectastain Elite ABC kit (Vector).

Experimental Animals and Protocol

Eight-week-old male USF2 (Tg) mice and sex- and age-matched WT littermates were used in the studies. All these mice were on B6C3H background and were cared for in accordance with National Institutes of Health Guide for the Care and Use of Laboratory Animals. Diabetes was induced in the mice at the age of 8 wk by injecting streptozotocin (STZ; 40 mg/kg) intraperitoneally for 5 consecutive days. STZ (Sigma, St. Louis, MO) was prepared in 0.1 mol/l sodium citrate buffer (pH 4.5) immediately before injection. Control animals received injections of citrate buffer alone. The development of diabetes was evaluated by measuring blood glucose using Glucometer 2 wk after the first injection, and the mice with a blood glucose level higher than 300 mg/dl were considered diabetic and were used for the study. There were four groups: 1) control WT; 2) control USF2 (Tg); 3) diabetic WT; and 4) diabetic USF2 (Tg). Each group contained 10 mice. These mice were kept for 15 wk. Throughout the studies, mice were provided with free access to water and normal standard mouse chow. Blood glucose levels and body weights were measured biweekly. At the end of the study, 24-h urine was collected. Mice were killed at 15 wk after diabetes onset. All protocols were approved by the institutional animal care and use committee of University of Kentucky. All experiments were conducted in accordance with the guidelines of the University of Kentucky Animal Care Committee.

Measurement of Urinary Albumin Excretion

At 15 wk, 24-h urine was collected on individual mice housed in metabolic cages with free access to chow and water. Total urine volume was measured. Urinary albumin was determined using the Albewell M Murine Microalbuminuria enzyme-linked immunosorbent assay kit (Exocell, Philadelphia, PA). Results were reported as micrograms of albumin per 24-h urine. Urinary creatinine concentration was measured using a picric acid assay (Exocell).

Immunoblot Analysis

Glomerular expression of USF2, fibronectin, TSP1, and active TGF-β was assessed by Western blot analysis. Mice in each group (n = 3 per group) were killed and kidneys were collected. The glomeruli were isolated by differential sieving (150-, 106-, 90-, and 53-μm sieves) (24) and lysed in Laemmli SDS sample buffer, and 30 μg of protein were subjected to SDS-PAGE on 12% gel under reducing condition and transferred onto PVDF membrane. After being blocked, the membrane was incubated with polyclonal anti-USF2 antibody (Santa Cruz Biotechnology), monoclonal anti-TSP1 antibody (A4.1, GIBCO-BRL), monoclonal anti-TGF-β1, 2, 3 antibody (R&D System), or rabbit anti-rat fibronectin antibody (from Life...
Technology for 1 h at room temperature. After being washed, the membrane was incubated with horseradish peroxidase-conjugated secondary antibody (Jackson Laboratory). The reaction was visualized using an enhanced chemiluminescence system (Pierce).

EMS

Mice were killed, and the kidneys were harvested. The glomeruli were isolated by a fractional sieving technique. Glomeruli were washed with cold PBS, and nuclear extracts were prepared as described previously (26, 36) and used for the EMSA assay. The 55-bp oligonucleotide of TSP1 promoter (−932 to −878) (36) was endlabeled with [32P] by T4 polynucleotide kinase (Invitrogen). A probe (2–5 × 106 cpm) was incubated with 3 μg of nuclear extracts in a 20-μl volume of binding reaction buffer [10 mM Tris-HCl (pH 7.5), 100 mM NaCl, 10% glycerol, 50 ng/ml poly(dI/dC)] on ice for 20 min. In competition experiments, an unlabeled USF2 consensus oligonucleotide (Santa Cruz Biotechnology) was mixed with the labeled probe before being added to the binding mixture to determine the specificity of nuclear binding. The binding reaction was then allowed to proceed for 20 min on ice. All binding mixtures were separated by 4–20% gradient Tris-buffered TBE gels (Bio-Rad). The reaction was visualized using an enhanced chemiluminescence system (Pierce). The slides were placed in PBS buffer containing 0.5 M casein for 30 min at room temperature (RT). The slides were washed in PBS before color development. The following antibodies were used: anti-TSP1 antibody (A4.1, GIBCO-BRL), polyclonal anti-USF2 antibody (Santa Cruz Biotechnology), anti-TGF-bet1, anti-TGF-α (R&D System) to detect active TGF-β, and polyclonal anti-rat fibronectin antibody (from Life Technology). The areas of mesangial staining for TSP1, active TGF-β, fibronectin, and USF2 were determined by marking the DAB-specific color hue and determining the number of pixels of stain using Image-ProPlus software. Thirty-five glomeruli were evaluated per mouse.

Statistical Analysis

All data are expressed as means ± SE. ANOVA was used to analyze variation within the group. Student’s t-tests were used to compare variation between groups. Statistical significance will be accepted at a value of P < 0.05.

RESULTS

Characterization of the USF2 Tg Mice

The USF2 transgenic mice were viable and fertile. There were no obvious physical abnormalities observed in these mice. Six-week-old male mice were used for characterization. RT-PCR results showed that transgene overexpressed in various tissues including heart, muscle, liver, lung, kidney, aorta, spleen, testes, brain, intestine, etc (Fig. 1B). To further analyze the expression of transgene in the kidney, we performed Northern blotting, Western blotting, and immunohistochemical staining. As shown in Fig. 2, in the kidney of transgene-positive mice, USF2 mRNA levels were 5-fold and protein levels were 3.5-fold above the level in control mice. In addition, a significant increase in positive staining of USF2 was shown in both glomeruli and tubular system in the USF2 transgenic mice (Fig. 2C). Taken together, these data indicate that overexpression of USF2 occurred in the kidneys as well as other tissues in the USF2 transgenic mice.

General Characteristics in Control and Diabetic Mice

To directly determine the effect of overexpression of USF2 on the development of diabetic nephropathy, USF2 transgenic mice and their WT littermates were made diabetic by STZ injection as described previously (26, 36) and used for the EMSA assay. The 55-bp oligonucleotide of TSP1 promoter (−932 to −878) (36) was endlabeled with [32P] by T4 polynucleotide kinase (Invitrogen). A probe (2–5 × 106 cpm) was incubated with 3 μg of nuclear extracts in a 20-μl volume of binding reaction buffer [10 mM Tris-HCl (pH 7.5), 100 mM NaCl, 10% glycerol, 50 ng/ml poly(dI/dC)] on ice for 20 min. In competition experiments, an unlabeled USF2 consensus oligonucleotide (Santa Cruz Biotechnology) was mixed with the labeled probe before being added to the binding mixture to determine the specificity of nuclear binding. The binding reaction was then allowed to proceed for 20 min on ice. All binding mixtures were separated by 4–20% gradient Tris-buffered TBE gels (Bio-Rad). The reaction was visualized using an enhanced chemiluminescence system (Pierce). The slides were placed in PBS buffer containing 0.5 M casein for 30 min at room temperature (RT). The slides were washed in PBS before color development. The following antibodies were used: anti-TSP1 antibody (A4.1, GIBCO-BRL), polyclonal anti-USF2 antibody (Santa Cruz Biotechnology), anti-TGF-bet1, anti-TGF-α (R&D System) to detect active TGF-β, and polyclonal anti-rat fibronectin antibody (from Life Technology). The areas of mesangial staining for TSP1, active TGF-β, fibronectin, and USF2 were determined by marking the DAB-specific color hue and determining the number of pixels of stain using Image-ProPlus software. Thirty-five glomeruli were evaluated per mouse.

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Fig. 2. Overexpression of USF2 in the kidney in transgenic mice. A: RNA samples were isolated from mouse kidneys and subsequently hybridized to [32P]-labeled probes corresponding to USF2 and β-actin. B: homogenates of mouse kidneys were subjected to SDS-PAGE gel, transferred, and probed with antibodies against USF2 and β-actin. β-Actin was used as an internal control. The – or + signs indicated transgene-negative or -positive animals as identified by PCR. The data shown were representative of 3 experiments. Relative USF2 levels were determined by scanning densitometry of blots. Data are represented as means ± SE. *P < 0.05. C: immunohistochemical staining showing the overexpression of USF2 in glomeruli and tubular system from the USF2 transgenic mice. The representative light photomicrographs were shown. The positive staining was shown as brown color. Original magnification ×100. USF2 immunostaining in glomeruli was analyzed by computer image analysis (measuring brown staining pixel density). Data are represented as means ± SE. *P < 0.05.

USF2 (Tg) groups of mice compared with their nondiabetic controls, and remained elevated throughout the study period. At 15 wk, there was no difference between the blood glucose levels in diabetic USF2 (Tg) mice and diabetic WT mice.

At the end of the studies, the ratio of kidney weights to body weights was significantly increased in nondiabetic USF2 (Tg) mice (−6 mo old) compared with nondiabetic WT group. The diabetes onset significantly augmented the ratio of kidney weights to body weights in USF2 (Tg) mice (Table 1). The 24-h urine volume and urinary albumin excretion were significantly greater in nondiabetic USF2 (Tg) group compared with nondiabetic WT group. Under diabetes conditions, 24-h urine volume and urinary albumin excretion were increased in both USF2 (Tg) and WT groups compared with their nondiabetic controls. There was a significant increase in 24-h urine volume and urinary albumin excretion in diabetic USF2 (Tg) mice compared with diabetic WT group. These studies demonstrated that USF2 (Tg) mice exhibited albuminuria at 6 mo of age, which were significantly augmented by diabetes onset.

Renal Histology Analysis in Control and Diabetic Mice

Given the marked effect of overexpression of USF2 gene on the urinary albumin excretion, we further determined whether there were differences in the kidney structure (Fig. 3, A and B). The PAS staining was performed. Glomerular size was determined to assess glomerular hypertrophy. The glomerular size was significantly increased in diabetic WT (D-WT vs. WT, 3.7 × 10^3 ± 68 vs. 2.5 × 10^3 ± 89, P < 0.05) or diabetic USF (Tg) mice [D-USF2 (Tg) vs. USF2 (Tg), 5.08 × 10^3 ± 102 vs. 3.3 × 10^3 ± 76, P < 0.05] compared with their control mice. We also determined the mesangial matrix expansion. The mean values for the mesangial matrix scores were shown in Fig. 3B. Mean values for mesangial matrix score were significantly increased in both diabetic groups compared with their nondiabetic controls. The diabetic USF2 (Tg) mice developed a greater increase in mesangial matrix score than that in diabetic WT mice.

Expression of USF2 in Glomeruli From Control and Diabetic Mice

We showed that high-glucose levels upregulated USF2 expression in mesangial cells in vitro (36), and to determine whether diabetes upregulated renal USF2 expression from diabetic mice, glomeruli were isolated and immunoblotting was performed (Fig. 4A). As expected, glomeruli USF2 protein levels were increased in diabetic WT mice compared with the nondiabetic WT control. In USF2 (Tg) mice, diabetes onset further increased glomeruli USF2 levels. These data provided

Table 1. General characteristics of control and diabetic mice at week 15

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<th>Diabetic</th>
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<td>USF2 (Tg)</td>
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<td>Body wt, g</td>
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<td>Blood glucose, mg/dl</td>
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<td>152 ± 14</td>
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<td>Urine albumin excretion, mg/dl</td>
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<td>Urine volume, ml/24 h</td>
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<td>Urine ACR, µg/mg</td>
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Data are means ± SE (n = 10). Eight-week-old male upstream stimulatory factor 2 transgenic (USF2 Tg) mice and age- and sex-matched wild-type littermates (WT) were made diabetic by streptozotocin injection and kept for 15 wk. *P < 0.05 vs. nondiabetic. †P < 0.05 USF2 (Tg) vs. nondiabetic WT. ‡P < 0.05 vs. diabetic WT. ACR, albumin-to-creatinine ratio; LK, left kidney wt.
the first evidence that type 1 diabetes onset stimulated USF2 expression in glomeruli.

**Binding of USF2 to a 55-bp TSP1 Promoter Region (−932 to −878) by EMSA**

Previously, we demonstrated that high glucose upregulated USF2 expression in mesangial cells and stimulated USF2 to bind to a 55-bp TSP1 promoter region (−932 to −878) (36). In this study, we determined whether nuclear extracts of glomeruli from USF2 (Tg) mice showed increased binding to the TSP1 promoter by using EMSA. As shown in Fig. 4B, a major band formed in EMSA. This band was significantly enhanced in both of the diabetic groups compared with their nondiabetic controls. There was also a marked increase in protein-DNA interaction in the diabetic USF2 (Tg) mice compared with the diabetic WT mice. Competition studies showed that unlabeled USF2 consensus oligonucleotide efficiently abrogated the formation of this complex (Fig. 4B, lane 1). Together, these data demonstrated that glomerular USF2 binding to the TSP1 promoter was increased under diabetes conditions.

**Renal Expression of Fibronectin in Control and Diabetic Mice**

To characterize further the mesangial injury, immunohistochemical staining, real-time PCR, and Western blotting were used to evaluate the expression of the extracellular matrix protein fibronectin in the kidney from four groups of mice (Fig. 5). There was a twofold increase in glomerular fibronectin immunostaining in the diabetic WT mice compared with nondiabetic WT controls and a threefold increase in glomerular fibronectin immunostaining in the diabetic USF2 (Tg) mice compared with nondiabetic USF2 (Tg) mice. Fibronectin immunostaining was greater in diabetic USF2 (Tg) mice compared with diabetic WT mice. Similarly, the mRNA (Fig. 5B) and protein levels of fibronectin (Fig. 5C) in isolated glomeruli were significantly increased in both diabetic mice compared with their control mice. The levels of fibronectin (mRNA and protein) were greater in diabetic USF2 (Tg) compared with diabetic WT mice.

**Renal Expression of TSP1 and Active TGF-β in Control and Diabetic Mice**

Our previous studies demonstrated that USF2 binds to TSP1 gene promoter and regulates high glucose-mediated TSP1 expression and TGF-β activity in glomerular mesangial cells (36). To determine whether overexpression of USF2 stimulates TSP1 expression and increase in active TGF-β levels in the...
kidney from USF2 (Tg) mice under basal and diabetic conditions, we performed real-time PCR, Western blotting, and immunohistochemical staining for TSP1 and active TGF-β (Figs. 6 and 7). TSP1 and active TGF-β immunostaining and mRNA and protein levels of TSP1 and active TGF-β were increased in both of the diabetic groups compared with their nondiabetic controls. There was also a marked increase in TSP1 and active TGF-β levels in the diabetic USF2 (Tg) mice compared with the diabetic WT mice.

**DISCUSSION**

USF2 was initially characterized as a transcription factor implicated in the regulation of the adenovirus major late gene.
and induced TSP1 gene expression and TGF-USF2 accumulation, which mediated high-glucose conditions demonstrated that high-glucose exposure stimulated nuclear 10, 13, 17, 22, 23, 34, 39). In our previous studies, we been demonstrated to regulate expression of many genes (4, 9, (31). Through binding to E boxes of target genes, USF2 has recognize in vitro a CACGTG core sequence termed E box (25). In mammals, USF2 is ubiquitously expressed with a molecular weight of 44 kDa. It belongs to the Myc family of transcription factors characterized by a basic/helix loop helix/leucine zipper domain responsible for dimerization and DNA binding. It can form homo- and heterodimers and recognize in vitro a CACGTG core sequence termed E box (31). Through binding to E boxes of target genes, USF2 has been demonstrated to regulate expression of many genes (4, 9, 10, 13, 17, 22, 23, 34, 39). In our previous studies, we demonstrated that high-glucose exposure stimulated nuclear USF2 accumulation, which mediated high-glucose conditions and induced TSP1 gene expression and TGF-β activity in glomerular mesangial cells, suggesting a role of USF2 in the development of diabetic renal complications. The current studies assessed the role of USF2 in short-term diabetes focusing on the effect of overexpression of USF2 on diabetic renal injury. The findings of the present study provide the first evidence that overexpression of USF2 accelerates the development of diabetic nephropathy.

It is known that one of the earliest clinically detectable functional abnormalities in diabetic nephropathy is microalbuminuria (37). Accordingly, we first determined whether overexpression of USF2 would affect the urinary albumin excretion in diabetic USF2 (Tg) mice. Accumulating evidence suggests that the kidney injuries observed in the diabetic mice are still early features of diabetic nephropathy. In addition, immunohistochemical studies, real-time PCR, and Western blotting analysis of the kidneys demonstrated that diabetic USF2 (Tg) mice and diabetic WT littermates exhibited greater fibronectin immunostaining, mRNA, and protein levels of fibronectin in glomeruli compared with their nondiabetic controls. Fibronectin expression was most pronounced in the diabetic USF2 (Tg) mice and diabetic WT littermates exhibiting greater fibronectin immunostaining, mRNA, and protein levels of fibronectin in glomeruli compared with their nondiabetic controls. Fibronectin expression was most pronounced in the diabetic USF2 (Tg) mice and diabetic WT littermates exhibiting greater fibronectin immunostaining, mRNA, and protein levels of fibronectin in glomeruli compared with their nondiabetic controls. Fibronectin expression was most pronounced in the diabetic USF2 (Tg) mice and diabetic WT littermates exhibiting greater fibronectin immunostaining, mRNA, and protein levels of fibronectin in glomeruli compared with their nondiabetic controls. Fibronectin expression was most pronounced in the diabetic USF2 (Tg) mice and diabetic WT littermates exhibiting greater fibronectin immunostaining, mRNA, and protein levels of fibronectin in glomeruli compared with their nondiabetic controls. Fibronectin expression was most pronounced in the diabetic USF2 (Tg) mice and diabetic WT littermates exhibiting greater fibronectin immunostaining, mRNA, and protein levels of fibronectin in glomeruli compared with their nondiabetic controls.

The degree of renal functional changes (albuminuria) correlates with the progression of renal structural changes including mesangial matrix expansion, glomerulosclerosis, and tubulointerstitial fibrosis (16). Therefore, next, we determined whether the exacerbation of urinary albumin excretion in diabetic USF2 (Tg) mice relates to structural changes in the kidneys. We found that the ratio of left kidney to body weight was greater in diabetic USF2 (Tg) mice than that in diabetic WT mice. We performed PAS staining to determine the mesangial matrix expansion in four groups of animals. We also determined the glomerular size to assess glomerular hypertrophy. The mean values of mesangial matrix scores significantly increased in USF2 (Tg) mice under both nondiabetic and diabetic conditions compared with control WT mice. Diabetic USF2 (Tg) mice exhibited a greater mean value for mesangial matrix scores than diabetic WT littermates. Glomerulosclerosis and tubulointerstitial fibrosis were not observed in any group of mice, suggesting that the kidney injuries observed in the diabetic mice are still early features of diabetic nephropathy. In addition, immunohistochemical studies, real-time PCR, and Western blotting analysis of the kidneys demonstrated that diabetic USF2 (Tg) mice and diabetic WT littermates exhibited greater fibronectin immunostaining, mRNA, and protein levels of fibronectin in glomeruli compared with their nondiabetic controls. Fibronectin expression was most pronounced in the diabetic USF2 (Tg) mice, contributing to the increased mesangial matrix expansion in these mice. These observations indicated that USF2 (Tg) mice at 6 mo of age developed glomerular hypertrophy and mesangial matrix expansion, which was augmented by diabetes onset.

We further determined the mechanisms for the acceleration of the functional and structural changes of diabetic nephropathy in USF2 (Tg) mice. Accumulating evidence suggests that TGF-β plays a key role in the development of diabetic nephropathy by upregulation of extracellular matrix components, including collagen, fibronectin, osteopontin, and the down-regulation of matrix-degrading enzymes (12, 40). We and
others demonstrated that the matricellular protein, TSP1, is a major regulator of TGF-β activation and extracellular matrix protein expression by renal mesangial cells under high-glucose conditions (21, 35, 38). Our studies also demonstrated that USF2 regulated high glucose-induced TSP1 expression and TGF-β activity in mesangial cells (36). In the current studies, we provided first evidence that hyperglycemia stimulated glomerular USF2 expression from diabetic WT control mice and USF2 (Tg) mice and enhanced USF2 binding to the TSP1 promoter. TSP1 and active TGF-β levels (mRNA and protein) in glomeruli were significantly increased in nondiabetic USF2 (Tg) mice, diabetic WT littermates, and diabetic USF2 (Tg) mice. Active TGF-β levels were most pronounced in the diabetic USF2 (Tg) mice, supporting our conclusion that differences in active TGF-β levels were responsible for the accelerated diabetic kidney injury in the USF2 (Tg) mice.

In addition to the importance of TGF-β in the development of diabetic kidney injury in USF2 (Tg) mice, other factors may need to be explored. It has been shown that USF2 regulates renin gene expression (19). Multiple evidence showed that the activation of intrarenal renin-angiotensin system (RAS) plays an important role in diabetic nephropathy. Blockade of RAS by angiotensin-converting enzyme inhibitors and angiotensin II receptor antagonists has been shown to attenuate proteinuria and slows the progression of diabetic nephropathy (1, 6–8, 14, 15). However, whether USF2 overexpression in the kidney upregulates intrarenal RAS and contributes to the development of nephropathy in USF2 (Tg) mice under both nondiabetic and diabetic conditions is not known. Given the importance of intrarenal RAS in diabetic nephropathy, the effect of USF2-mediated renin expression on the development of diabetic nephropathy will be investigated.

In summary, we provided the first evidence that hyperglycemia stimulated USF2 expression in glomeruli from diabetic control mice, which was associated with increased TSP1 expression, active TGF-β levels, and fibronectin accumulation in glomeruli, leading to the development of diabetic nephropathy. In addition, overexpression of USF2 in the kidney further augmented the above features and exacerbated the diabetic kidney injury.

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REFERENCES


