Cloning and Characterization of a Novel Subunit of Protein Serine/Threonine Phosphatase 4 from Mesangial Cells

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Abstract. Mesangial cells play an important role in maintaining glomerular structure and function and in the pathogenesis of glomerular diseases. With a novel approach using a rapid large-scale DNA sequencing strategy and computerized data processing, a new human gene, PP4Rmeg was cloned. The full-length cDNA clone of human PP4Rmeg coded for a novel 950–amino acid protein, which was similar to a subunit of protein serine/threonine phosphatase 4 (PP4). Recombinant PP4Rmeg produced in COS-7 cells bound to the catalytic subunit of PP4. PP4Rmeg is therefore structurally and functionally related to the recently reported regulatory subunit of PP4, PP4R1. Amino acid sequence analysis of rat PP4Rmeg homologue revealed that the sequences were well conserved between human and rat (86.3% identity). Northern blot analyses of human tissues and cultured cells demonstrated that the regulatory subunits were expressed abundantly in human cultured mesangial cells, although their expression was relatively ubiquitous. In situ hybridization studies in normal human renal tissues confirmed their expression in glomeruli in vivo. The expression was upregulated in glomeruli of anti-Thy1 glomerulonephritis rats before mesangial proliferation. These data demonstrate that PP4Rmeg is a novel regulatory subunit of PP4, which is expressed ubiquitously but abundantly in mesangial cells. Its pathophysiologic role in mesangial cells and glomerulus remains unknown. As PP4 is an essential protein for nucleation, growth, and stabilization of microtubules at centrosomes/spindle pole bodies during cell division, PP4Rmeg may play a role in regulation of mitosis in mesangial cells.

Mesangial cells play a central role in maintaining glomerular structure and function. Numerous glomerular diseases, including chronic glomerulonephritis and diabetic nephropathy, two major causes of end-stage renal failure, are associated with proliferation of mesangial cells and/or accumulation of mesangial extracellular matrix, which eventually leads to the progression of glomerulosclerosis. To identify novel genes expressed and functioning in mesangial cells, we used a rapid large-scale DNA sequencing strategy and computerized data processing to compare the transcripts in cultured human mesangial cells with various cells and organs (1).

Using this novel methodology, we previously reported discovery of a new mesangium-predominant gene, meggin, which is a new member of the serine protease inhibitor (serpin) superfamily (2,3). Here, we cloned and characterized another novel gene, which was expressed ubiquitously but abundantly in mesangial cells.

Sequencing analysis of this gene demonstrated its structural homology with a regulatory subunit of protein serine/threonine phosphatase 4 (PP4R1) (4). Protein serine/threonine phosphatases (PP) play an important role in the control of most biologic processes by catalyzing the dephosphorylating reactions and serving as an off switch of cell signaling (5). The four major PP families that have been identified are PP1, PP2A, PP2B, and PP2C. This classification is based on their substrate selectivity, inhibitor sensitivity, and requirement for divalent cations (6–10).

PP4 is classified as a PP2A family member. The catalytic subunit of PP4 (PP4c) is 65% identical to the catalytic subunit of PP2A (PP2Ac). However, PP4c does not associate with the regulatory subunits of PP2A (11). Instead, PP4c seems to associate with distinct regulatory subunits (4).

The biologic function of PP4 has not been understood well. However, several lines of evidence suggest its potential involvement at centrosomes/spindle pole bodies for nucleation, growth, and/or stabilization of microtubules (12), which play an important role in each of the mitotic processes by forming the mitotic spindle and functioning in many of the subcellular movements.

In the present study, we determined the structure of the novel gene and investigated its biologic function and localization. Using anti-Thy1 glomerulonephritis, a model of mesangio proliferative glomerulonephritis of rats, we also investi-
gated the temporal profile of its expression in association with mesangial proliferation.

Materials and Methods

Cloning of Human PP4\textsubscript{Rmeg}

Details of construction of the 3'-directed human mesangium cDNA library have been described elsewhere (1). Briefly, human glomeruli were isolated by differential sievings from a normal human kidney and were cultured in medium 199 (Life Technologies, Rockville, MD) containing 25 mM HEPES, 10% Nu-serum (Collaborative Biomedical Products, Bedford, MA), and antibiotics (50 μg/ml penicillin, streptomycin, and Fungizone) in a 5% CO\textsubscript{2} incubator. PolyA\textsuperscript{+} RNA was isolated from human mesangial cells at passage 6 using the standard guanidine isothiocyanate method and oligo dT cellulose column (Amersham Pharmacia Biotech, Uppsala, Sweden). A vector primer is dam-methylated at the MboI sites (GATC) and has a 3' protrusion of homo dT stretch at one end. The double-stranded cDNA moiety was cleaved with MboI. The vector that was attached with the 3'-cDNA (from polyA to the nearest MboI site) was circularized by ligation and was transformed into Escherichia coli. The resulting transformants were selected randomly and were lysed individually by brief boiling. The lysate was used as a template for PCR. The resulting short double-stranded DNA was used for the cycle sequencing reaction and was analyzed using an autosounder.

To identify the 5' end of PP4\textsubscript{Rmeg} cDNA, we used the 5'-Full RACE Core Set (Takara, Tokyo, Japan). The reverse transcriptase (RT) reaction was performed with 1.0 μg of human mesangial cell polyA\textsuperscript{+} RNA with a gene-specific oligonucleotide. After degradation of the template mRNA with RNase H, the first-strand cDNA was ligated by T4 RNA ligase, and an aliquot was used as a template for the first PCR amplification with gene-specific primers. The resulting PCR product was then used as a template for the second PCR amplification with nested gene-specific primers. The PCR products were cloned into the pCRII vector (Clontech, Palo Alto, CA), and DNA sequences were determined by dideoxy chain termination reaction using a DNA autosounder.

Cloning of Rat PP4\textsubscript{Rmeg}

To determine the sequence of rat PP4\textsubscript{Rmeg}, we performed PCR with primers corresponding to highly homologous parts between human PP4\textsubscript{Rmeg} and mouse cDNA sequences that were obtained from the expression sequence tag database. Messenger RNA from cultured rat mesangial cells at passage of 10 to 20 with a Micro-FastTrack 2.0 mRNA Isolation Kit (Invitrogen, Groningen, the Netherlands) was reversed transcribed with Superscript II (Life Technologies) to generate template cDNA. The template was amplified in a DNA thermal cycler (Perkin Elmer Japan, Chiba, Japan) for 30 cycles using optimum conditions for each primer. To prevent misreading, we designed PCR primers so that each base could be determined in at least two different PCR products. We used a 5'RACE System, version 2.0 (Life Technologies) for the confirmation of the DNA sequence around the putative initiation codon. The PCR products were ligated into pGEM-T easy vector (Promega, Madison, WI), and DNA sequences of more than four clones were determined by dideoxy chain termination reaction with T7 and SP6 primers using a DNA autosounder.

RT-PCR

Total RNA was isolated from cultured human mesangial cells (passage 10) and A431 cells (purchased from American Type Culture Collection, Manassas, VA) using ISOGEN (Nippon Gene, Tokyo, Japan) according to the manufacturer’s protocol. Approximately 2 μg of total RNA was reverse transcribed using an RNA-PCR kit (Takara). Ten microliters of cDNA was applied for PCR amplification. PCR amplification was performed in a 25-μl reaction containing 2.5 U of ExTaQ (Takara), 2.5 mM each of the four deoxyribonucleoside triphosphates, and 50 pmol of the KpnI-PP4\textsubscript{Rmeg} (5'-CCG GTA CCG GGC GAC CAC AAC ATG GCG GAC CT-3') and SaciI-PP4\textsubscript{Rmeg} (5'-TCG AGC TCC CGC TCT AAC AGT TGG TTC TCA ACG ATC-3') primers. Specimens were amplified in a DNA Thermal Cycler. Each cycle consisted of denaturation at 94°C for 30 s, annealing at 55°C for 30 s, and extension at 72°C for 30 s.

The PCR products were separated by electrophoresis in a 4% agarose gel and extracted using a QIAEX II kit (QIAGEN, Hilden, Germany). These products were ligated to pUC18 vector (Takara) after restriction enzyme digestion, and DNA sequences were confirmed by dideoxy chain termination reaction using a DNA autosounder.

Production of PP4\textsubscript{Rmeg} Transfectants

Human PP4\textsubscript{Rmeg} cDNA was engineered with a c-Myc tag on the C-terminus as described below. The 5' terminal fragment of human PP4\textsubscript{Rmeg} (corresponding to 1 to 2210 bp) was obtained with digestion with EcoRI and HindIII. At the same time, the 3' terminal fragment was synthesized using a PCR-based method with the primers PP4\textsubscript{Rmeg}/2112 (5'-CGA GCT TGC AGT TAT TCT TGG AGA TCA GAT CAA CTG CCT CCA GGT CAC GAC CT-3') and BamHI-PP4\textsubscript{Rmeg}AS (5'-CCG GAT CCA CGT AGG ATG AGG ACC TGG CTG TCA ACG ATC-3'). These two fragments were confirmed by sequence analysis, followed by simultaneous ligation into pcDNA 3.1/myc-His B vector (Invitrogen) with a Takara Ligation Kit Version 2.0. The pcDNA 3.1/myc-His B vector containing PP4\textsubscript{Rmeg} was transfected into COS-7 cells cultured in Dulbecco’s modified Eagle’s medium (Nissui Pharmaceutical, Tokyo, Japan) supplemented with 10% fetal bovine serum. Transfections were performed using 5 μg of PP4\textsubscript{Rmeg} expression vector and 2.5 μl of LIPOFECTAMINE Reagent (Life Technologies) according to the manufacturer’s protocol. Sixty hours posttransfection, cells were dislodged by scraping in 1 ml of phosphate-buffered saline and stored at −80°C until use. Approximately 8 × 10\textsuperscript{5} cells were lysed in 400 μl of Buffer A (20 mM Tris-HCl [pH 7.5], 100 mM NaCl, 0.5% Triton X-100, 1 mM ethylenediaminetetraacetate, 1 mM ethyleneglycol-bis(β-aminoethyl ether)-N,N'-tetraacetic acid, 1 mM diithiothreitol, and a cocktail of protease inhibitors, which included leupeptin, pepstatin, aprotinin, benzamidine, and soybean trypsin inhibitors) by repetitive passage (8 to 10 times) through a 22-gauge needle. The cell lysates were clarified by centrifugation for 10 min at 4°C, and the supernatant was taken as cell lysates and solubilized in sodium dodecyl sulfate (SDS) sample buffer, which represented starting material.

Immunoprecipitation

The ability of recombinant PP4\textsubscript{Rmeg} (myc-PP4\textsubscript{Rmeg}) to bind PP4c was assessed by immunoprecipitation using specific antibodies. Cell lysates (350 μg of protein) were incubated with 2 μl of c-Myc antibody (Clontech) overnight while rotating at 4°C. Immune complexes were isolated by adding 40 μl of a 50% slurry of Buffer A-washed GammaBind Plus Sepharose (Amersham Pharmacia Biotech) resin. The protein-antibody-beads complexes were pelleted by centrifugation, and the supernatant was taken, an aliquot of which was solubilized in SDS sample buffer, which represented unbound proteins. After the beads were washed six times with Buffer A, bound proteins were eluted with 30 μl of 2× SDS sample buffer and then with 25 μl of 1× SDS sample buffer, which represented immunopre-
cipitated proteins. Samples were analyzed by immunoblot analysis using an affinity-purified antibody raised against the amino acid residues 56 to 69 (ASENIFNRQMVARS) in PP4R1 (4) and an affinity-purified antibody directed against the C terminus of PP4c (4).

**Immunoblot Analysis**

Approximately 20 μl of starting material, unbound protein, and immunoprecipitated protein were analyzed by SDS-polyacrylamide gel electrophoresis (SDS-PAGE) and immunoblotting. Proteins were transferred to nylon-reinforced nitrocellulose in 10 mM 3-(cyclohexylamino)propanesulfonic acid buffer (pH 11.0) containing 10% methanol. The blots were incubated with affinity-purified antibody raised against the amino acid residues 56 to 69 (ASENIFNRQMVARS) in PP4R1 (4) and an affinity-purified antibody directed against the C terminus of PP4c (4), followed by incubation with goat anti-rabbit IgG-alkaline phosphatase conjugate. Immunocomplexes were visualized with 5-bromo-4-chloro-3-indolyl phosphate and nitro blue tetrazolium as substrates for alkaline phosphatase.

**Northern Blot Analysis**

The expression of PP4 regulatory subunits (PP4Rs) mRNA was assessed in various human primary cultured cells and tissues, as well as in glomeruli isolated from anti-Thy1 glomerulonephritis rats. Cultured human mesangial cells, dermal fibroblasts, proximal tubule epithelial cells, umbilical vein endothelial cells, and aortic smooth muscle cells were purchased from Takara, and their mRNA were isolated at passage 5 to 15 using a Micro-FastTrack 2.0 Kit (Invitrogen). A human multiple tissue Northern blot containing polyA+ RNA from heart, brain, placenta, lung, liver, skeletal muscle, kidney, and pancreas was purchased from Clontech. Total RNA was isolated from glomeruli of anti-Thy1 glomerulonephritis rats described below, using an ISOGEN kit (Nippon Gene).

PolyA+ RNA from cultured human cells (2 μg) or total RNA from anti-Thy1 glomerulonephritis glomeruli (4 μg) were electrophoretically separated in 1% agarose gels containing 2.2 mol/L formaldehyde, followed by capillary transfer to nitrocellulose membrane GeneScreenPlus (NEN, Boston, MA). The membrane was prehybridized in Quikhyb Hybridization solution (Stratagene, La Jolla, CA) at 68°C for 1 h, followed by hybridization in Quikhyb Hybridization solution containing labeled probe and salmon sperm DNA at 68°C for 2 h. After hybridization, membranes were washed with 0.2× SSC/0.1% SDS at 60°C.

As a probe for human PP4 regulatory subunits (PP4Rs), we used a 625-bp-long cDNA fragment cut with PvuII (corresponding to 2734 to 3359 bp). As a probe for rat PP4Rs, we used a 1141-bp-long cDNA fragment (corresponding to 894 to 2034 bp). These DNA fragments were radiolabeled using Random Primer DNA Labeling Kit (Takara) and purified with ProbeQuant G-50 Micro columns (Amersham Pharmacia Biotech).

Quantification of the PP4R mRNA signals was obtained by densitometry using National Institutes of Health image software (version 1.62; Bethesda, MD). The intensities of the signals were normalized using β-actin mRNA or 28S ribosomal RNA as loading controls.

**In Situ Hybridization**

**In situ** hybridization was performed as described previously (13). Briefly, fresh kidney biopsy tissues were embedded in OCT compound, frozen quickly, and stored at −80°C until use. Sections of tissues were cut 4 μm thick and fixed in 4% paraformaldehyde in phosphate-buffered saline deproteinized by HCl and digested with proteinase K (Sigma Chemical, St. Louis, MO). The specimens were incubated in a prehybridization buffer, drained, and hybridized overnight with digoxigenin (DIG)-labeled oligonucleotide probe in the prehybridization buffer. As a probe, we used 34-bp-long synthesized oligonucleotide corresponding to nucleotides 2879 to 2912. After hybridization, the DIG-labeled probe was visualized by immunohistochemical staining using a mouse monoclonal anti-DIG antibody (Boehringer Mannheim, Mannheim, Germany), horseradish peroxidase-conjugated rabbit anti-mouse antibody (DAKO, Kyoto, Japan), and horseradish peroxidase-conjugated swine anti-rabbit antibody (DAKO). Color was developed with diaminobenzidine tetrahydrochloride at 0.05 M Tris-HCl (pH 7.6) and 0.03% H2O2. Sections were briefly counterstained with hematoxylin, rinsed, dehydrated, cleared in xylene, and mounted.

**Anti-Thy1 Glomerulonephritis Rat Experiment**

Anti-Thy1 glomerulonephritis was induced in 21 male Wistar rats (Nippon Clea, Tokyo, Japan) that weighed approximately 200 g using a hindpaw line producing anti-rat Thy1.1 antibody from European Collection of Animal Cell Culture (Sulisbury, UK); purification of anti-Thy1.1 monoclonal antibody was performed as reported (14). To induce anti-Thy1 glomerulonephritis, purified anti-rat Thy1.1 antibody (2.4 mg/kg body wt) was injected intravenously. Three rats were killed at each time point (days 2, 4, 7, 14, and 28) along with three control rats. Rat kidneys were removed, followed by glomerular isolation by standard sieving method (15) and preparation of total RNA for Northern blot analysis. A portion of tissue was fixed in methyl-Carnoy’s solution, embedded in paraffin, sectioned 4 μm thick, and stained with the periodic acid-Schiff reagent and counterstained with hematoxylin. Immunohistochemical staining with mouse antiproliferating cell nuclear antigen (PCNA) monoclonal antibody PC10 (DAKO) was performed as described previously (16). The number of intraglomerular cells and PCNA-positive glomerular cells on 20 randomly selected glomeruli was determined. Glomerular cross-sections containing only a minor portion of the glomerular tuft (<20 discrete capillary segments per cross-section) were not used.

**Results**

**Cloning of PP4Rmeg**

A large-scale sequencing of a 3'-directed cDNA library of cultured human mesangial cells was performed to determine partial sequences of 1836 randomly picked clones (1,2). The sequences of the clones was compared with the DNA database GenBank using the FASTA program (17). Several clones, which have not been recorded in any other databases, were found to be abundantly expressed in human mesangial cells. We obtained a clone, which was abundant among those detected in our human mesangial cell cDNA library. This clone consisted of 0.25% of all the mRNA population.

Using PCR techniques, we isolated a full-length cDNA. Nucleotide sequencing analysis of this clone revealed an open reading frame of 2850 nucleotides for a predicted protein of 950 amino acids (Figure 1). The sequence around the initiation codon (AAGATGG) was consistent with Kozak’s consensus sequence (AGCCATGG). Stop codons in all three reading frames were identified upstream of the initiation codon.

Nucleic acid homology searches of the database using the BLASTN program revealed that this gene was highly homologous to a recently identified regulatory subunit of protein
Figure 1. Amino acid sequences of human and rat PP4 Rmeg. The amino acid sequences were well conserved between human and rat PP4 Rmeg (86.3% homology). Thirteen regions homologous to the heat repeats found in the A subunit of PP2A (18) are underlined. The heat repeat sequences were highly conserved between human and rat. The portion enclosed by a box indicates the 18 amino acids substituting for 18-Ser in PP4R1. The accession numbers for the nucleotide sequence of human and rat PP4 Rmeg are AF200478 and AF332004, respectively (DNA Data Bank of Japan, European Molecular Biology Laboratory, and GenBank).
phosphatase 4 (PP4R1) (4). The deduced amino acid sequence of PP4Rmeg was completely identical to PP4R1, except for the replacement of serine-18 in PP4R1 by 18 amino acids (FGVD-DYSDSDVIIIPSA) in PP4Rmeg. PP4Rmeg has 13 regions homologous to the “heat” repeats found in the A subunit of PP2A (18).

We confirmed by RT-PCR that cultured human mesangial cells and the A431 cell line contained both PP4Rmeg and PP4R1 transcripts (Figure 2). Nucleotide sequence analyses of the 275- and 326-bp PCR products established that they were PP4R1 and PP4Rmeg, respectively.

The size of the myc-tagged PP4Rmeg protein produced by the in vitro translation system using the rabbit reticulocyte lysates with canine pancreatic microsomal membranes was 135 kD, which was much higher than the calculated molecular weight of the deduced amino acid sequence of the tagged PP4Rmeg (107 kD; data not shown). This finding suggests the existence of some posttranslational modification(s). The size of the myc-tagged protein was almost identical when the in vitro translation was performed in the absence of canine microsomal membranes, excluding the possibility of N-glycosylation of PP4Rmeg.

To investigate whether PP4Rmeg was conserved in other species, we cloned a partial cDNA of the rat homologue of PP4Rmeg from cultured rat mesangial cells. The determined DNA sequences covered the putative open reading frame, and the 18 amino acids that we found in the N-terminus of human PP4Rmeg also existed in rat PP4Rmeg. The DNA sequence of this region was almost identical with that of human PP4Rmeg. At the amino acid level, rat PP4Rmeg was 86.3% identical to human PP4Rmeg (Figure 1). The regions of the heat repeat sequences were highly conserved in rat PP4Rmeg.

Binding of PP4Rmeg to PP4c

The high homology of PP4Rmeg with the recently reported regulatory subunit of PP4, PP4R1, suggested that PP4Rmeg might bind to PP4c. To test this, we transfected COS-7 cells with Myc-PP4Rmeg and recombinant Myc-PP4Rmeg (M.W.: 135 kD, Figure 3A) was immunoprecipitated from the cell lysates using anti-Myc antibody. The immune complexes were analyzed for PP4c by immunoblotting. As shown in Figure 3B, PP4c co-precipitated with recombinant Myc-PP4Rmeg from cell lysates of Myc-PP4Rmeg transfectants. No PP4c was detected in the anti-Myc immune complexes from lysates of mock-transfected cells. These results indicate that recombinant PP4Rmeg bound to endogenous PP4c, suggesting that PP4Rmeg functions as a regulatory subunit of PP4.

PP4Rmeg Is Abundantly Expressed in Human Mesangial Cells

The high homology made it difficult to discriminate between PP4Rmeg and PP4R1. Consequently, we performed Northern blot analysis using a probe that recognizes a common portion of the PP4 regulatory subunits (PP4Rs).

A single transcript of 4.5 kb was detected in cultured mesangial cells (Figure 4A). PP4Rs were also detected in other human cells, e.g., dermal fibroblasts, tubular epithelial cells, umbilical vein endothelial cells, and aortic smooth muscle cells, but were most highly expressed in mesangial cells. The PP4R mRNA were ubiquitously expressed in the various organs and most highly expressed in heart and placenta (Figure 4B).

The expression of PP4R mRNAs in vivo was examined in

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**Figure 2.** Detection of PP4Rmeg and PP4R1 transcripts by reverse transcriptase-PCR in cultured human mesangial cells and A431 cells. Total RNA from two independently cultured mesangial and A431 cells were reverse transcribed, and the fragments containing 18-Ser in PP4R1 (275 bp) or the substitutive 18 amino acids in PP4Rmeg (326 bp) were amplified by PCR.

**Figure 3.** Association of PP4Rmeg with PP4c. (A) The cell lysates obtained from mock- or Myc-PP4Rmeg-transfected COS-7 cells were analyzed by immunoblotting with anti-Myc antibody to detect recombinant Myc-PP4Rmeg. (B) The mock- or Myc-PP4Rmeg-transfectant lysates were reacted with anti-Myc antibody and the thus-precipitated immune complexes were analyzed by immunoblotting with anti-PP4R1 (anti-PP4Rmeg) antibody (top) or anti-PP4c antibody (bottom). The “applied” fraction represents starting material, which is cell lysate solubilized in sodium dodecyl sulfate sample buffer. The “bound” fraction represents immunoprecipitated proteins. The “flow-through” fraction represents unbound proteins present in the supernatant after centrifugation of the protein-antibody-beads complex.
normal human renal tissues by in situ hybridization. The strongest signals were detected mainly within the glomerulus (Figure 5). By contrast, the signals in the tubular and interstitial regions were less intense.

**Upregulation of the PP4 Regulatory Subunits Expression in Anti-Thy1 Glomerulonephritis Rats**

To investigate whether the PP4 regulatory subunits expression is altered in vivo in glomerular disease, we used anti-Thy1 glomerulonephritis rats. This is a well-established model of mesangial proliferative glomerulonephritis (19). Periodic acid-Schiff staining of the renal tissues demonstrated characteristic features of anti-Thy1 glomerulonephritis, including mesangial hypercellularity, matrix accumulation, and microaneurysm formation (19). Northern blot analysis showed that PP4 mRNA expression reached peak on day 2 and returned to the control levels thereafter (Figure 6A). Total cell number in glomeruli decreased on day 2, did not recover on day 4, and demonstrated only a slight increase on day 7 (Table 1). Immunohistochemical staining showed that the number of PCNA-positive cells in glomeruli reached its peak on day 7 (Table 1). Whereas the number of PCNA-positive cells on day 1 was approximately half of that on day 2, the PP4 expression level was almost identical to the peak value on day 2, suggesting that expression of PP4 proceeds mesangial proliferation (Figure 6B, Table 1).

**Discussion**

Here we report the cloning and characterization of a novel subunit of PP4. PP dephosphorylate many kinds of proteins and play biologically important roles. The result that the amino acid sequences of PP4 were well conserved between human and rat reflects that PP4 has biologically basic functions. The sequences were especially well conserved in the regions of the heat repeat, which may be a potential candidate as a binding site to other subunits. It is likely that PP4 binds to the C terminus of PP4, because this is where the A subunit of PP2A and PP4 share the greatest homology; however, the precise binding site remains to be determined.

Structural and functional analyses of PP4 revealed that it was closely related to the recently reported novel regulatory subunit of PP4, PP4 (4). The amino acid sequences of

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**Figure 4.** Detection of PP4 (PP4meg and PP4R1) transcripts in tissues and cells. Expression of PP4 in primary culture cells (A) and various human tissues (B) was examined by Northern blotting. Top, PP4 (PP4meg and PP4R1). Middle, β-actin. Bottom, the ratios of intensities of PP4 to β-actin transcripts calculated by densitometry using NIH image software. HUVECs, human umbilical vein endothelial cells.

**Figure 5.** In situ hybridization detection of PP4 transcripts in human renal tissues. The signals for PP4 regulatory subunits PP4meg and PP4R1 are observed in a glomerulus of normal subjects. Magnification, ×40.
PP4\textsubscript{Rmeg} and PP4\textsubscript{R1} were almost identical except that serine-18 in PP4\textsubscript{R1} was replaced by 18 amino acids (FGVDDYSSED-VIIIPSA) in PP4\textsubscript{Rmeg}. Despite the additional amino acid insertion at the N-terminus, PP4\textsubscript{Rmeg} seems to be biologically similar to PP4\textsubscript{R1}. Our immunoprecipitation studies demonstrated that recombinant PP4\textsubscript{Rmeg} can associate with endogenous PP4\textsubscript{c} in cell lysates, supporting the idea that PP4\textsubscript{Rmeg} functions as a regulatory subunit of PP4. In good agreement with this, Kloeker and Wadzinski (4) previously demonstrated that PP4\textsubscript{R1} migrated as a doublet on SDS-PAGE and exhibited a fairly broad peak (approximately 105 kD) by mass spectrometry, suggesting the possibility of the isoform(s) of PP4\textsubscript{R1}.

According to the genomic information in the GenBank database, PP4\textsubscript{Rmeg} seems to be localized on chromosome 18. The PP4\textsubscript{Rmeg}-specific sequence, which is 51 bp long, is located on the 5' part of the third exon consisting of 136-bp nucleotides. The sequences of the 3' end of intron 2 and the PP4\textsubscript{Rmeg}-specific part are consistent with consensus sequences for donor sites of alternative splicing. PP4\textsubscript{Rmeg} and PP4\textsubscript{R1} therefore may be splicing variants of a common gene. Both PP4\textsubscript{Rmeg} and PP4\textsubscript{R1} are expressed in human mesangial cells and A431 cells. However, the difference of function and enzymatic activity between these two molecules remains to be determined.

In the present study, we showed ubiquitous expression of PP4 regulatory subunits in various human organs. This result is in accordance with the fact that PP4 is the protein with biologically basic functions. Although our Northern blot analysis demonstrated that PP4\textsubscript{R}s were expressed to some degree in most, if not all, cultured cells examined thus far, we observed higher expression of PP4\textsubscript{R}s mRNA in cultured mesangial cells. The result of the present in situ hybridization studies also supported high expression of PP4\textsubscript{R}s in glomerular cells in vivo.

Our immunoprecipitation studies demonstrating the association of PP4\textsubscript{Rmeg} with PP4\textsubscript{c} suggest that a functional role for PP4\textsubscript{Rmeg} is similar to PP4\textsubscript{R1}. This may give us a clue to its biologic functions. PP4 has been localize at centrosomes/spindle pole bodies in human and Drosophila cells (11). The Drosophila melanogaster strain containing a mutated PP4\textsubscript{c} gene exhibits a semilethal phenotype with abnormal mitotic spindle microtubules (12). Most cell-cycle–dependent regulation of microtubule assembly occurs through changes in microtubule-associated protein phosphorylation state (reviewed in reference 20). Thus, PP4 may regulate cell mitosis by locally dephosphorylating centrosomal or microtubule-associated proteins, thereby regulating microtubule growth initiation or stability. We speculate that PP4\textsubscript{Rmeg} controls cell mitosis by regulating the activities of key phosphoproteins. Although some proteins, including \(\gamma\)-tubulin and CP60, have been considered to be potential candidates (12), the in vivo substrates have not identified. To uncover the mechanism of cytokinesis, it will be important to identify the substrates and to determine the precise function of PP4 in cell mitosis.

In this context, of particular interest is the potential involve-

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### Table 1.
The number of intraglomerular cells and PCNA-positive cells in the renal tissues of anti-Thy1 glomerulonephritis rats at the time points from day 2 to day 28 and of day 1 and day 2

<table>
<thead>
<tr>
<th>Time Points</th>
<th>Total Cells</th>
<th>PCNA-Positive Cells</th>
</tr>
</thead>
<tbody>
<tr>
<td>Days 2 to 28</td>
<td></td>
<td></td>
</tr>
<tr>
<td>control</td>
<td>44.9 ± 11.2</td>
<td>1.6 ± 1.9</td>
</tr>
<tr>
<td>day 2</td>
<td>35.4 ± 7.0\textsuperscript{a}</td>
<td>3.5 ± 2.9\textsuperscript{b}</td>
</tr>
<tr>
<td>day 4</td>
<td>37.5 ± 9.9\textsuperscript{b}</td>
<td>4.2 ± 3.1\textsuperscript{a}</td>
</tr>
<tr>
<td>day 7</td>
<td>51.8 ± 11.4\textsuperscript{c}</td>
<td>11.0 ± 5.0\textsuperscript{a}</td>
</tr>
<tr>
<td>day 14</td>
<td>46.9 ± 11.0</td>
<td>1.0 ± 1.5</td>
</tr>
<tr>
<td>day 28</td>
<td>46.9 ± 10.0</td>
<td>0.3 ± 0.6</td>
</tr>
<tr>
<td>Days 1 and 2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>control</td>
<td>54.2 ± 7.9</td>
<td>1.1 ± 0.8</td>
</tr>
<tr>
<td>day 1</td>
<td>43.2 ± 5.6\textsuperscript{a}</td>
<td>3.3 ± 1.5\textsuperscript{a}</td>
</tr>
<tr>
<td>day 2</td>
<td>38.0 ± 6.0\textsuperscript{a}</td>
<td>4.8 ± 1.5\textsuperscript{a}</td>
</tr>
</tbody>
</table>

\(\text{a}\ P < 0.001, \text{b}\ P < 0.01, \text{c}\ P < 0.05 \text{ versus control.}\)
ment of PP₄Rₘₑᵍ in the regulation of mesangial cell division and proliferation. This stimulated us to investigate expression profiles of PP₄Rₘₑᵍ in mesangial injury and repair. Our present results using anti-Thy1 glomerulonephritis rats suggest a link between the upregulation of PP₄Rₘₑᵍ expression and mesangial proliferation. After intravenous administration of anti-Thy1 antibody, the number of endogenous glomerular cells decreases as a result of mesangiolysis. This phase is transient and followed by the recovery phase with mesangial proliferation. These results are consistent with our hypothesis that PP₄Rₘₑᵍ serves as a regulator of cell division in glomeruli. However, functional studies are required to conclude that PP₄Rₘₑᵍ plays a role in this process.

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