Regulation of Angiotensin II Type 1 Receptor mRNA and Protein in Angiotensin II–Induced Hypertension

Lisa M. Harrison-Bernard, Samir S. El-Dahr, Denise F. O’Leary, L. Gabriel Navar

Abstract—Chronic elevations of circulating angiotensin II (Ang II) cause sustained hypertension and enhanced accumulation of intrarenal Ang II by an AT$_1$ receptor–dependent process. The present study tested the hypothesis that chronic elevations in circulating Ang II regulate AT$_1$ mRNA and protein expression in a tissue-specific manner. Sprague-Dawley rats were infused with Ang II (80 ng/min) or vehicle subcutaneously for 13 days via osmotic minipump. On day 12, systolic blood pressure averaged 186±12 mm Hg in Ang II–infused rats compared with rats given vehicle (121±2 mm Hg). Plasma renin activity was markedly suppressed in the Ang II–infused rats compared with vehicle-infused rats (0.1±0.01 versus 4.9±0.9 ng of Ang I · mL$^{-1}$ · h$^{-1}$; $P<0.05$). Semiquantitative reverse transcription polymerase chain reaction using rat AT$_{1A}$ and glyceraldehyde-3-phosphate dehydrogenase (GAPDH)–specific primers was followed by Southern blot hybridization using specific radiolabeled cDNA or oligonucleotide probes. The results showed that the ratios of AT$_{1A}$/GAPDH mRNA in the kidney (0.19±0.05 versus 0.26±0.03) and liver (2.8±0.9 versus 3.0±0.5) were comparable in Ang II– and vehicle-infused rats. In contrast, AT$_{1R}$/GAPDH mRNA levels were increased in the adrenal glands of Ang II–infused rats (0.49±0.04 versus 0.36±0.02; $P<0.05$). Western blot analysis showed that AT$_1$ protein levels in the kidney and liver were also similar in the two groups. Therefore, these results indicate that renal and liver AT$_1$ receptor gene expression is maintained in Ang II–induced hypertension. The failure to downregulate AT$_1$ receptor mRNA and protein levels thus allows the sustained effects of chronic elevations in Ang II to elicit progressive increases in arterial pressure. (Hypertension. 1999;33[part II]:340-346.)

Key Words: kidney ■ liver ■ adrenal gland ■ gene expression ■ antibodies

Chronic administration of angiotensin II (Ang II) is a useful experimental model of Ang II–dependent hypertension that mimics 2-kidney, 1 clip (2K1C) Goldblatt hypertension. The mechanisms responsible for the progressive nature of Ang II–induced hypertension are multifarious and incompletely understood. We previously demonstrated that chronic infusion of initially a subpressor dose of Ang II into uninephrectomized rats produces a slowly developing hypertension that is associated with diminished renal renin content and mRNA, enhanced renal ACE activity, maintained renal and hepatic angiotensinogen mRNA levels, and an AT$_1$–mediated augmentation of intrarenal Ang II content.$^{1-4}$ However, the contribution of the expression of the AT$_1$ receptor to the hypertensinogenic effect of Ang II has not been established. Because most of the hypertensinogenic actions of the renin-angiotensin system are mediated by the binding of Ang II to the AT$_1$ receptor, the predominant receptor subtype in adult animals, and the availability of AT$_1$ receptors essentially determines the efficacy of the renin-angiotensin system, we studied the tissue-specific expression of the AT$_1$ receptor after chronic low-dose infusions of Ang II in the rat. In particular, the regulation of AT$_1$ receptor mRNA and protein expression was determined in the kidney, liver, and adrenal gland.

Methods

Animals and Tissue Preparation

Male Sprague-Dawley rats (Charles River Labs, Wilmington, MA) were housed in wire cages and maintained in a temperature-controlled room regulated on a 12-hour light/dark cycle. Rats had free access to water and standard rat chow (Ralston-Purina). The experimental protocol was approved by the Tulane University Animal Care and Use Committee. Rats (230±4 g body wt; n=17) were anesthetized with sodium pentobarbital (50 mg/kg IP), and an osmotic minipump (model 2002; Alza Corp) was implanted subcutaneously at the dorsum of the neck. Rats were selected at random to receive Ang II infusion (n=8; Novabiochem) at a rate of 80 ng/min (350 ng · kg$^{-1}$ · min$^{-1}$) or vehicle (n=9; 5% acetic acid) for a period of 13 days. Systolic blood pressures were measured in conscious rats 1 day before surgery and on days 6 and 12 of the infusion using tail-cuff plethysmography (model 52-0338; Harvard Apparatus). Blood and tissue samples (kidneys, liver, adrenal glands) were harvested on day 13 after rapid decapitation. Trunk blood was collected into chilled tubes containing EDTA. Plasma was separated and stored at −20°C until assayed for plasma renin activity using a commercially available Ang I RIA kit (Incastar) as described previously.$^3$ Liver and kidneys were removed for protein and RNA extraction. Adrenal glands were removed for RNA extraction. Samples were snap-frozen in liquid nitrogen and stored at −80°C until processed.

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AT₁<sub>A</sub> Receptor mRNA Analyses

Total RNA was extracted using the RNeasy Midi Kit (Qiagen) according to the manufacturer's specifications. The extracted RNA was quantified spectrophotometrically by absorbance at 260 nm, dissolved in sterile water, and stored at −80°C until use. Integrity of RNA was documented by agarose gel electrophoresis and observation of 28S and 18S ribosomal RNA.

RT-PCR

cDNA was synthesized by use of SuperScript II RT (GIBCO BRL). The reaction mixture contained DNase I–digested RNA (kidney, 5 μg; liver, 3 μg; adrenal, 2.5 μg), 10× PCR buffer (200 mmol/L Tris·HCl, pH 8.4, 500 mmol/L KCl, 10 mmol/L MgCl₂), 100 ng random hexamers, 10 mmol/L concentration each of deoxynucleoside triphosphate, 0.1 mmol/L DTT, and 200 U RT for a total volume of 23 μL. RT was omitted in control samples. Positive control for the RT step consisted of control RNA provided by the manufacturer. The reaction mixture was incubated at 25°C for 10 minutes and 42°C for 50 minutes, heated to 70°C for 15 minutes, and chilled on ice. RNase H (2 U) was added to each tube and incubated at 37°C for 20 minutes. RT reaction was then diluted with 10× PCR buffer, followed by the addition of upstream and downstream primers and 2.5 U Taq DNA polymerase (GIBCO BRL) for a final volume of 50 μL. The reaction was initiated by heat denaturation of RNA-cDNA hybrid at 95°C for 1 minute, annealing of the primers (50 pmol for hAT₁<sub>a</sub>, 25 pmol glyceraldehyde-3-phosphate-dehydrogenase [GAPDH]), and extension at 72°C. The cycle was repeated 25 times using a programmable PCR thermocycler (Perkin-Elmer Cetus Instruments). Details of each PCR are described. PCRs for GAPDH and hAT₁<sub>a</sub> were performed from the same RT products to allow the data to be expressed as a ratio to GAPDH. The appropriate PCR reaction cycle number was determined for the two targeted mRNAs by using 0.5 μCi [α-<sup>32</sup>P]dCTP in the PCR and performing 15 to 35 cycles of amplification. PCR products were run on 2% agarose gel, and the bands were excised, dried at 37°C overnight, and counted using scintillation fluid. Twenty-five–cycle amplification was on the linear portion of the plot of the log of the cpm as a function of cycle number for each PCR product. Semi-quantification of hAT₁<sub>a</sub> and GAPDH mRNA in the liver and kidney was carried out in the presence of 0.5 μCi [α-<sup>32</sup>P]dCTP. Products were analyzed as described above.

Primers

hAT₁<sub>a</sub> primers are from the 3'-untranslated regions of the rat AT₁<sub>a</sub> receptor cDNA. The upstream primer is complementary to nucleotides 1370 to 1389 (5′-GCACCTGGCAATGTAATGC-3′), and the downstream primer corresponds to nucleotides 1737 to 1756 (5′-TTGAGCAAGAACTGACC-3′). The predominant cDNA amplification product is predicted to be 385 bp. Ten μL of RT product was amplified as described above with annealing at 58°C for 45 seconds and extension at 72°C for 90 seconds. The upstream primer of GAPDH is complementary to nucleotides 524 to 547 of the rat GAPDH cDNA (5′-AATGATCTCCTGACCAACAACCTG-3′), and the downstream primer corresponds to nucleotides 1055 to 1078 (5′-GGAGCCCATGTAGGAAGGTT-3′). The predicted size of the PCR product is 555 bp. Two μL of RT product was amplified as described above with annealing at 55°C and extension at 72°C for 60 seconds each.

Southern Blot Hybridization

Electrophoresis of 10 to 20 μL PCR products was carried out in 1% agarose gel. DNA was transferred to a positively charged nylon membrane (GeneScreen Plus; New England Nuclear) using capillary method. Blots were prehybridized for 1 hour at 46°C with 5× SSC, 1× Denhardt’s solution, 0.05 mol/L PO₄ buffer (pH6.7), 2 mg denatured herring sperm DNA, 0.10 mmol/L dextran sulfate, and 50% formamide. Blots were hybridized overnight with 10⁷ cpm/mL oligo probe for hAT₁<sub>a</sub> and GAPDH using 5× SSC, 0.5× Denhardt’s solution, 0.02 M PO₄ buffer, 1 mg herring sperm DNA, 0.2 mmol/L dextran sulfate, and 50% formamide. Blots were prehybridized at 65°C for 1 hour with 1% SDS in 0.1× SSPE and hybridized overnight with 10⁷ cpm/mL GAPDH cDNA probe in 7% SDS, 0.25 mol/L sodium phosphate buffer, 2 mg denatured herring sperm DNA, 0.2 g BSA fraction V, and 0.1 mmol/L EDTA. Blots were washed successively in 1×, 0.2×, and 0.1× SSC containing 0.1% SDS at room temperature with gentle agitation (30 minutes each).

Slot Blot Analysis

Slot blots were prepared by serial 2-fold dilutions (4 to 1 μg) of total RNA from individual animals as described previously. Blots were hybridized to the hAT₁<sub>a</sub> oligo probe and rehybridized with a GAPDH oligo probe to account for loading variations (2 to 3 months allowed for ³²P decay). Signals were detected by autoradiography and quantified by scanning laser densitometry (Ultrorcan; Pharmacia LKB).

DNA Probe Radiolabeling

Probes were labeled with 50 μCi [α-³²P]dCTP using random primers DNA labeling system (GIBCO BRL) and purified on Sephadex G-50. Nick columns (Pharmacia). The cDNA probe used was a human GAPDH cDNA (Clontech). Five pmol of the oligonucleotide (lower AT₁<sub>a</sub> or GAPDH primer) was 5′-end labeled with 50 to 70 μCi [γ-³²P]dATP using T4 polynucleotide kinase (20 U; GIBCO BRL) and purified on a Sephadex G25 column (Pharmacia).

AT₁<sub>A</sub> Receptor Protein Analysis

Proteins were extracted from kidney and liver samples after homogenization as described previously and assayed by the method of Lowry et al.⁸

Western Blot Analysis of AT₁<sub>A</sub> Receptor

Kidney (50 μg) or liver (25 μg) samples were electrophoretically separated by 3% to 10% stacking Tris-glycine gel at 100 V for 2 hours (10% SDS, 24 mmol/L Tris base, 192 mmol/L gly cine) and transferred (20% methanol, 12 mmol/L Tris base, 96 mmol/L glycine) to nitrocellulose membrane (0.45; BioRad) for 90 minutes at 25 V according to the manufacturer’s specifications (XCell II Mini-Cell; Novex). Molecular weight markers (10- to 250-kDa rainbow; Amersham; and 10-kDa protein ladder, GIBCO BRL) were used to determine approximate molecular mass. Western blot analysis was performed as described previously with minor modifications. Blots were incubated with the primary antibody (1) anti-peptide (8 to 17 amino acids, AT<sub>1</sub> monoclonal antibody 6313/G2, 1:50; GP Vinson) or (2) anti-peptide AT<sub>1</sub> polyclonal antibody 1:200 (15 to 24 amino acids, SC-1173; Santa Cruz) for 3 hours, washed, incubated with the secondary antibody conjugated to horseradish peroxidase (1:1500) for 1 hour, and washed. Detection was accomplished using enhanced chemiluminescence Western blotting (ECL; Amersham), and the blots were exposed to x-ray film (Hyperfilm-ECL; Amersham). For preadsorption studies, the polyclonal antibody and the synthetic peptide antigen (20 μg; SC-1173P) were incubated overnight at 4°C. Kidney (50 μg) and liver (25 μg) samples were separated in duplicate on each of 2 gels. One gel was stained with 0.1% Coomassie blue R250 to visualize the protein bands for total protein quantification. The proteins from the second gel were electrophoretically transferred to nitrocellulose and incubated with the primary polyclonal antibody or preadsorbed antibody as described above.

Statistical Analysis

Results are expressed as mean ± SEM. For slot blots, regression lines were calculated for each tissue sample from the ratio of the densitometric values of the 3 serial dilutions, and only those samples exhibiting linearity of the hybridization signals with values of r²>0.9 were accepted for further consideration. For Southern and slot blot analyses, AT₁<sub>a</sub> signals were factored for GAPDH. The data were analyzed using unpaired t test or Mann-Whitney rank sum test. Statistical significance is defined at a value of P<0.05.
Results

Body Weight, Blood Pressure, and Plasma Renin Activity

Body weights in the two groups at the initiation of the study were similar (Ang II, 226±4 g, n=8; vehicle, 225±4 g, n=9). On day 13 of the infusion, average body weight in the Ang II–infused animals was significantly reduced compared with vehicle (292±7 versus 343±9 g). Systolic blood pressures (Figure 1) were identical in the 2 groups before implantation of the osmotic minipumps (121±2 mm Hg). On days 6 and 12 of infusion, pressures were significantly elevated to 168±3 and 186±12 mm Hg in the Ang II–infused rats compared with vehicle-infused rats (118±3 and 119±3 mm Hg). Plasma renin activity was markedly suppressed in the Ang II–infused rats compared with vehicle-infused rats (0.1±0.01 versus 4.9±0.9 ng of Ang I · mL⁻¹ · h⁻¹, n=7 and 9).

AT1 Receptor Antibody Specificity

We documented the specificity of the anti-peptide polyclonal AT1 receptor antibody by performing Western blot analysis of liver and kidney protein using the antibody preadsorbed with the synthetic peptide antigen. Figure 2 illustrates a Western blot autoradiograph comparing liver and kidney AT1 receptor protein detected using the primary antibody shown on the left and preadsorbed antibody on the right. Densitometric analysis of the bands indicates that the intensity of the signal was >90% decreased using the preadsorbed antibody. Equal loading was determined by Coomassie blue staining of the duplicate gel. The results demonstrate that the polyclonal AT1 receptor antibody is specific for the ∼46-kDa AT1 receptor protein in these tissues. We previously reported that adsorption of the monoclonal AT1 antibody by the antigenic peptide eliminates renal vascular and tubular AT1 receptor antibody immunostaining, demonstrating that the monoclonal antibody is specific for the AT1 receptor protein. The antigenic peptide sequences for the two antibodies correspond to portions of the AT1 receptor protein that are identical for the AT1A and AT1B receptor subtypes.

Kidney AT1 Receptor mRNA and Protein Expression

Western blot analysis of AT1 receptor protein from whole kidney homogenates using the monoclonal antibody in Ang II–infused animals showed that the receptor protein levels remain unchanged during chronic Ang II–induced hypertension (42±6 versus 36±3 du; n=5) (Figure 3A). Similar results were obtained using the polyclonal antibody for Ang II–infused (9±3 du; n=4) and vehicle-infused (6±1 du; n=5) rats. Renal AT1A mRNA expression was assessed using semiquantitative RT-PCR and Southern blot analysis (Figure 3B). Renal AT1A mRNA levels were not significantly different between the vehicle- and Ang II–infused animals. The ratio of renal AT1A to GAPDH densitometric signals was 0.66±0.07 in vehicle-infused (n=9) and 0.47±0.10 in Ang II–infused (n=8) animals. In addition, semiquantification of kidney AT1A mRNA by incorporation of [α-32P]dCTP confirmed the results obtained by Southern blot analysis. The ratio of AT1A and GAPDH PCR products (cpm) was 1.1±0.4 (n=4) in vehicle-infused and 1.1±0.3 (n=4) in Ang II–infused rats. AT1A mRNA slot blot analysis of 4, 2, and 1 μg of total kidney RNA is shown in Figure 3C and demonstrates that AT1A mRNA levels were not different between the 2 groups, in agreement with the RT-PCR analysis. The ratios of kidney AT1A and GAPDH densitometric signals were 4.2±0.4 versus 4.5±0.3, 3.2±0.2 versus 3.3±0.3, and 3.6±0.5 versus 3.6±0.3 for vehicle-infused (n=9) versus Ang II–infused (n=7) animals at 4, 2, and 1 μg RNA, respectively.

Liver AT1 Receptor mRNA and Protein Expression

Western blot analysis of liver AT1 receptor protein from Ang II– and vehicle-infused animals showed that the receptor protein levels were not altered during Ang II–induced hypertension (52±3 versus 52±3 du, polyclonal primary antibody; 11±2 versus 10±1 du, monoclonal: Figure 4A). Semiquantification of liver AT1A mRNA by RT-PCR demonstrated that the receptor gene expression is not altered by chronic Ang II infusion (Figure 4B). The ratio of liver AT1A to GAPDH Southern blot densitometric signals was 3.0±0.5 in vehicle-infused (n=9) and 2.8±0.9 in Ang II–infused (n=8) animals. Semiquantification of liver AT1A mRNA by incorporation of [α-32P]dCTP confirmed the results obtained by Southern blot analysis. The ratio of AT1A and GAPDH PCR products (cpm)
was $0.42 \pm 0.09$ (n=5) in vehicle-infused and $0.30 \pm 0.03$ (n=4) in Ang II-infused animals ($P=0.14$). Slot blot analysis of liver AT_{1A} mRNA in vehicle- and Ang II–infused animals is shown in Figure 4C. Liver AT_{1A} gene expression was not altered during Ang II–induced hypertension. The ratios of liver AT_{1A} and GAPDH densitometric signals were $2.9 \pm 0.3$ versus $3.1 \pm 0.1$, $3.0 \pm 0.2$ versus $3.2 \pm 0.3$, and $3.8 \pm 0.7$ versus $4.1 \pm 0.5$ for vehicle-infused (n=9) versus Ang II–infused (n=8) animals at 4, 2, and 1 μg RNA, respectively.

Adrenal AT_{1A} Receptor mRNA Expression
Adrenal AT_{1A} mRNA was analyzed as described above. RT-PCR and Southern blot analysis demonstrated a significant elevation in AT_{1A} mRNA in the adrenal gland of Ang II–infused animals (Figure 5A). The ratios of adrenal AT_{1A} to GAPDH Southern blot densitometric signals were $0.36 \pm 0.02$ in vehicle-infused (n=8) and $0.49 \pm 0.04$ in Ang II–infused (n=8) animals ($P<0.01$). By slot blot analysis, AT_{1A}/GAPDH mRNA tended to be higher but did not reach statistical significance (Figure 5B). The ratios of adrenal AT_{1A} and GAPDH densitometric signals were $0.58 \pm 0.05$ versus $0.68 \pm 0.08$, $0.75 \pm 0.05$ versus $0.87 \pm 0.08$, and $0.98 \pm 0.12$ versus $0.87 \pm 0.08$ for vehicle-infused (n=8) versus Ang II–infused (n=6) animals at 4, 2, and 1 μg RNA, respectively.

Discussion
In agreement with previous studies, chronic low-dose infusion of Ang II produced significant elevations in systolic blood pressure and reductions in plasma renin activity. After 13 days of infusion, we found that kidney and liver AT_{1A} mRNA and protein levels were maintained under conditions of chronic elevations in Ang II. However, in the adrenal gland, AT_{1A} mRNA expression was significantly elevated. These results indicate that renal AT_{1} receptor gene expression is not suppressed in Ang II–induced hypertension. The failure to downregulate AT_{1A} receptor mRNA and protein levels thus allows the sustained effects of chronic elevations in Ang II to elicit progressive increases in arterial pressure.

The AT_{1} receptor is 1 of 2 major Ang II receptor subtypes, which has been characterized pharmacologically and cloned. In rodents, 2 subtypes of AT_{1} receptors exist (AT_{1A}, AT_{1B}). The AT_{1A} and AT_{1B} receptor subtypes are >95% homologous at the amino acid level, but their tissue distributions and chromosomal locations are different. In the rat kidney, AT_{1A} mRNA expression has been reported to be 3- to 8-fold higher than AT_{1B} mRNA levels. Using RT-PCR techniques, Bouby et al reported that AT_{1A} mRNA was the predominant subtype in all microdissected nephron segments, with the exception of the glomerulus, where AT_{1B} mRNA levels were higher than AT_{1A} mRNA levels. In agreement with the AT_{1} mRNA localization, we have previously shown by immunohistochemical analysis that the AT_{1} receptor protein is present in all nephron segments. The liver is almost exclusively of the AT_{1A} subtype. Therefore, the AT_{1A} receptor subtype is involved in the majority of the hepatic and renal effects of Ang II. However, the adrenal gland expresses equal or 2-fold higher AT_{1B} mRNA levels compared with AT_{1A} mRNA. In the present study, the

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**Figure 3.** Kidney AT_{1} receptor mRNA and protein expression. A, Top, Western blot of renal AT_{1} receptor protein levels in Ang II– and vehicle-infused rats detected using a monoclonal antibody (lanes 1 through 5, vehicle infused; lanes 6 through 10, Ang II infused). Bottom, Similar renal AT_{1} receptor protein density in vehicle-infused (hatched bar; n=5) and Ang II–infused (solid bar; n=5) rats. B, Top, Representative Southern blot showing AT_{1A} and corresponding GAPDH mRNA levels (lanes 1, 3, and 5, vehicle infused; lanes 2, 4, and 6, Ang II infused). Bottom, Ratio of the densitometric analysis of the autoradiographic signals for AT_{1A} and GAPDH in vehicle-infused (hatched bar; n=9) and Ang II–infused (solid bar; n=8) rats. C, Top, Representative autoradiograph of AT_{1A} mRNA slot blot hybridized with radiolabeled AT_{1A}-specific oligonucleotide. Membranes were reprobed with radiolabeled GAPDH oligonucleotide probe (lanes 1, 3, and 5, vehicle infused; lanes 2, 4, and 6, Ang II infused). Bottom, Average data for AT_{1A} mRNA detected by slot blot for vehicle-infused (○; n=9) and Ang II–infused (●; n=7) rats.
monoclonal and polyclonal antibodies used for Western blot analysis detect both the AT_{1A} and AT_{1B} receptors. The peptide sequences used to generate the antibodies were from the amino-terminal extracellular tail of the protein in which both the AT_{1A} and AT_{1B} amino acids sequences are identical. The results of the Western blot analysis using these 2 different AT_{1} antibodies indicated that kidney and liver AT_{1} protein levels were not significantly altered by chronic Ang II infusion. To determine the regulation of the predominant AT_{1} receptor–subtype mRNA expression, RT-PCR and slot blot analyses were performed using an AT_{1A}-specific oligonucleotide. The nucleotide sequences chosen were from the 3’ untranslated region of the AT_{1A} cDNA. Interestingly, the 5’ and 3’ flanking sequences of the AT_{1B} cDNA are only 35% identical with the AT_{1A} cDNA. Therefore, this study permitted us to assess AT_{1} receptor expression at both the protein and mRNA levels to determine the contribution of regulation of the AT_{1} receptor at the level of gene transcription as well as at the level of protein expression.

In vitro studies have demonstrated that AT_{1} mRNA levels are altered in response to Ang II. Decreases in AT_{1} mRNA have been described in aortic vascular smooth muscle cells and cultured rat glomerular mesangial cells, whereas increases were reported in cultured rabbit proximal tubule cells. These data suggest that the regulation of AT_{1} mRNA by vascular and tubular structures within the kidney may be differentially regulated and demonstrate that the regulation of the receptor by its ligand may be cell or tissue specific, or both.

Angiotensin-dependent hypertensive animal models have also been used to address the regulation of the AT_{1} receptor by alterations in the components of the renin-angiotensin system. In 2K1C Goldblatt hypertensive animals, AT_{1A} receptor mRNA levels were not changed in the contralateral intact kidneys but were decreased in the clipped kidneys 2 days and 1 week after clipping. AT_{1A}, but not AT_{1B}, mRNA levels were decreased in both kidneys 4 weeks after clipping in 2K1C rats. Decreases in vascular and glomerular AT_{1} receptor density have been reported in both the clipped and nonclipped kidney of 2K1C rats. In contrast, AT_{1} receptor mRNA was elevated in both the clipped and non-

Figure 4. Liver AT_{1} receptor mRNA and protein expression. 
A, Top, Western blot of liver AT_{1} receptor protein in Ang II– and vehicle-infused rats detected using polyclonal (top) and monoclonal (bottom) antibodies. Blots are from separate gels run using protein from the same animals in each group (lanes 1, 3, 5, 7, and 9, vehicle infused; lanes 2, 4, 6, 8, and 10, Ang II infused). Bottom, Comparable liver AT_{1} receptor protein expression in vehicle-infused (hatched bar) and Ang II-infused (solid bar) rats (n=5) for the polyclonal (left) and monoclonal (right; du >5) primary antibodies. B, Top, Representative blots showing AT_{1A} and corresponding GAPDH mRNA levels (lanes 1, 3, and 5, vehicle infused; lanes 2, 4, and 6, Ang II infused). Bottom, Ratio of the densitometric analysis of the autoradiographic signals for AT_{1A} and GAPDH in vehicle-infused (hatched bar; n=9) and Ang II-infused (solid bar; n=8) rats. C, Top, Representative autoradiograph of AT_{1A} mRNA slot blot hybridized with radiolabeled AT_{1A}-specific oligonucleotide in vehicle- and Ang II–infused rats (lanes 1, 3, and 5, vehicle infused; lanes 2, 4, and 6, Ang II infused). Bottom, Graph plotting the average data for AT_{1A} mRNA detected by slot blot for vehicle-infused (○; n=9) and Ang II–infused (●; n=8) rats.
clipped kidneys after 10 weeks of 2K1C. The renal expression of the AT1 receptor during the development of 2K1C hypertension may exhibit a temporal profile. Elevated expression of the renal AT1 receptor during the latter stages of 2K1C hypertension may explain the maintenance of an elevated blood pressure at a time when plasma renin activity is no longer elevated. In the present study, after 2 weeks of elevations in Ang II, overall kidney AT1 receptor mRNA and protein levels were maintained at levels similar to vehicle-infused animals, suggesting that the continued synthesis of the AT1 receptor enabled the sustained effects of circulating Ang II on arterial blood pressure.

Previous studies have evaluated the effects of chronic infusions of Ang II on renal AT1 receptor expression. Wang et al reported that 2 weeks of Ang II infusion at doses that do not elevate blood pressure decreases both AT1A and AT1B mRNA levels and AT1 receptor density in the rat kidney. However, Sechi et al showed that although renal AT1 mRNA levels were similar in rats infused with Ang II for 1 week compared with vehicle-infused rats, Ang II binding was slightly but significantly decreased by ~15%. Ang II infusion has been shown to increase and decrease the affinity and number of glomerular Ang II–binding sites. Amiri and Garcia demonstrated that 7-day infusions of nonpressor or pressor doses of Ang II did not alter pregglomerular or glomerular Ang II receptor density. Therefore, there is continued uncertainty regarding the effects of chronic infusions of Ang II on renal AT1 mRNA expression. This may be due to the duration and dose of Ang II infusion, level of blood pressure, the methodologies used to measure AT1 mRNA and density, or a combination. It is possible that the direct effects of Ang II on the expression of its receptor may be offset by the ambient blood pressure. It has been shown that infusion of Ang II that did not produce a change in blood pressure did not alter AT1 mRNA in aorta and mesenteric arteries. However, pressor infusion of Ang II increased AT1 mRNA in these vessels. Less is known about the organ-specific regulation of the AT1 receptor during Ang II infusions that produce hypertension.

Several studies, including our own, have failed to detect changes in AT1 mRNA levels in the kidney in response to alterations in circulating Ang II levels. This failure to detect changes in the total kidney tissue may reflect opposing changes in glomerular/vascular and tubular AT1 mRNA, as has been shown in response to low sodium diet and chronic AT1 receptor blockade in rabbits. However, the present study did not address the regional and segment-specific regulation of intrarenal AT1 receptor expression during the development of Ang II–induced hypertension.

In response to Ang II, the adrenal gland has been shown to increase Ang II receptors. In the rat adrenal cortex, AT1A mRNA increased in response to salt depletion, whereas AT1B mRNA decreased. However, opposite findings have also been reported in the adrenal gland in response to low salt diet. After 2 weeks of Ang II infusion in the rat, Iwai and Inagami found that adrenal AT1 mRNA levels were elevated but were not altered in the kidney. Our findings are in agreement with most of the studies that reported that the expression of the AT1 receptor in the adrenal gland is upregulated by its ligand. We found a
modest (~36%) but significant increase in adrenal AT1a gene expression in Ang II-infused animals with use of the sensitive technique of RT-PCR; although slot blot analysis did not detect these differences.

Significant reductions in body weight in Ang II–infused rats (350 ng · kg⁻¹ · min⁻¹, 2 weeks) have been reported to be due to increased peripheral metabolism that is independent of elevations in blood pressure.⁴⁴

In summary, chronic Ang II infusion in the rat that produces a significant elevation in arterial pressure is accompanied by elevations in adrenal AT1a mRNA levels and the maintenance of kidney and liver AT1 mRNA and protein levels. The combined effects of elevations in circulating Ang II levels and preservation of the AT1 receptor in these organs contribute to the hypertensinogenic effects of Ang II.

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