

Cloning and Characterization of Two New Isoforms of the Rat Kidney Urea Transporter: UT-A3 and UT-A4

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Abstract. Urea transport in the kidney is important for the production of concentrated urine and is mediated by a family of transporter proteins, identified from erythropoietic tissue (UT-B) and from kidney (UT-A). Two isoforms of the renal urea transporter (UT-A) have been cloned so far: UT-A1 and UT-A2. We used rapid amplification of cDNA ends to clone two new isoforms of the rat UT-A transporter: UT-A3 and UT-A4. UT-A3 and UT-A4 are 87% homologous. The UT-A3 cDNA encodes a peptide of 460 amino acids, which corresponds to the amino-terminal half of the UT-A1 peptide and is 62% identical to UT-A2. The UT-A4 cDNA encodes a peptide

of 466 amino acids, which is 84% identical to UT-A2. Transient transfection of HEK-293 cells with the UT-A3 or UT-A4 cDNA results in phloretin-inhibitable urea uptake, which is increased by forskolin. Thus, both new isoforms encode functional urea transporters that may be vasopressin-regulated. UT-A3 and UT-A4 mRNA are expressed in the renal outer and inner medulla but not in the cortex; unidentified UT-A isoforms similar to UT-A3 may also be expressed in the testis. It is concluded that there are at least four different rat UT-A urea transporters.

Urea is a major end product of protein metabolism. Although urea can cross cell membranes slowly by passive diffusion, its transport rate in kidney and erythrocytes is enhanced by specific transporter proteins (1). In the kidney, urea transport is important for the production of concentrated urine. The first evidence for a vasopressin-regulated, facilitated urea transport process in a mammalian inner medullary collecting duct (IMCD) segment was reported about 10 yr ago (2). The function of this renal vasopressin-regulated urea transporter has been further characterized in subsequent studies (3–9). The cDNA sequence of the first renal urea transporter UT2 was identified by expression cloning from rabbit inner medulla (10). The rat and human cDNA for this form of the urea transporter have also been cloned (11,12). A longer cDNA isoform, UT1, was later cloned, which appears to be a vasopressin-regulated urea transporter in the rat kidney IMCD (13). The cDNA of the human erythrocyte urea transporter (HUT11) was initially cloned from human bone marrow cells (14), and homologous cDNA for the rat erythrocyte urea transporter (rUT11, UT3) have been cloned subsequently (15,16), and are found to be expressed in kidney, brain, and testis.

The physiologic and molecular characterization of these urea transporters shows that they are remarkably homologous, and therefore they may be regarded as a family, similar to the aquaporins. A new, systematic nomenclature has recently been proposed for the urea transporters (1) and will be used in this report. The urea transporter family includes two main groups: the renal urea transporters (UT-A) and erythrocyte urea transporters (UT-B), which are likely to be encoded by different genes (reviewed in reference (1)). There are probably other urea transporters, which have not been identified. For example, the two known isoforms of the renal urea transporter UT-A1 (UT1) and UT-A2 (UT2), which are expressed in the renal tubule (17,18), are localized only to the apical membrane of IMCD cells and thin descending limb (18,19). Thus, they cannot account for the phloretin-inhibitable urea transport described in the basolateral membrane of IMCD (20), which must occur through a different, as yet unidentified urea carrier.

Using cloning by rapid amplification of cDNA ends (RACE), we searched for new members of the urea transporter family. We report two new cDNA isoforms of the renal UT-A urea transporter: UT-A3 and UT-A4, cloned from the rat inner medulla, and the partial characterization of their functional properties in a heterologous expression system.

Materials and Methods

Rapid Amplification of cDNA Ends

3' RACE was performed using the reagents provided in the 5'/3' RACE kit (Boehringer-Mannheim, Indianapolis, IN), following the protocols suggested by the manufacturer. Briefly, first-strand cDNA was synthesized from 2.5 mg of total RNA from rat renal

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medulla (TRI Pure Isolation Reagent, Boehringer-Mannheim), using an oligo(dT)-anchor primer (5'-GACCACGCGTATCGATGTCGACTTTTTTTTTTTTTTTT-3') and avian myeloblastosis virus reverse transcriptase. The reaction mixture was incubated for 60 min at 55°C, followed by incubation at 65°C for 10 min. Amplification by PCR was performed on 1.5 ml of the cDNA, using Expand™ High Fidelity PCR System (Boehringer-Mannheim), the PCR anchor primer (5'-GACCACGCGTATCGATGTCGAC-3'), and the sense primer PA (5'-GCATCGCATTGACATCTTCTCTAC-3'), corresponding to nucleotides 210 to 232 of the UT-A1 cDNA (13), for 10 cycles of 1 min at 94°C, 1 min at 58°C, 3 min at 72°C, followed by 25 cycles of 45 s at 94°C, 1 min at 58°C, 3 min + 20 s/cycle at 72°C. A second PCR amplification was performed using the sense primer PB (5'-CTTCACATGACAGATGAGCGAC-3'), corresponding to nucleotides 364 to 385 of UT-A1 cDNA, and the PCR anchor primer. The products of the second PCR amplification were gel-purified and sequenced using AmpliTaq DNA Polymerase FS (ABI PRISM Dye Terminator Cycle sequencing kit, Perkin Elmer, Foster City, CA). Sequences were analyzed on an automatic DNA sequencing system (ABI PRISM Genetic Analyzer, Perkin Elmer). 5' RACE was performed using a similar protocol with nested antisense primers corresponding to nucleotides 600 to 631, and 481 to 457 of the UT-A1 cDNA. The resulting PCR products were gel-purified and sequenced to verify that the 5' end sequences of the UT-A3, UT-A4, and UT-A1 cDNA were identical.

To exclude that discrepancies in the sequence of otherwise identical cDNA segments among the new isoforms and the previously published sequence of UT-A1 (13) could result from artifact, we amplified the UT-A1 cDNA by reverse transcription (RT)-PCR from total RNA from rat inner medulla, and compared its sequence with the sequences of UT-A3 and UT-A4 cDNA as well as with the sequence of the corresponding segments of PCR-amplified rat genomic DNA.

In Vitro Transcription-Translation and Immunoblotting

The coding region of the cDNA of UT-A1 (nucleotides 493/3262), UT-A2 (nucleotides 816/2283), UT-A3 (nucleotides 493/1790), and UT-A4 (nucleotides 493/2217) was subcloned into the *Hind*III, *Xho*I-digested mammalian expression vector pcDNA3 (Invitrogen, Carlsbad, CA), under the control of the T7 promoter. *In vitro* translation from the above constructs was performed using a coupled transcription/translation reagent system (TNT Coupled Reticulocyte Lysate System, Promega, Madison, WI) in the presence of L-[³⁵S]-methionine (1000 Ci/mmol, Amersham, Arlington Heights, IL), following the protocol suggested by the manufacturer, in the absence and in the presence of canine pancreatic microsomes (Promega). The products obtained were analyzed by electrophoresis on 10% sodium dodecyl sulfate (SDS)-polyacrylamide gel, followed by autoradiography. For Western blotting, the translated products were size-separated by SDS-polyacrylamide gel electrophoresis and electroblotted onto polyvinylidene difluoride membranes (Gelman Scientific, Ann Arbor, MI). Blots were incubated with a primary rabbit polyclonal antibody generated toward the carboxy-terminal portion of rat UT-A1 and UT-A2 (21), followed by a secondary goat anti-rabbit IgG, and the bound antibody was visualized using chemiluminescence (ECL kit, Amersham).

cDNA Expression and Cell Transfection

To test the function of UT-A3 and UT-A4 as urea transporters, the coding regions of UT-A3 cDNA (364/1790) and UT-A4 cDNA (364/2217) were subcloned in pcDNA3. Similar pcDNA3 constructs for

UT-A2 cDNA (816/2283) were used for functional comparison. These constructs were transiently transfected into the human embryonic kidney cell line HEK-293. HEK-293 cells were obtained from American Type Culture Collection (Rockville, MD) at passage 31, and used until passage 45, after which fresh cultures were started from frozen passage 32 cells. Cells were maintained in T75 flasks, in 5% CO₂/95% air in a 37°C incubator, with minimum essential medium, L-glutamine, and 5% fetal calf serum. Cells (2 to 3 × 10⁵/cm²) were transfected with the calcium phosphate transfection system kit (Life Technologies, Gaithersburg, MD), using 30 to 40 μg of plasmid construct DNA per flask. After 4 h, cells were subjected to glycerol shock for 2 min with 2 ml of 18% glycerol at room temperature, followed by replacement with fresh medium. The next day cells were plated in 24-well plates (Corning, Marietta, GA) at a density of 1.6 × 10⁵ cells/well. Flux measurements were carried out at 48 ± 6 h after transfection.

Northern Hybridization Analysis and RT-PCR Analysis of mRNA Expression

A rat multiple tissue Northern blot (Clontech, Palo Alto, CA) was hybridized with ³²P-labeled DNA probes (Prime-A-Gene kit, Promega). The following cDNA segments were amplified by PCR, labeled, and used as DNA probes in sequential hybridizations of the same membrane to identify the different isoforms: probe P1, corresponding to nucleotides 26 to 481 of UT-A1 cDNA, is expected to hybridize to transcripts that share this same sequence, *i.e.*, UT-A1, UT-A3, and UT-A4; probe P2 includes nucleotides 63 to 492 of UT-A2 cDNA, specific for the UT-A2 transcript only; probe P3 includes nucleotides 1764 to 1986 of UT-A3 cDNA, specific for UT-A3 only. Hybridization (65°C), washings (0.1 × SSC, 0.1% SDS, 50°C), and stripping of the probes from the membrane for multiple hybridizations were performed according to the protocols suggested by the manufacturer.

For RT-PCR analysis of mRNA expression, rat kidney tissue was dissected into cortex, outer medulla, and inner medulla and homogenized for extraction of total RNA using TRI Pure Isolation Reagent (Boehringer-Mannheim). Reverse transcription from 1 μg of total RNA and amplification of the first-strand cDNA were performed using the Super Script One-Step RT-PCR System (Life Technologies), following the protocol suggested by the manufacturer. DNA sequence analysis was performed using the Wisconsin Sequence Analysis Software Package, version 9.1-UNIX (Genetic Computer Group, Madison, WI).

Measurement of [¹⁴C]-Urea Transport

Cells were washed with 0.5 ml of HCO₃-free, Hepes-buffered minimum essential medium containing (in mM): 5 urea, 143 NaCl, 4.36 KCl, 1.8 CaCl₂, 0.81 MgCl₂, 5.55 D-glucose, 25 Hepes, pH 7.64, at 20°C, preincubated at 37°C in room air for 30 min, and transferred on a water thermostated platform at 21 ± 2°C. At known intervals, the preincubation medium was substituted with medium containing 2 μCi/ml ¹⁴C-urea (Amersham) with or without phloretin (50 to 250 mM; Sigma, St. Louis, MO). The influx was stopped simultaneously for all wells by three rapid washes with ice-cold solution containing (in mM): 150 NaCl, 1 CaCl₂, 1 MgCl₂, and 0.05 phloretin. The cells in each well were solubilized in 0.5 ml of 25 mM NaOH with 0.5% deoxycholate; 100 μl from each well was used to measure protein with BCA assay (Pierce, Rockford, IL), and 500 μl was counted in 3 ml of Optifluor (Packard Instruments, Meriden, CT) in a liquid scintillation counter.

Statistical Analyses

The net cpm/mg protein *versus* the elapsed exposure time to the tracer (15, 5, 2.5, 1.5, and 0.5 min) were fit to a straight line by the least squares method or a single exponential. The initial slope of the fit line divided by the specific activity (cpm/nmol) was the calculated flux: nmol/g protein per minute. The standard error of each flux value was calculated by dividing the standard error of the slope by the specific activity. The influx was linear for 5 min for urea influx measurements. Samples were measured in cells transfected with vector containing the cDNA as well as in the cells sham-transfected with vector only. Measurements of urea influx were repeated four times in separate experiments, using different batches of transfected cells. Differences were considered statistically significant for $P < 0.05$, using unpaired two-tailed t test.

Results

Cloning of UT-A3 and UT-A4 cDNA

Our approach in searching for new isoforms of the rat urea transporter UT-A was based on cloning by rapid amplification of cDNA ends (RACE) (22). The amplification products of the first-strand cDNA generated by 3' RACE revealed a 3.8-kb band corresponding to UT-A1, plus two smaller products of approximately 1.9 and 2.4 kb, which were designated as UT-A3 and UT-A4, respectively, and sequenced. 5' RACE was performed to obtain the 5' end of the new cDNA and to confirm that the sequences of UT-A3, UT-A4, and UT-A1 cDNA (which we reverse-transcribed from rat inner medulla) had identical 5' ends.

UT-A3 cDNA has an open reading frame of 1380 nucleotides (Figure 1A), equivalent to a peptide of 460 amino acids with a predicted molecular weight of 50 kD. UT-A3 cDNA is identical to the nucleotide sequence corresponding to the N-terminal half of UT-A1, but diverges from UT-A1 cDNA in the codon for UT-A3's last amino acid (D₄₆₀ replaces G₄₆₀). UT-A3 also has a unique 3' untranslated region (3' UTR), which is not common to any other UT-A isoform. To validate this part of the cDNA sequence, it was compared and found to be identical to the corresponding sequence of rat genomic DNA.

UT-A4 cDNA has an open reading frame of 1398 nucleotides (Figure 1B), encoding a peptide of 466 amino acids, with a predicted molecular weight of 51 kD, which is 87% homologous to the UT-A3 peptide sequence. The cDNA of UT-A4 is identical to UT-A1 in the first 1100 nucleotides; the remaining 1485 nucleotides correspond to the 3' terminal cDNA of UT-A1, suggesting that it results from alternative splicing between 5' terminal and 3' terminal groups of exons in the UT-A gene. A schematic representation of the cDNA of the four UT-A isoforms is shown in Figure 2A. The nucleotide sequence of the regions that UT-A3, UT-A4, and UT-A1 have in common are identical among the cDNA that we generated. However, compared with the UT-A1 cDNA sequence originally reported (13), we find consistent nucleotide discrepancies, resulting in the following amino acid differences: L₁₇ replaces P₁₇ and G₉₆ replaces A₉₆. Since in our hands the cDNA and genomic DNA sequences of these codons are also identical, the differences may be due to polymorphisms.

Both UT-A3 and UT-A4 peptides have a consensus glyco-

sylation site at Asn₂₇₉, and UT-A4 has an additional consensus site at Asn₃₅₇. UT-A3 has two consensus sequences for cAMP-dependent phosphorylation sites at Ser_{81,88}, and four for protein kinase C (PKC) phosphorylation sites at Ser_{23,79,205} and Thr₄₄₇. UT-A4 has three consensus sequences for cAMP-dependent phosphorylation sites at Ser_{81,88,452}, and three for PKC phosphorylation sites at Ser_{23,79,205}.

We have analyzed the sequences of these new urea transporter isoforms, as well as the other known urea transporters, and, based on previously stated criteria (1), we propose the structural models for UT-A3 and UT-A4 which are shown in Figure 2B; those for UT-A1 and UT-A2 are shown for comparison. The models propose a symmetrical configuration in which an intracellular amino-terminal domain is followed by three transmembrane segments, a large extracellular loop containing an N-glycosylation site, three more segments that completely span the membrane, a smaller integral membrane domain, and an intracellular carboxy-terminal domain. Consensus phosphorylation sites for protein kinase A and PKC, potentially important in the regulation of activity, are within the intracellular compartment.

In Vitro Translation

The *in vitro* translation products of the UT-A3 and UT-A4 cDNA subcloned into pcDNA3 are shown along with those of UT-A1 and UT-A2 in Figure 3A. The UT-A3 construct yielded a product with an apparent molecular weight of approximately 35 kD, whereas the UT-A4 construct yielded a product of approximately 37 kD. An increase in size of approximately 4 kD was observed when UT-A3 and UT-A4 were translated in the presence of pancreatic microsomes, presumably reflecting *in vitro* glycosylation of the two proteins (Figure 3B). As expected, only UT-A4 was recognized when both UT-A3 and UT-A4 translation products were tested by immunoblotting with an antibody directed toward the last 20 amino acids of UT-A1/UT-A2 carboxy terminus (21,18) (Figure 3C).

Functional Analysis of UT-A3 and UT-A4 Proteins

The functional activity of UT-A3 and UT-A4 proteins as urea transporters was analyzed by measuring the influx of ¹⁴C-urea in HEK-293 cells transiently transfected with pcDNA3-UT-A3 or pcDNA3-UT-A4, and their activity compared with those of HEK-293 cells transfected with pcDNA3 only, as negative control, and with pcDNA3-UT-A2, as a positive control. HEK-293 cells were chosen because they do not express UT-A transporters (23); therefore, any phloretin-inhibitable urea uptake must be from newly synthesized protein after transfection with the above constructs. Cells transfected with either UT-A3 or UT-A4 display phloretin-inhibitable urea transport above control level (sham-transfected cells), and the transport activities of these new isoforms appear comparable to those of UT-A2 (Figure 4A).

Since both UT-A3 and UT-A4 have consensus sites for cAMP-dependent phosphorylation, we tested the effects of inducing intracellular accumulation of cAMP on the rates of urea transport of transiently transfected cells, as an indicator of potential susceptibility to vasopressin regulation.

A		B	
1	aaaaagaggaaagacagagccggcctagacagcagacatcaggacacccctctagggccag	60	1 aaaaagaggaaagacagagccggcctagacagcagacatcaggacacccctctagggccag
61	ctctgtttctgcttaagtctcaaggaaagactgcaagatcatctgaggtgggtctctgta	120	61 ctctgtttctgcttaagtctcaaggaaagactgcaagatcatctgaggtgggtctctgta
121	acagcgtcagctccacaaagtcatcgctgcaaagttcaggagatgggagatctttctctgt	180	121 acagcgtcagctccacaaagtcatcgctgcaaagttcaggagatgggagatctttctctgt
181	tttcttactgagtggttccgggtgtgagtgcatgccattgacatcttctacctctgtgg	240	181 tttcttactgagtggttccgggtgtgagtgcatgccattgacatcttctacctctgtgg
241	acaacaaggacaaggctcgaatcccctcagctacttcatcagccgagcctgcatgact	300	241 acaacaaggacaaggctcgaatcccctcagctacttcatcagccgagcctgcatgact
301	ggctattttgaccacttgaagtcataaataagaagttctcaagaccaccaagaccaagg	360	301 ggctattttgaccacttgaagtcataaataagaagttctcaagaccaccaagaccaagg
361	acacttcaatgacagatgagcagaccatcccctgaaggagatgctgacaacaaccgcag	420	361 acacttcaatgacagatgagcagaccatcccctgaaggagatgctgacaacaaccgcag
	M S D H P L K E M S D N N R S		M S D H P L K E M S D N N R S
421	ccccctcttgccagagcctctttccagcagatacaagttgtatgagtcagagctaaagcag	480	421 cccccctcttgccagagcctctttccagcagatacaagttgtatgagtcagagctaaagcag
	P L L P E P L S S R Y K L Y E S E L S S		P L L P E P L S S R Y K L Y E S E L S S
481	ccctacctggcctcaagctcccaggatacacaccagcctcccctgctggaaatgcc	540	481 ccctacctggcctcaagctcccaggatacacaccagcctcccctgctggaaatgcc
	N T W P S S S Q D T H P R R A S A G R G		N T W P S S S Q D T H P R R A S A G R G
541	tgaagaaaaggatctccgatcatcggatgaagacagccacatagtgaaagattgaaagcc	600	541 tgaagaaaaggatctccgatcatcggatgaagacagccacatagtgaaagattgaaagcc
	E E K D L R S S D E D S H I V K I E K P		E E K D L R S S D E D S H I V K I E K P
601	caacgagcggagtaaacggagagaaagcaggttgcccgcagggtctctgagcggcggg	660	601 caacgagcggagtaaacggagagaaagcaggttgcccgcagggtctctgagcggcggg
	N E R S K R R R E S E L P R R A S A G R G		N E R S K R R R E S E L P R R A S A G R G
661	aggcttcagcctcttccaagctgtgagctacccactcagtgacatgaaggaatgcaagaa	720	661 aggcttcagcctcttccaagctgtgagctacccactcagtgacatgaaggaatgcaagaa
	G F S L F Q A V S Y L T G D M K E C K N		G F S L F Q A V S Y L T G D M K E C K N
721	ctggctgaaagataagccctggctcctcagttcagctgggtcctgcccgggagcagc	780	721 ctggctgaaagataagccctggctcctcagttcagttcagctgggtcctgcccgggagcagc
	W L K D K P L V L Q P L D W V L R G A A		W L K D K P L V L Q P L D W V L R G A A
781	tcaggtgatgtttgtcaacaaccccttagtgggctcatcatcttcatagggctcctgat	840	781 tcaggtgatgtttgtcaacaaccccttagtgggctcatcatcttcatagggctcctgat
	Q V M F V N N P L S G L I I F I G L L I		Q V M F V N N P L S G L I I F I G L L I
841	ccagaatccctggggagcaggttgctggggcaactggggaactgggtctcaaccttggctgc	900	841 ccagaatccctggggagcaggttgctggggcaactggggaactgggtctcaaccttggctgc
	Q N P W W T I A G A L G T V V S T L A A		Q N P W W T I A G A L G T V V S T L A A
901	ccttgcttgagccagcagcaggtcagccatcgccctcggactccatgggtcaacgggat	960	901 ccttgcttgagccagcagcaggtcagccatcgccctcggactccatgggtcaacgggat
	L A L S Q D R S A I A S G L H G Y N G M		L A L S Q D R S A I A S G L H G Y N G M
961	gctgggtgggactcctgggtgctgtcttctcagagaagttagactactactggtgctct	1020	961 gctgggtgggactcctgggtgctgtcttctcagagaagttagactactactggtgctct
	L V G L L V A V F S E K L D Y Y W W L L		L V G L L V A V F S E K L D Y Y W W L L
1021	gtttcctgtgaccttcgcatccatggcctgccagttatttctagtgccctgagcaccgt	1080	1021 gtttcctgtgaccttcgcatccatggcctgccagttatttctagtgccctgagcaccgt
	F P V T F A S M A C P V I S S A L S T V		F P V T F A S M A C P V I S S A L S T V
1081	cttcgcaagtgaggacctgccagctcttcaactgccttcaacatcgcccttaacactgta	1140	1081 cttcgcgaagtgaggacctgccagctcttcaactgccttcaacatcgcccttaacactgta
	F A K W D L P V F T L P F N I A L T L Y		F A K W D L P V F T L P F N I A V T L Y
1141	cctggcagctcagggccactacaaccttttctcccacagcagcttggtaagcctgcgtc	1200	1141 cctggcagccacgggccaactacaaccttttctcccacagcagcttggtaagcctgcgtc
	L A A T G H Y N L F P T L V L K L G F A V		L A A T G H Y N L F P T L V L K L G F A V
1201	ttcagcggcccaacatcacctggctcagagatgagatgcttttctgttacaacccatccc	1260	1201 taccacacccaacatcacctggctcagatgctccaagtgcttttctgtctgagagccatccc
	S A P N I T W S E I E M P L L L Q T I F		T T P N I T W S D V Q V P L L L R A I F
1261	ogtgggggtggcaggtctacggctgtgacaacccctggacagcagcggcgtgatcctggt	1320	1261 cgttggaaatcggcgaagtgatggctgtgacaacccctggacagcagcagcagcagcagc
	V G V G Q V Y G C D N P W T G G V I L V		V G I G Q V Y G C D N P W T G G I F L V
1321	ggctctgtttatctctctccctcactctgttggcagcagcagcagcagcagcagcagc	1380	1321 tgcctcgttctgtctctcactctcactctgttggcagcagcagcagcagcagcagcagc
	A L F I S S P L I C L H A A I G S I V G		A P F V S S P L I C L H A A I G S T I G
1381	gctgctggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	1440	1381 gatgttagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
	L L A A L T V A T P F E T I Y T G L W S		M L A A L S I A T P F D S I Y F G L C G
1441	ctacaactgtctctctctgtgctgcaatggagcagcagcagcagcagcagcagcagc	1500	1441 ctcaatagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
	Y N C V L S C V A I G G M F Y V L T W Q		F N S T L A C I A I G G M F Y V I T W Q
1501	gacacactgttgccacttctgtgctgctgctgctgctgctgctgctgctgctgctgct	1560	1501 gacgacactgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct
	T H L L A L V C A L F C A Y T G A A L S		T H L L A I A C A L F A A Y L G A A L A
1561	caatgatggcagtggtgtggtggtggtggtggtggtggtggtggtggtggtggtggt	1620	1561 caaatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct
	N M M A V V G V P P G T W A F C L S T L		N M L S V F G L P P C T W P F C L S A L
1621	caactcctctctctcaacaacaacccctggcagcagcagcagcagcagcagcagcagc	1680	1621 caactcctctctctcaacaacaacccctggcagcagcagcagcagcagcagcagcagc
	T F L L L T S N N P G I H K L P L S K V		T F L L L T T N N P G I Y K L P L S K V
1681	caactaccagagcccaacccatcttctctgacagcagcagcagcagcagcagcagcagc	1740	1681 caactaccagagcccaacccatcttctctgacagcagcagcagcagcagcagcagcagc
	T Y P E A N R I Y F L S Q E K N R R A S		T Y P E A N R I Y F L S Q E K N R R A S
1741	gcccccaatggtgactagttcagcagcagcagcagcagcagcagcagcagcagcagc	1800	1741 gatgatacaaaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
	P P N G D		M I T K Y Q A Y D V S
1801	atggtctcaactctgggccaagcagccggcagcagcagcagcagcagcagcagcagcagc	1860	1801 gtaaatgagcctccagaaccaccctgcccagcagcagcagcagcagcagcagcagcagc
1861	acotgttcaaatcaaacccctcttctccctaatccagagcagcagcagcagcagcagcagc	1920	1861 ccttctctcaatagcagtggtgctcttggagccctcaatgagatgtgagcagcagcagc
1921	cccagatcttataacaacccttgtagcattaaaggaagcgtgtagcagcaaaaaaaaa	1980	1921 atcaagccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
1981	aaaaa 1985		1981 gggggaactctgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
			2041 atgttcattagcctgcaatgcaagagcgtgggttcaactaatgagttcaactgtctcag
			2101 gccagctcttctcctcaacccatccccacccctatccacacccccccccctcatctca
			2161 gctgggtgtttgtgccaagatttcttaccatgacaaggaagcagcagcagcagcagcagc
			2221 tccactcagaagcatttattcttccatctcctgtaaaccaaacactcagcagcagcagc
			2281 agcaagtaattctgactgagttacttggaaatggctctcagagagagagagaaaa
			2341 tgttagtgcctctgggaagttattctctagatctcgggagatgctcaaggcttgggac
			2401 oggacacctgaattcattgaaaatgcaatgtatcttcttgcaccatgaaaatatttcc
			2461 agaaacatcatctggaaggagcagccttcccaactccaatcatagtgtaagcaaacg
			2521 ccttctggtgtaataattcaaaatcagtagtcattaaacttgaatttgcataaaaaaaa
			2581 aaaa 2584

Figure 1. (A) UT-A3 cDNA and amino acid sequence. (B) UT-A4 cDNA and amino acid sequence. These sequences have been submitted to GenBank. The accession numbers are: AF041788 (UT-A3), AF042167 (UT-A4).

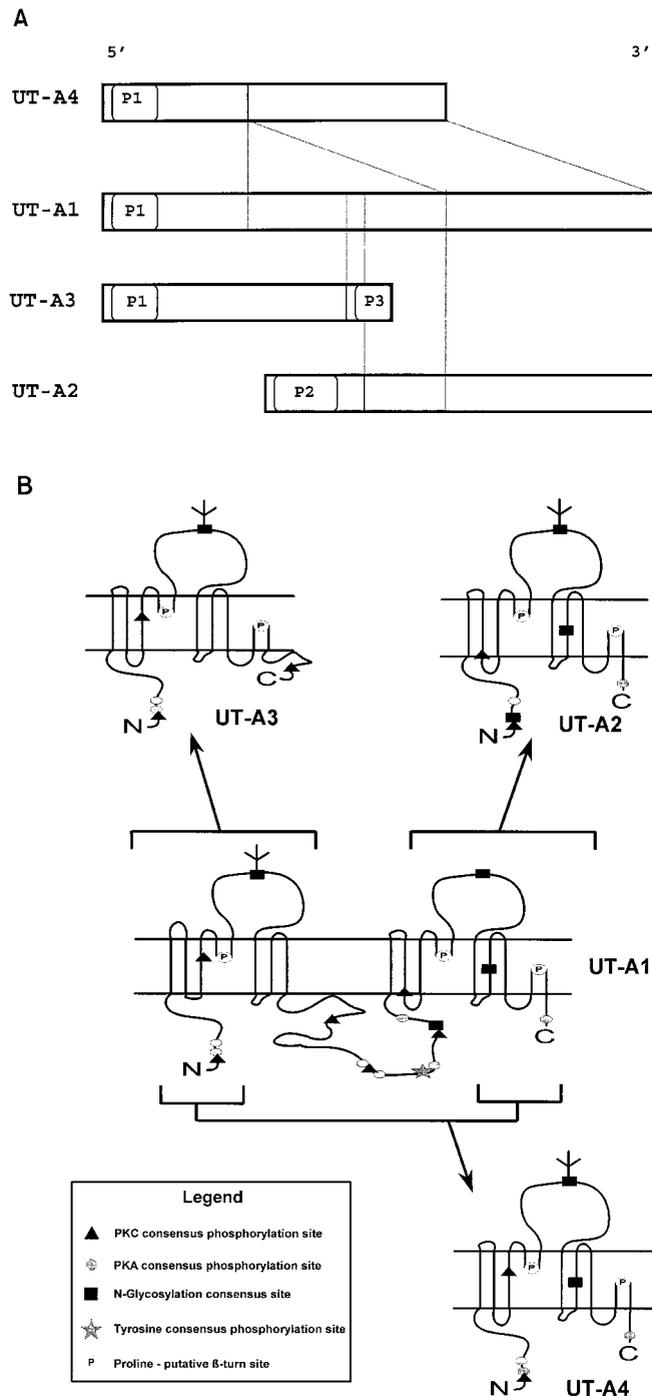


Figure 2. (A) Schematic illustration of the relationships between the cDNA of UT-A1, and the cDNA of the other isoforms UT-A2, UT-A3, and UT-A4. (B) Model of predicted membrane topology for UT-A3 and UT-A4 peptides and structural relationships with UT-A1 and UT-A2. (The UT-A1 and UT-A2 model are redrawn from reference (1).)

Phloretin-inhibitable urea transport was examined for UT-A3, UT-A4, and UT-A2, with or without forskolin, an activator of adenylate cyclase (Figure 4B). Forskolin induced a statistically significant increase in the transport activity of UT-A3 and UT-A4, 26% and 73%, respectively.

As expected, forskolin did not increase the transport rate of UT-A2, which was slightly decreased (16%).

UT-A3 and UT-A4 mRNA Expression in Rat Tissues

The expression of UT-A3 and UT-A4 mRNA was examined in multiple rat tissues by Northern hybridization, using three different DNA probes, spanning specific portions of the UT-A2, UT-A1, and UT-A3 cDNA (Figure 5). The position of the probes relative to specific cDNA sequences is illustrated in Figure 2. Probe P2, corresponding to a unique 5' end cDNA sequence of UT-A2, hybridizes to a single transcript of 3.1 kb in the whole kidney, consistent with expression of UT-A2 limited to the kidney. Probe P1, corresponding to nucleotides 26 to 481, which are common to UT-A1, UT-A3, and UT-A4, hybridizes with transcripts of 4.0 kb and 2.1 kb in the kidney, consistent with the mRNA size of UT-A1 and UT-A3, respectively. There also is a weaker signal of 3.7 kb. The significance and specificity of the smaller signals (about 1.7 kb) appearing in most lanes is unclear at this time. Probe P3, corresponding to the unique 3' UTR sequence of UT-A3, hybridizes with two transcripts of 3.7 kb and 2.1 kb in the kidney. The 2.1-kb transcript, identified with both probe P1 and probe P3, is consistent with expression of UT-A3 in the kidney. The nature of the 3.7-kb mRNA detected with probe P1 and probe P3 in the kidney is unclear at this time and needs further characterization. Among other tissues, only the testis expresses transcripts recognized by probe P3 with estimated size of 1.7 and 3.3 kb. Whether they represent shorter variants of the two transcripts detected by the same probe in the kidney remains to be established.

We could not detect any 2.5-kb mRNA, the size expected for UT-A4, in any tissue, suggesting that the abundance or stability of the UT-A4 transcript may be too low for detection by Northern hybridization. To detect expression of UT-A4 and to examine the distribution of UT-A3 and UT-A4 mRNA within regions of the kidney, we performed RT-PCR analysis of total RNA from renal cortex, outer medulla, and inner medulla (Figure 6). A sense primer corresponding to nucleotides 790 to 812 of UT-A3 cDNA and an antisense primer corresponding to nucleotides 1771 to 1790 of the 3' UTR of UT-A3 were used to amplify a portion of UT-A3, and yielded a PCR product of the expected size of 1.0 kb in outer medulla (lane 1) and in inner medulla (lane 5), but not in cortex (lane 3). Because no unique sequence for UT-A4 is available, primers were designed to span segments of UT-A4 and of UT-A1 that could be distinguished by their size. Two PCR amplifications with nested primers detected 570 bp of UT-A4 in outer medulla (lane 2), and in inner medulla (lane 6), but not in cortex (lane 4). These same primers also detect a larger product of approximately 1.9 kb (lane 6) in inner medulla, but not in outer medulla or in cortex, consistent with expression of UT-A1 limited to the inner medulla, as shown previously (19,13). Thus, UT-A3 and UT-A4 are both expressed in the outer and inner medulla, with a relatively lower level of expression for UT-A4 mRNA.

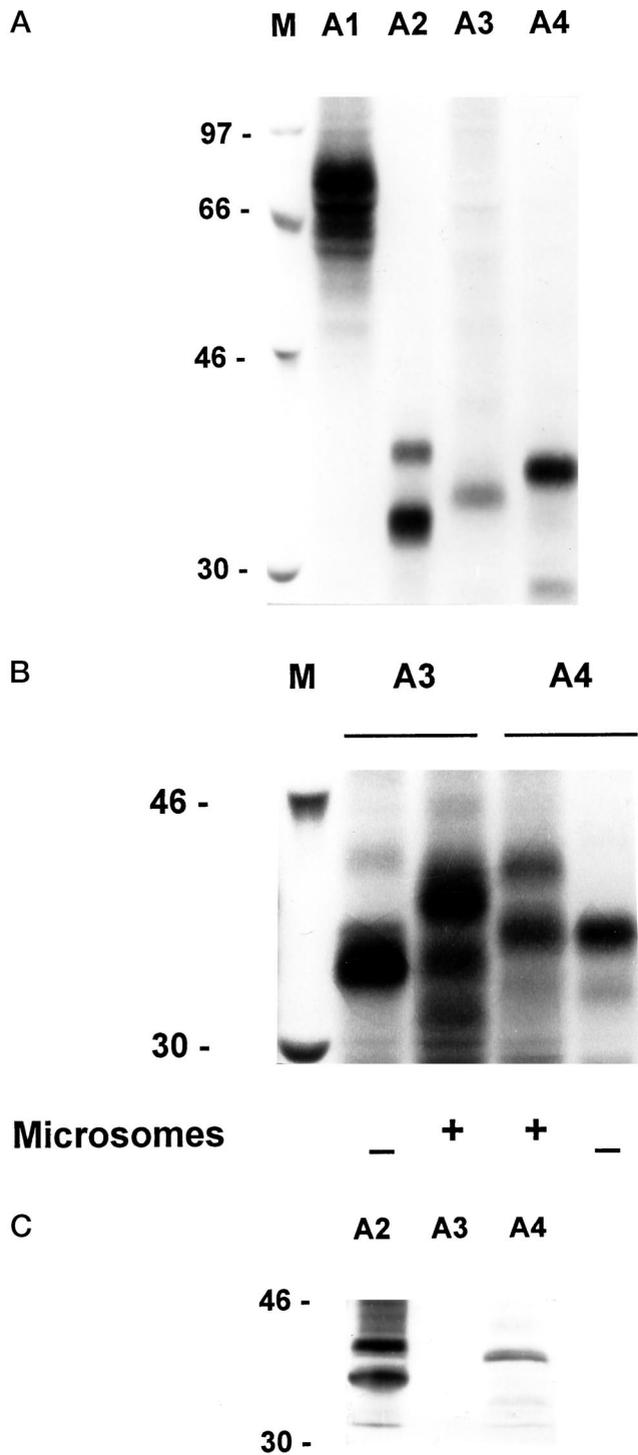


Figure 3. Analysis of *in vitro* translation products of the UT-A isoforms. (A) Sodium dodecyl sulfate-polyacrylamide gel electrophoresis of *in vitro* translation products of pcDNA3-UT-A1 (A1), pcDNA3-UT-A2 (A2), pcDNA3-UT-A3 (A3), and pcDNA3-UT-A4 (A4). Molecular size markers (M) are shown in the first lane. (B) *In vitro* translation products of pcDNA3-UT-A3 (A3) and pcDNA3-UT-A4 (A4) obtained in the presence (+) and in the absence (-) of pancreatic microsomes. Molecular size markers (M) are shown in the first lane. (C) Immunoblot of *in vitro* translation products of pcDNA3-UT-A2 (A2), pcDNA3-UT-A3 (A3), and pcDNA3-UT-A4 (A4), with a primary rabbit polyclonal antibody generated toward the carboxy terminus of the rat UT-A1/UT-A2 peptides (21).

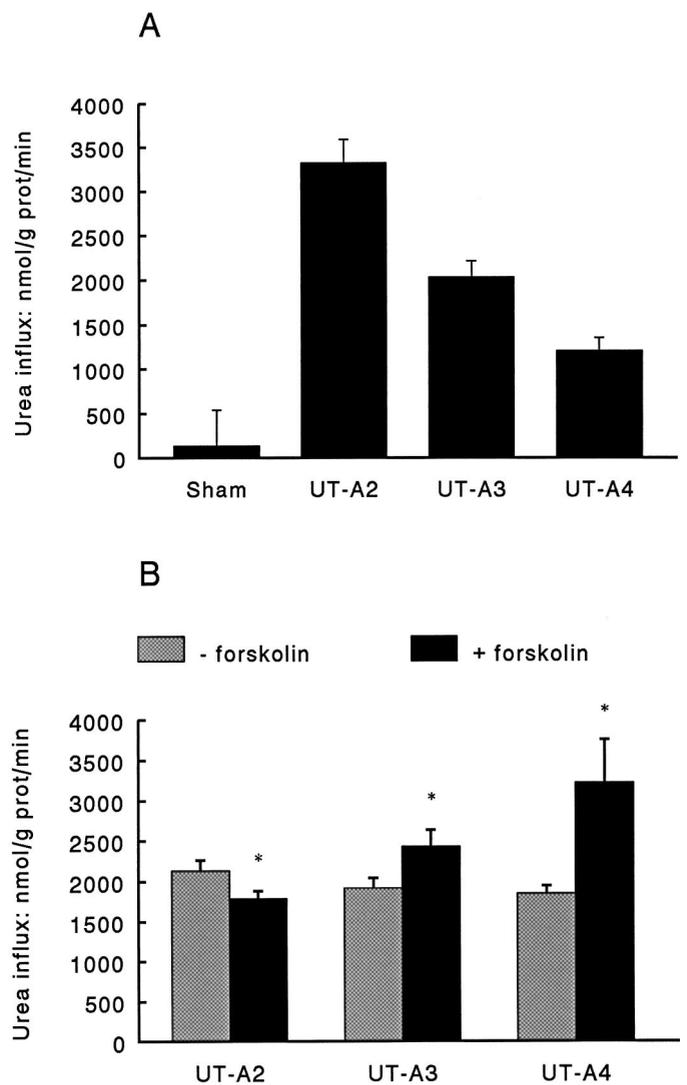


Figure 4. (A) Phloretin-inhibitable uptake of [¹⁴C] urea in HEK-293 cells transiently transfected with pcDNA3-UT-A2, pcDNA3-UT-A3, pcDNA3-UT-A4, or pcDNA3 without insert (Sham), in the presence of 50 μM phloretin. (B) Effect of forskolin on phloretin-inhibitable urea uptake of HEK cells transiently transfected with pcDNA3-UT-A2, pcDNA3-UT-A3, and pcDNA3-UT-A4 (10 μM forskolin, 24 h preincubation). The unlabeled urea concentration in the uptake solution was 5 mM. Values are shown as mean ± SD (n = 4). *P < 0.01.

Discussion

We have identified two new isoforms of the UT-A urea transporter: UT-A3 and UT-A4. Analysis of the homology of UT-A3 and UT-A4 cDNA sequences with those of UT-A1 and UT-A2 shows that each of the two new isoforms corresponds to different portions of UT-A1. Thus, it appears likely that UT-A3 and UT-A4 as well as UT-A1 and UT-A2 may be encoded by a single gene. Interestingly, the structural models proposed for UT-A3 and UT-A4 show symmetric configurations similar to UT-A2, and come very close to the model predicted for the erythrocyte urea transporter UT-B (UT11/UT3) (14), to which UT-A3 and UT-A4 are 61% homologous. Another interesting feature of the new isoforms is that both

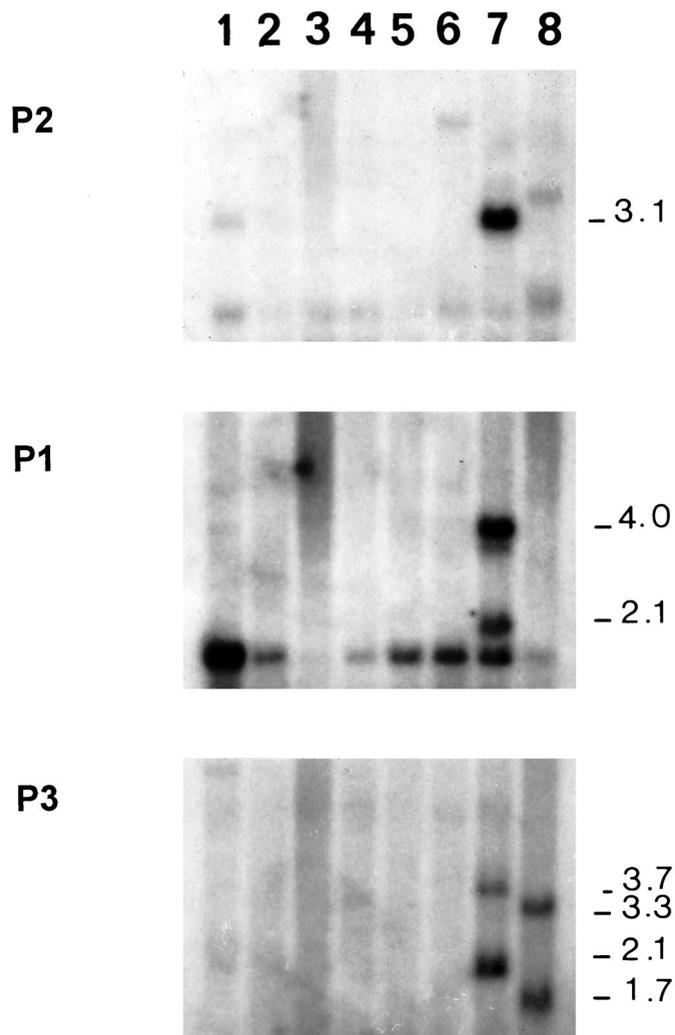


Figure 5. Northern hybridization of rat multiple tissue blot. Lanes are as follows: 1, heart; 2, brain; 3, spleen; 4, lung; 5, liver; 6, skeletal muscle; 7, kidney; 8, testis. (Top Panel) Membrane hybridized with DNA probe P2, (nucleotides 63/492 of UT-A2 cDNA; Figure 2A). (Middle Panel) Membrane hybridized with probe P1 (nucleotides 26/481 of UT-A1, UT-A3, and UT-A4 cDNA; Figure 2A). (Bottom Panel) Membrane hybridized with probe P3 (nucleotides 1746/1986 of UT-A3 cDNA; Figure 2A). (The faint bands of 3.3 and 1.7 kb seen in lane 8 of the top panel may be due to incomplete elimination of the signal from previous hybridization of the same membrane with probe P3. There is not sufficient homology between probes P2 and P3 to expect cross-hybridization.)

UT-A3 and UT-A4 peptides include all of the following three amino acid motifs: KWDLPF₁LPFN, ATGHYNLFFP, and SSPLICLHAAIGS, which are present as intra-protein tandem repeats within each of the two UT-A1 halves (UT-A1a and UT-A1b), and which, as we have previously noted (1), are found in all urea transporters, including UT-B. Thus, these may represent highly conserved "signature sequences" in the urea transporter family.

UT-A3 and UT-A4 are functionally active urea transporters, and display levels of phloretin-inhibitable urea uptake in the range of those reported previously for the other two known

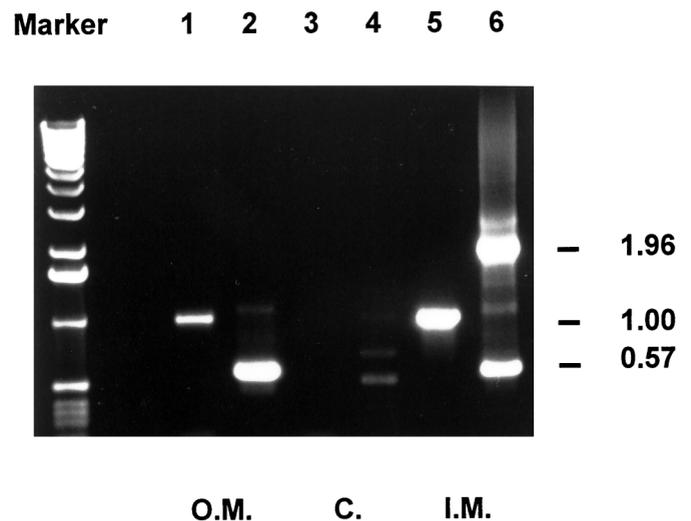


Figure 6. Renal expression of UT-A3 and UT-A4 detected by reverse transcription-PCR, using RNA from rat kidney outer medulla (lanes 1 and 2), cortex (lanes 3 and 4), and inner medulla (lanes 5 and 6). The size of the specific amplification products (indicated in kilobases) is shown on the left, and the first lane contains DNA size markers (M, 1-kb ladder). A single amplification was used for UT-A3, spanning nucleotides 790 to 1790 of UT-A3 cDNA, resulting in a 1.0-kb product (lanes 1, 3, and 5). The amplification to detect UT-A4, spanning nucleotides 1008 to 2964 of UT-A1 cDNA, yields two products: the smaller, about 0.57 kb, representing UT-A4 (lanes 2, 4, and 6) and the larger, about 1.96 kb, resulting from UT-A1 (lane 6).

isoforms UT-A1 and UT-A2. In addition, they appear to be susceptible to regulation via a cAMP-dependent pathway based on the stimulatory effect of forskolin on their urea uptake activity. Several consensus sequences for protein kinase A-dependent phosphorylation sites are present in both UT-A3 and UT-A4, of which those located at the intracytoplasmic amino-terminal and carboxy-terminal domains may be important for *in vivo* regulation of their functional activity as urea transporters. Our observations support the possibility that the activity of UT-A3 and UT-A4 may be regulated by vasopressin, through activation of adenyl cyclase and generation of cAMP.

We do not have a precise explanation of the reason why the *in vitro* translation products of UT-A3 and UT-A4 are lower than their predicted molecular weight. In our hands, the *in vitro*-translated products of UT-A1 and UT-A2 also show a lower molecular weight than predicted, similar to observations by Shayakul *et al.* (13), who, using the same reagent system, reported a molecular weight of 76 kD for the translated product of the rat UT-A1, while the predicted molecular weight is 95 kD.

Analysis of the expression of the different UT-A mRNA isoforms in rat tissue confirms that the UT-A transporters are localized primarily within the kidney, but indicates that expression of some UT-A isoforms also occurs in the testis, which was never reported previously; expression of an isoform of UT-B, the erythrocyte urea transporter, has been detected in the testis (16,24). In addition, our findings show that the UT-A mRNA expressed in the testis are smaller than their renal

counterparts, perhaps as a result of tissue-specific regulatory mechanisms. Our observations also point to the existence of another, as yet uncharacterized UT-A isoform of approximately 3.7 kb in the kidney. The intrarenal distribution of UT-A3 and UT-A4 mRNA expression was examined by RT-PCR, confirming the presence of both mRNA in the rat kidney. The pattern of expression of UT-A3 and UT-A4 indicates that their mRNA is expressed in outer and inner medulla but not in cortex. Thus, the distribution of UT-A3 and UT-A4 is similar to that of UT-A1 and UT-A2, for which expression appears confined to the medullary region (17–19).

In conclusion, we have identified UT-A3 and UT-A4 as two new isoforms of the UT-A urea transporter, which are expressed in the renal inner medulla. They are functionally active urea transporters and their activity appears to be stimulated by cAMP-dependent pathways, suggesting that they may be regulated by vasopressin. The high homology of these new isoforms and the previously identified UT-A transporters support their origin from a single gene. Our findings indicate that other, as yet uncharacterized, related forms of this family of transporters may be expressed in the testis. Additional studies will be necessary to understand the regulation of the expression and function of multiple urea transporters in the kidney and in other organs.

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