SGLT2 Mediates Glucose Reabsorption in the Early Proximal Tubule

Volker Vallon,*†‡ Kenneth A. Platt,§ Robyn Cunard,*† Jana Schroth,† Jean Whaley,‖ Scott C. Thomson,*† Hermann Koepsell,¶ and Timo Rieg*†

Departments of *Medicine and ‡Pharmacology, University of California San Diego, La Jolla, California; †VA San Diego Healthcare System, San Diego, California; §Lexicon Pharmaceuticals, The Woodlands, Texas; ‖Bristol-Myers Squibb R&D, Pennington, New Jersey; and ¶Institute for Anatomy and Cell Biology, University of Würzburg, Würzburg, Germany

ABSTRACT
Mutations in the gene encoding for the Na⁺-glucose co-transporter SGLT2 (SLC5A2) associate with familial renal glucosuria, but the role of SGLT2 in the kidney is incompletely understood. Here, we determined the localization of SGLT2 in the mouse kidney and generated and characterized SGLT2-deficient mice. In wild-type (WT) mice, immunohistochemistry localized SGLT2 to the brush border membrane of the early proximal tubule. Sglt2−/− mice had glucosuria, polyuria, and increased food and fluid intake without differences in plasma glucose concentrations, GFR, or urinary excretion of other proximal tubular substrates (including amino acids) compared with WT mice. SGLT2 deficiency did not associate with volume depletion, suggested by similar body weight, BP, and hematocrit; however, plasma renin concentrations were modestly higher and plasma aldosterone levels were lower in Sglt2−/− mice. Whole-kidney clearance studies showed that fractional glucose reabsorption was significantly lower in Sglt2−/− mice compared with WT mice and varied in Sglt2−/− mice between 10 and 60%, inversely with the amount of filtered glucose. Free-flow micropuncture revealed that for early proximal collections, 78 ± 6% of the filtered glucose was reabsorbed in WT mice compared with no reabsorption in Sglt2−/− mice. For late proximal collections, fractional glucose reabsorption was 93 ± 1% in WT and 21 ± 6% in Sglt2−/− mice, respectively. These results demonstrate that SGLT2 mediates glucose reabsorption in the early proximal tubule and most of the glucose reabsorption by the kidney, overall. This mouse model mimics and explains the glucosuric phenotype of individuals carrying SLC5A2 mutations.

glucose reabsorption have been cloned and identified\(^1^-^5\); however, direct experimental in vivo evidence on their tubular sites of action and quantitative contributions is still sparse.

The concept has been developed that the low-affinity/high-capacity Na\(^+\)-glucose co-transporter SGLT2 (Slc5a2) mediates the bulk uptake of glucose across the apical membrane of the early proximal tubule, whereas the high-affinity/low-capacity SGLT1 (Slc5a1) reduces luminal glucose concentrations to very low concentrations in further distal parts of the proximal tubule.\(^1^,^3^-^7\) This concept is based on mRNA and transport studies in isolated nephron segments and membrane vesicles from various tissue zones of rat and rabbit kidneys.\(^6^-^1^4\) Real-time PCR suggested SGLT2 mRNA expression in many human tissues,\(^1^5\) but, because of the lack of good antibodies (Ab), the implication for extrarenal malabsorption, but these individuals with these mutations have little or no glucosuria.\(^1^8\) In comparison and providing strong evidence for a prominent role in renal glucose reabsorption, individuals with gene mutations in SGLT2 have persistent renal glucosuria.\(^1^9^-^2^2\)

To determine in an experimental and direct way the role of SGLT2 in proximal tubular glucose reabsorption, we generated and studied gene-targeted mice lacking Sglt2 and applied a new Ab for SGLT2. The results demonstrate for the first time that the SGLT2 protein is localized to the brush border of the early proximal tubule, where it is responsible for all glucose reabsorption and is the major pathway of glucose reabsorption in the kidney, overall.

**RESULTS**

**Generation of Sglt2\(^{-/-}\) Mice and Renal mRNA Expression of Glucose Transporters**

The strategy to generate gene-targeted mice lacking Sglt2 is outlined in Figure 1. Real-time reverse transcriptase–PCR confirmed the knockout of Sglt2 in the kidney of Sglt2\(^{-/-}\) mice (Figure 2A). Whereas the renal mRNA expression of Glut1, Glut2, and Glut12 were not significantly different between genotypes, the expression of Glut1 mRNA was reduced by approximately 40% in Sglt2\(^{-/-}\) versus wild-type (WT) mice (Figure 2A). This was confirmed for SGLT1 expression at the protein level (Figure 2B).

**Localization of Renal SGLT2 Protein Expression in the Kidney**

Western blot analysis of whole kidneys in WT and Sglt2\(^{-/-}\) mice with an affinity-purified polyclonal Ab raised against rat SGLT2 showed a specific band with a molecular weight in the predicted range of SGLT2 (approximately 73 kD; Supplemental Figure S1). This band was absent from the SGLT2\(^{-/-}\) mouse kidneys. Immunohistochemical analysis with the same SGLT2 Ab revealed specific staining of the apical brush border membrane of early proximal convoluted tubules, whereas no signal was detected in late proximal convoluted tubules (iden-
Renal expression of Glut1, Glut2, and Glut12 was unaltered but the expression of Sglt2 is reduced in Sglt2/−/− mice. (A) Renal mRNA expression of Glut1, Glut2, and Glut12 are unchanged whereas Sglt1 is reduced in Sglt2/−/− relative to WT mice. Real-time PCR confirms the knockout of Sglt2 in kidney of Sglt2/−/− mice. ND, not detectable. *P < 0.01 versus WT mice. (B) Western blotting shows reduced renal SGLT1 protein expression (related to β-actin) in Sglt2/−/− versus WT mice (n = 4 per genotype). *P < 0.05 versus WT mice. Gene knockout of Sglt1 in mice (Sglt1−/−) confirms the specificity of the signal.

Glucose Handling by the Whole Kidney and along the Proximal Convoluted Tubule in Anesthetized Mice

Renal clearance experiments under anesthesia confirmed a similar mean arterial BP and heart rate in Sglt2/−/− versus WT mice (101 ± 3 versus 101 ± 8 mmHg; 527 ± 12 versus 520 ± 14/min; n = 6 to 8 mice; NS). Moreover, plasma glucose concentrations, GFR, and the amount of filtered glucose were similar in SGLT2−/− and WT mice (155 ± 16 versus 139 ± 10 mg/dl; 187 ± 19 versus 218 ± 20 μl/min; 1683 ± 321 versus 1713 ± 274 mmol/min; NS); however, absolute and fractional renal reabsorption of glucose were significantly lower in Sglt2/−/− compared with WT mice (P < 0.001). The amount of filtered glucose was a primary determinant of glucose excretion as well as fractional glucose reabsorption in Sglt2/−/− mice, the latter varying inversely with the amount of filtered glucose (between 60 and 10%). Glucosuria in Sglt2/−/− mice was associated with doubling of absolute and fractional excretion of fluid in Sglt2/−/− mice compared with WT mice, whereas the absolute and fractional excretion of Na+, K+, and Cl− were not different (Table 2).

Free-flow collections of tubular fluid were performed along accessible proximal convoluted tubules at the kidney surface to establish a profile for fractional reabsorption of glucose (FR-glucose) versus fluid (FR-fluid; Figure 6A). Mean values for single-nephron GFR and the amount of glucose filtered per nephron were not different in Sglt2/−/− versus WT mice (8.5 ± 0.6 versus 8.7 ± 0.6 nl/min; 65 ± 4 versus 66 ± 6 pmol/min; n = 23 nephrons in five Sglt2/−/− mice and 18 nephrons in four WT mice; NS for both comparisons). For early proximal collections (confirmed by FR-fluid <40%: mean ± SEM for FR-fluid 21 ± 3 and 26 ± 4% in WT and Sglt2/−/− mice, respectively; n = 9 to 10 nephrons; NS), 78 ± 6% of the filtered glucose was reabsorbed in WT mice, whereas mean FR-glucose was not different from 0 (0.2 ± 0.6%) in Sglt2/−/− mice (P < 0.001 versus WT mice; Figure 6B). For late proximal collections (confirmed by FR-fluid ≥40%: mean ± SEM for FR-fluid 59 ± 3 and 52 ± 3% in WT and Sglt2/−/− mice, respectively; n = 9 to 13 nephrons; NS), FR-glucose was 93 ± 1% in WT mice and 21 ± 6% in Sglt2/−/− mice (P < 0.001 versus WT
collections between WT and Sglt2\(^{-/-}\) mice (early 22 ± 5 versus 27 ± 5%; late 49 ± 4 versus 49 ± 3%; NS; Figure 6C).

**DISCUSSION**

These studies demonstrate for the first time that SGLT2 protein is expressed in the brush border membrane of the early proximal convoluted tubule and that net glucose reabsorption in the early proximal tubule is absent in transgenic Sglt2 null mice. These data provide direct and unequivocal evidence that SGLT2 mediates all glucose reabsorption in the early proximal tubule. This is consistent with a previously proposed role of SGLT2 as the low-affinity/high-capacity glucose reabsorption pathway in the early proximal tubule.\(^6\)

These data further show that on the whole-kidney level, SGLT2 is a major determinant of glucose reabsorption. These findings are consistent with the phenotype of individuals with familial renal glucosuria, who carry specific mutations in the SLC5A2 gene.\(^{19–26}\) A total of 44 different mutations have been described for the SCL5A2 gene, including missense and nonsense mutations, small deletions (in-frame and frame shift), and splicing mutations, scattered throughout the gene.\(^{25}\) Individuals with these mutations have normal blood glucose levels but persistent glucosuria. Heterozygous carriers often exhibit mild glucosuria (<10 g/1.73 m\(^2\) per d), whereas massive glucosuria is confined to the homozygous or compound heterozygous states (>10 g/1.73 m\(^2\) per d); glucosuria can range from <1 to >150 g/1.73 m\(^2\) per d.\(^{18,19,27,28}\) Similarly, Sglt2\(^{-/-}\) mice excreted much of the filtered glucose with urinary glucose to creatinine concentrations of approximately 1850 \(\mu\)mol/mg; in comparison, urinary glucose concentrations of heterozygous Sglt2\(^{+/-}\) mice was 6 \(\mu\)mol/mg (n = 3) and thus not different from WT mice (approximately 6 \(\mu\)mol/mg), indicating that one intact Sglt2 allele is sufficient to achieve normal renal glucose reabsorption.

These data show that Sglt2\(^{-/-}\) mice reabsorb glucose in nephron segments downstream of the early proximal tubule, including distal aspects of the proximal convoluted tubule. The whole-kidney clearance studies show that increasing glomerular filtration of glucose does not enhance absolute renal glucose reabsorption in Sglt2\(^{-/-}\) mice, indicating that the capacity of the remaining glucose transport system in these mice is saturated. This reabsorption may be mediated by SGLT1, the high-affinity/low-capacity co-transporter, and/or by NaGLT1, the low-affinity co-transporter. Further studies are needed to demonstrate conclusively the quantitative role of SGLT1 and NaGLT1 in renal glucose transport. Notably, renal SGLT1 mRNA and protein expression both are reduced (by approximately 40%) in mice lacking Sglt2. The findings indicate that an upregulation of SGLT1 expression does not occur in the kidney when the amount of glucose delivered out of the early proximal tubule is increased. This does not exclude, however, that more glucose is transported via SGLT1 in Sglt2\(^{-/-}\) mice; in fact, the micropuncture data indicate that WT and Sglt2\(^{-/-}\) mice reabsorbed approximately 15 and 21%, respectively, of
Figure 4. Urinary glucose concentration is enhanced in Sglt2−/− mice despite normal blood glucose levels and GFR: Studies in awake mice. (A) Glucose measured in spontaneous urine collections and subsequent blood collections from tail vein. (B) GFR determined by plasma FITC-inulin kinetics. (C) Food and fluid intake assessed in regular cages. (D) BP measurements using a tail-cuff system in trained awake mice (n = 9 to 10 per group). *P < 0.05 versus WT mice.

The filtered glucose between early and distal sites of proximal tubular collections. Thus, downregulation of SGLT1 mRNA and protein may be a mechanism of these segments to limit the increase in glucose reuptake under conditions of increased luminal glucose delivery. Preliminary studies in gene-targeted mice heterozygous for Sglt1 (which have approximately 50% of the Sglt1 mRNA expression of WT mice) show no evidence of urinary glucose loss (urinary glucose/creatinine 5 ± 2 versus 5 ± 3 μmol/mg in WT mice; n = 3 per genotype; H.K., V.V., unpublished data, 2010), indicating that the downregulation of SGLT1 expression in Sglt2−/− mice does not explain their major urinary glucose loss.

Mice lacking SGLT2 have normal BP, GFR, plasma levels of Na⁺ and K⁺, and no significant increase in urinary excretion of amino acids, arguing against a general proximal tubular dysfunction in these mice. Moreover, modest polyuria may be compensated by increased fluid intake, and polypagia may serve to compensate for urinary glucose and calo-

table 1. Systemic parameters in age-matched male Sglt2−/− and WT mice

<table>
<thead>
<tr>
<th>Parameter</th>
<th>WT</th>
<th>Sglt2−/−</th>
</tr>
</thead>
<tbody>
<tr>
<td>Body weight (g)</td>
<td>30 ± 1</td>
<td>30 ± 1</td>
</tr>
<tr>
<td>Kidney weight (mg/g body wt)</td>
<td>11.9 ± 0.3</td>
<td>11.9 ± 0.2</td>
</tr>
<tr>
<td>Heart rate (/min)</td>
<td>576 ± 19</td>
<td>579 ± 19</td>
</tr>
<tr>
<td>Hematocrit (%)</td>
<td>42.4 ± 0.5</td>
<td>42.8 ± 0.5</td>
</tr>
<tr>
<td>Urine osmolality (mmol/kg)</td>
<td>1849 ± 96</td>
<td>1488 ± 73</td>
</tr>
<tr>
<td>Urine vasopressin (pmol/mmol creatinine)</td>
<td>36 ± 3</td>
<td>39 ± 4</td>
</tr>
<tr>
<td>Plasma aldosterone (pg/ml)</td>
<td>136 ± 14</td>
<td>80 ± 12</td>
</tr>
<tr>
<td>PRC (ng angiotensin I/ml per h)</td>
<td>445 ± 39</td>
<td>613 ± 61</td>
</tr>
<tr>
<td>Plasma Na⁺ (mM)</td>
<td>155 ± 1</td>
<td>156 ± 2</td>
</tr>
<tr>
<td>Plasma K⁺ (mM)</td>
<td>4.0 ± 0.1</td>
<td>4.0 ± 0.1</td>
</tr>
<tr>
<td>Plasma osmolality (mmol/kg)</td>
<td>328 ± 2</td>
<td>332 ± 2</td>
</tr>
</tbody>
</table>

Data are means ± SEM; n = 6 to 10 per group. PRC, plasma renin concentration.  
*P < 0.05.  
**P < 0.01.
Three pKOS genomic clones, pKOS-61, pKOS-78, and pKOS-91, were isolated from the library screen and confirmed by sequence and restriction analysis. Gene-specific arms (5′-ACTAGCCCCTTGGAGACGATGCTGGAGAGA-3′) and (5′-GCTCTCTGTCACCACCTGAAGCTTGGCT-3′) were appended by PCR to a yeast selection cassette containing the URA3 marker. The yeast selection cassette and pKOS-78 were co-transformed into yeast, and clones that had undergone homologous recombination to replace a 2419-bp region containing exons 1 through 5 with the yeast selection cassette were isolated. The yeast cassette was subsequently replaced with a LacZ/Neo selection cassette to complete the Slc5a2 targeting vector. The NotI linearized targeting vector was electroporated into 129/SvEvBrd (Lex-2) embryonic stem (ES) cells. G418/FIAU-resistant ES cell clones were isolated, and correctly targeted clones were identified and confirmed by Southern analysis using a 502-bp 5′ internal probe (15/16), generated by PCR using primers Slc5-15 (5′-TGGTTAGGCTTGATC-3′) and Slc5-16 (5′-ACAGGGCTGTATTGAAGAG-3′), and a 295-bp 3′ external probe (13/14), amplified by PCR using primers Slc5-13 (5′-CCATCTTTACAGGACTGTC-3′) and Slc5-14 (5′-AATGTAATCGAAGAGCTGCC-3′). Southern analysis using probe 15/16 detected a 11.0-kb WT band and an 8.7-kb mutant band in NcoI-digested genomic DNA, whereas probe 13/14 detected a 7.3-kb WT and a 4.8-kb mutant band in EcoRI-digested genomic DNA (Figure 1B). Four targeted ES cell clones were identified and microinjected into C57BL/6 blastocysts to generate chimeric animals that were bred to C57BL/6 females. Germine transmission was observed with one clone, and heterozygous offspring were backcrossed for 10 generations to the C57BL/6 background. Heterozygous mice were then interbred to produce homozygous Slc5a2−/− mice and WT mice, which were used to establish breeding colonies for Slc5a2−/− and WT mice. Genotypes were confirmed by PCR amplification of tail-snip DNA (Figure 1C). Male mice of matched age (3 to 5 months) were used in the experiments described. Mice were housed in a 12:12-hour light-dark cycle in standard rodent cages with free access to standard rodent chow (1% NaCl; Harlan Teklad, Madison, WI) and tap water.

**CONCISE METHODS**

All animal experimentation was conducted in accordance with the Guide for Care and Use of Laboratory Animals (National Institutes of Health, Bethesda, MD) and was approved by the local Institutional Animal Care and Use Committee.

**Generation of Mice Lacking Sglt2 (Slc5a2)**

Slc5a2 mutant mice were generated at Lexicon Pharmaceuticals (The Woodlands, TX) as outlined in Figure 1A. The Slc5a2 targeting vector was derived using the Lambda KOS system. The Lambda KOS phage library, arrayed into 96 superpools, was screened by PCR using exon 1-specific primers Slc5-1 (5′-GTCCCTGATTGATAATCCTGC-3′) and Slc5-2 (5′-TGGACAAATCCAGAAGTG-3′). The PCR-positive phage superpools were plated and screened by filter hybridization using the 251-bp amplicon derived from primers Slc5-1 and Slc5-2 as a probe.

**Table 2. Renal clearance experiments in age-matched male Sglt2−/− and WT mice**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>WT</th>
<th>Sglt2−/−</th>
</tr>
</thead>
<tbody>
<tr>
<td>AE-glucose (nmol/min per g body wt)</td>
<td>0.14 ± 0.04</td>
<td>40.4 ± 10.7a</td>
</tr>
<tr>
<td>AE-Na+ (nmol/min per g body wt)</td>
<td>3.8 ± 0.6</td>
<td>3.6 ± 0.6</td>
</tr>
<tr>
<td>AE-K+ (nmol/min per g body wt)</td>
<td>6.1 ± 0.6</td>
<td>6.0 ± 0.6</td>
</tr>
<tr>
<td>AE-CI− (nmol/min per g body wt)</td>
<td>3.2 ± 0.4</td>
<td>3.2 ± 0.7</td>
</tr>
<tr>
<td>AE-H2O (nl/min per g body wt)</td>
<td>45 ± 10</td>
<td>77 ± 10b</td>
</tr>
<tr>
<td>FE-glucose (%)</td>
<td>0.26 ± 0.04</td>
<td>63.6 ± 7.6a</td>
</tr>
<tr>
<td>FE-Na+ (%)</td>
<td>0.36 ± 0.03</td>
<td>0.36 ± 0.05</td>
</tr>
<tr>
<td>FE-K+ (%)</td>
<td>17.7 ± 1.5</td>
<td>18.5 ± 2.3</td>
</tr>
<tr>
<td>FE-CI− (%)</td>
<td>0.42 ± 0.05</td>
<td>0.44 ± 0.11</td>
</tr>
<tr>
<td>FE-H2O (%)</td>
<td>0.62 ± 0.09</td>
<td>1.20 ± 0.20a</td>
</tr>
</tbody>
</table>

Data are means ± SEM; n = 6 to 8 per group. AE, absolute renal excretion; FE, fractional renal excretion.

aP < 0.01.

bP < 0.05.

**Figure 5. Renal excretion of glucose in Sglt2−/− is a function of the amounts of glucose filtered:** Clearance studies under anesthesia (n = 9 to 10 per group).
mogenates were centrifuged at 16 000 × g for 30 minutes to obtain a membrane pellet. The pellet was resuspended in homogenizing buffer, and protein concentration was determined using a DC Protein assay (Bio-Rad, Hercules, CA). Samples used for SGLT2-Ab were diluted in 2× SDS gel loading buffer (100 mM Tris, 4% SDS, 20% glycerol, 0.2% bromphenol blue) and heated for 15 minutes at 70°C. Samples used for SGLT2-Ab were diluted in 4× LDS reducing sample buffer (Invitrogen, Carlsbad, CA) and heated for 15 minutes at 65°C. Samples were loaded on precast 4 to 12% Bis-Tris SDS-PAGE gels (Invitrogen) using MOPS buffer. The membranes were blocked with 5% nonfat dry milk (Bio-Rad) in PBS (pH 7.4) containing 0.1% Tween 20 (PBS-T) for 1 hour. Immunoblotting was performed at 4°C overnight with the primary SGLT2-Ab (see previous section) diluted 1:1000 and SGLT1-Ab diluted 1:2000 in PBS-T containing 1% BSA.

Reverse Transcription and Real-Time PCR
Whole-kidney RNA was prepared with the RNeasy Mini Kit. DNase digestion was performed with Turbo DNase (Ambion, Austin, TX), and cDNA was prepared with the Superscript II First Strand Synthesis System. For quantification, specific primers were used with Power SYBR Green PCR Master Mix (10 minutes at 95°C with 50 cycles of 15 seconds at 95°C and 1 minute at 60°C) in a Chromo4 Real-time PCR Detector (MJ Research and Bio-Rad). Given the homology of the Sglt isoforms, we used Taqman PCR Universal Mastermix with the following primers to improve specificity and sensitivity of these reactions: Sglt1 Mm00451203_m1 and Sglt2 Mm00453831_m1 (Applied Biosystems). The primers used for Glut1, Glut2, and Glut12 are listed in Table 3. Amplification efficiencies were normalized against the housekeeping gene Rpl19, and relative fold increases were calculated using the Pfaffl technique of relative quantification, which accounts for real-time efficiencies. Each experiment was performed in triplicate.

Table 3. Real-time PCR primers used

<table>
<thead>
<tr>
<th>Target</th>
<th>Forward</th>
<th>Reverse</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glut1</td>
<td>AACATGGAAACCACCGCTACG</td>
<td>GGGTGAAGTGAGTGATGG</td>
</tr>
<tr>
<td>Glut2</td>
<td>ATCGCCCTCTGCTTCAGAC</td>
<td>GAACACGTAAGGCAACAGGA</td>
</tr>
<tr>
<td>Glut12</td>
<td>CACAGGAGGGCTGCTCATA</td>
<td>AGTTATGCGAGCAGCTCTT</td>
</tr>
<tr>
<td>Rpl19</td>
<td>TGCCAGGTCAAGGAGGCCTT</td>
<td>GGAGTTGCGATTGGCGATTTC</td>
</tr>
</tbody>
</table>

Blood and Urine Analysis
Urine was obtained by picking up the mice to elicit reflex urination, then holding them over a clean Petri dish for sample collection. For obtaining paired measurements, blood was collected by tail snip immediately after urine collection. Plasma and urine glucose was measured using a glucose oxidase method. Glut1, Glut2, and Glut12 were analyzed using a Taqman PCR Universal Mastermix with the following primers to improve specificity and sensitivity of these reactions: Sglt1 Mm00451203_m1 and Sglt2 Mm00453831_m1 (Applied Biosystems). The primers used for Glut1, Glut2, and Glut12 are listed in Table 3. Amplification efficiencies were normalized against the housekeeping gene Rpl19, and relative fold increases were calculated using the Pfaffl technique of relative quantification, which accounts for real-time efficiencies. Each experiment was performed in triplicate.

Food and Fluid Intake
Daily food and fluid intakes were determined over 3 days while the mice were maintained in their regular cages.
determined by the hexokinase/glucose-6-phosphate dehydrogenase method (Infinity, Thermo Electron, Louisville, CO). Urinary calcium and creatinine were determined photometrically (Arsenazo III Method and enzymatically, respectively; Thermo Electron, Melbourne, Australia). Urinary amino acid concentrations were determined by HPLC. In a separate set of mice, blood was collected by puncturing the retrobulbar plexus under brief isoflurane anesthesia to determine hematocrit and plasma Na\(^+\) and K\(^+\) (measured by flame photometry; Cole-Parmer Instrument Co., Vernon Hills, IL). Plasma aldosterone was determined by RIA (Diagnostic Systems Laboratories, Webster, TX). Plasma renin concentration was determined by RIA (GammaCoat; DiaSorin, Stillwater, MN) as the generation of angiotensin I after addition of excess renin substrate from 24-hour nephrectomized rats.\(^{38}\) As an indirect measure of circulating vasopressin, concentration of vasopressin in urine was measured using a commercial assay (IBL, Hamburg, Germany) and related to creatinine.\(^{39}\) Urine and plasma osmolalities were measured by vapor pressure (Vapro; Wescor, Salt Lake City, UT).

**BP, Heart Rate, and GFR Measurement in Awake Mice**

Systolic BP and heart rate were determined in awake animals over a period of 5 days using the tail-cuff system (BP-2000; Visitech-Systems, Apex, NC) after appropriate training (for 5 days), as described previously.\(^{38,40,41}\) GFR measurements were performed in conscious mice using the plasma kinetics of FITC-inulin after a single-dose intravenous injection as described previously.\(^{42}\)

**Whole-Kidney and Proximal Tubular Reabsorption of Glucose in Anesthetized Mice**

Mice were anesthetized with thiobutabarbital (100 mg/kg intraperitoneally) and ketamine (100 mg/kg intramuscularly) and prepared for renal micropuncture.\(^{43–45}\) A catheter was placed in the femoral artery for continuous BP recording. For assessment of two-kidney and single-nephron GFR, \(^{3}H\)inulin was added to the infusion to deliver 20 \(\mu\)Ci/h. Urine was quantitatively collected using a bladder catheter. For determination of glucose reabsorption along the proximal tubule, quantitative fluid collections were made from early and late surface loops of the proximal convoluted tubule. Tubular fluid volume was determined from transfer to a constant bore capillary. The concentrations of glucose in plasma, urine, and tubular fluid were determined enzymatically (Infinity; Thermo Electron, Melbourne, Australia) in a regular photometer and a flow-through microfluorometer (NanoFlo; WPI, Sarasota, FL), respectively.\(^{44}\) The concentrations of chloride in plasma, urine, and tubular fluid were determined photometrically (Infinity, Thermo Electron) and by a microadaptation of the electrometric titration method,\(^{45}\) respectively.

**Statistical Analysis**

Data are presented as means ± SEM. Statistical differences between Sglt2\(^{-/-}\) and WT mice were analyzed by the unpaired two-tailed t test. \(P < 0.05\) was considered to be statistically significant.

**ACKNOWLEDGMENTS**

This work was supported by the National Institutes of Health (DK56248, DK28602, and P30DK079337), the Department of Veterans Affairs (including a Career Development Transition Award to R.C.), the Deutsche Forschungsgemeinschaft (SFB487 grant C1), and Bristol-Myers Squibb and Astra-Zeneca.

We thank Donald Pizzo for expert advise on the immunohistochemistry.

**DISCLOSURES**

Studies were supported by Bristol-Myers Squibb and Astra-Zeneca.

**REFERENCES**


