Mechanisms of Urinary $K^+$ and $H^+$ Excretion: Primary Structure and Functional Expression of a Novel H, K-ATPase

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Abstract. The kidney plays an essential role in regulating potassium and acid balance. A major site for these regulations is in the collecting tubule. In the present study, we report the primary sequence of a novel $\alpha$ subunit of the P-ATPase gene family, which we isolated from the urinary bladder epithelium of the toad Bufo marinus, the amphibian equivalent of the mammalian collecting tubule. The cDNA encodes a protein of 1,042 amino acids which shares $\sim67\%$ identity with the $\alpha$ subunit of the ouabain-inhibitable Na,K-ATPase and $\sim69\%$ identity with the $\alpha$ subunit of the SCH28080-inhibitable gastric H,K-ATPase. When coexpressed in Xenopus oocytes with a $\beta$ subunit isolated from the same cDNA library, the ATPase is able to transport rubidium (a potassium surrogate) inward, and hydrogen outward, leading to alkalization of the intracellular compartment and acidification of the external medium. The novel ATPase has a unique pharmacological profile showing intermediate sensitivity to both ouabain and SCH28080. Our findings indicate that the bladder ATPase is a member of a new ion motive P-ATPase subfamily. The bladder ATPase is expressed in the urinary tract but not in the stomach or the colon. This H,K-ATPase may be one of the molecules involved in $H^+$ and $K^+$ homeostasis, mediating the transport of these ions across urinary epithelia and therefore regulating their urinary excretion.

Potassium is primarily an intracellular ion where its concentration is high (150 mM), whereas the normal concentration of the extracellular fluid is low ($\sim$4 mM) (Wright and Giebisch, 1992). This ionic gradient is generated by an ion motive P-ATPase, the ouabain-inhibitable Na,K-ATPase, present in the plasma membrane of all cells. The P-type ATPases are members of the phosphorylating class of ion transport ATPases which includes the ubiquitous Na,K-ATPase, the gastric H,K-ATPase, the sarcoplasmic and plasma membrane Ca-ATPases, plant and fungi H-ATPases, and the bacterial K-ATPase (Pedersen and Carafoli, 1988).

The potassium gradient across the cell membrane promotes the outflow of $K^+$ ions across $K^+$-selective channels, generating the intracellular negative membrane potential of most animal cells (Wright and Giebisch, 1992). The gradient is thus essential to control the excitability of nerve and muscle cells. A small change in plasma potassium concentration can have dramatic adverse effects. Hyperkalemia can be rapidly lethal by inducing membrane depolarization of heart muscle, and life-threatening arrhythmias. On the other hand hypokalemia also leads to severe clinical symptoms, including muscle weakness and paralysis, arrhythmias, and renal failure (Wright and Giebisch, 1992). The extracellular potassium concentration must therefore be maintained within very narrow margins (i.e., 3.5 to 5 mM). The maintenance of a normal extracellular potassium concentration requires not only that the distribution of potassium between the extracellular and the intracellular fluid is maintained by Na,K-ATPase but also that the potassium excretion equals its intake, allowing global potassium balance. The potassium balance is mainly achieved by the control of urinary potassium excretion, and to a lesser extent by the control of $K^+$ absorption from the digestive tract (Wright and Giebisch, 1992). In the kidney, the major sites of controlled $K^+$ secretion and/or reabsorption are located in the cortical and medullary portion of the collecting tubule (CCT and MCT) (Wright and Giebisch, 1992). In the secretory process, $K^+$ is taken up by the basolateral Na,K-ATPase and flows into the lumen across the apical membrane through $K^+$ selective ion channels. Under conditions of low dietary intake, potassium secretion is negligible, and net potassium reabsorption takes place (Wright and Giebisch, 1992). The molecular mechanisms of potassium reabsorption are not yet elucidated but recent biochemical and pharmacological evidences suggest that active $K^+$ transport is mediated by a K- or H,K-ATPase (Wingo, 1989; Wingo and Armitage, 1992; Okusa et al., 1992; Zhou and Wingo, 1992; Silver and Frindt, 1993). $K^+$ and H,K-ATPase activities were measured in the distal nephron of mammals (Doucet and Marsy, 1987;...
sequence (5′ sense CCACCTCATCCAAATCATG) and one degenerate oligomer designed against a P-ATPase conserved region located near the COOH-terminal end (3′ antisense TGGQ0ETGTTCAATG/CTGGCCCAATA) (Jaisser et al., 1993a). This 1.6-kb fragment, including part of the previously characterized cDNA, was subcloned in Bluescript and used to re-screen the cDNA library. A new clone was isolated but the 1.1-kb insert did not overlap the former 5′-2-kb cDNA, missing 450 bp. Since we were unable to find any overlapping clone, a full-length 3.7-kb clone was reconstructed using PCR and classical DNA recombinant technology (Sambrook et al., 1989). The full-length cDNA was sequenced in both directions, as well as the initial cDNAs cloned from the library. The nucleotide sequence of the 450-bp region obtained by PCR was confirmed by sequencing three clones obtained from three independent PCR reactions.

Northern Blot Analysis

Northern blot analysis were performed using 1.5 μg poly A (+) RNA obtained from various tissues from the toad Bufo marinus and from the TBM 18-23 clonal cell line, which derives from the urinary bladder (Asher et al., 1988). Hybridizations were done with a 500-bp B. marinus H,K-ATPase α subunit probe (covering 250 bp of the 5′ untranslated region and 250 bp of the divergent NH2-terminal coding region) and a 400-bp B. marinus Na,K-ATPase α1 subunit probe (covering the 3′ untranslated region). Probes were labeled with 32P-dCTP. Final washes of the blot were done with 0.2 × SSC, 0.1% SDS at 65°C for 30 min (Sambrook et al., 1989). Autoradiograms were exposed for 3 d (Na,K-ATPase α subunit) or 10 d (H,K-ATPase α subunit). Similar results were obtained using a 3′ untranslated probe of the H,K-ATPase α subunit.

cRNA Synthesis and Expression in Xenopus Oocytes

The 3.7-kb full-length cDNA was subcloned in the pSD3 vector containing a 110-bp poly A (+) tail before the HindIII linearization site (Horisberger et al., 1991b). Preliminary experiments showed that cRNA obtained from SP6 in vitro transcription of the full-length cDNA was poorly translated in a reticulocyte lysate. We deleted 170 bp of the 5′ untranslated region, removing a GC-rich region. This improved dramatically the translatability in vitro and in the Xenopus oocytes. Xenopus oocytes were injected either with 7 ng H,K-ATPase α subunit, 7 ng B. marinus Na,K-ATPase α1 subunit or 2 ng of the recently described B. marinus P-ATPase β subunit (βα) cRNAs, alone or in combination.

Rubidium Uptake

2 to 3 d after injection, oocytes were used to measure 86Rb uptake as a marker of K+ transport (Jaunin et al., 1992). Depending on the experimental protocol, oocytes were first preincubated with or without potassium in order to increase intracellular Na+, a maneuver required to insure full activation of the Na,K-ATPase (Horisberger et al., 1991a). Then, they were incubated in modified Barth's medium (MBM) containing 10 μM ouabain for 10 min in the presence of 1 mM K to inhibit the endogenous Na,K-ATPase, as previously described (Jaisser et al., 1992). Thereafter, ouabain was washed in MBM without KCl with or without the inhibitors or the diluent (DMSO) at appropriate concentrations, in the presence of 1 to 5 mM BaCl2. Barium can be omitted without affecting significantly the results. 86Rb uptake was done as described (Jaunin et al., 1992). Results were expressed on the correction for the specific activities of 86Rb. The activation (Kact) and inhibition (Ki) were obtained by fitting the 86Rb uptake data to a single site model (inserts).

Intracellular pH (pH1) Measurements

pH-sensitive microelectrodes were manufactured using the liquid ion exchanger H-ionophore II–Cocktail A (Fluka) as described earlier (Horisberger and Giebisch, 1988). These electrodes had a resistance of 2 to 10 Gohms. They were calibrated in pH 6.5 and pH 7.5 solution immediately before and after each intracellular measurement, as described later in Fig. 6. Only electrodes with a response of >54 mV/decade were used. A conventional microelectrode filled with 3 M KCl was used to measure the oocyte membrane potential (Vm) and pH1 was calculated from the voltage read with the pH electrode minus Vm.

Extracellular pH Measurements

A qualitative assay of extracellular medium acidification was designed to demonstrate H+ secretion by Xenopus oocytes. The assay was performed 2 d af-
ter coinjection of α2β3, β3 alone, or α3β2β4 cRNAs. Oocytes were transferred for 5 min in a weakly buffered solution (NaCl 110 mM, KCl 1 mM, CaCl2 0.5 mM, MgCl2 0.5 mM, MOPS 500 μM, adjusted to pH 8 with NaOH), containing the pH indicator Red phenol (200 mg/l). In some experiments, ouabain (1 mM) was added to the solution. Oocytes were placed individually in a small drop of the same solution under oil. The volume of the droplet was then reduced to 0.5 to 1.0 μl by gently removing the temperature, a color picture was taken.

Results

Primary Structure and Tissue Distribution of a P-ATPase α Subunit from Bladder Epithelium

Using a set of degenerate oligonucleotides designed to amplify a PCR product common to all Na,K- and H,K-ATPases α subunits from different species (Jaisser et al., 1993a), we have cloned, characterized and sequenced a 3.7-kb cDNA from a toad bladder epithelium library. The full cDNA sequence and the predicted amino acid sequence are shown in Fig. 1. The novel α subunit encodes a protein of 1,042-amino acids long with many features characteristic of the ion-motive P-ATPase gene family, including a highly conserved phosphorylation site (Cys-Ser-Asp399-Lys) and the FITC-binding site (Met-Lys531-Gly-Ala) (Horisberger et al., 1991). In the present study, we selected a novel/3 subunit of B. marinus. The deduced amino acid sequence starts with the presumed initial methionine. The full-length cDNA includes 222 bp of 5' untranslated region, 3,126 bp of coding region, 310 bp of 3' untranslated region, and a poly A tail. Putative transmembrane domains are underlined. The consensus phosphorylation site (D399) and FITC-binding site (K531) are indicated in bold. These sequence data are available from EMBL/GenBank under accession number Z25809.

![Nucleotide and deduced amino acid sequence of the bladder epithelium cDNA](image)

Figure 1. Nucleotide and deduced amino acid sequence of the bladder H,K-ATPase α subunit of B. marinus. The deduced amino acid sequence starts with the initial methionine. The full-length cDNA includes 222 bp of 5' untranslated region, 3,126 bp of coding region, 310 bp of 3' untranslated region, and a poly A tail. Putative transmembrane domains are underlined. The consensus phosphorylation site (D399) and FITC-binding site (K531) are indicated in bold. These sequence data are available from EMBL/GenBank under accession number Z25809.

Functional Expression of α2 and β3 in Xenopus oocytes

To examine the possibility that the α2 subunit could function as a K-ATPase to reabsorb potassium from the extracellular fluid or as a H,K-ATPase to secrete protons in exchange for potassium reabsorption, we have used the Xenopus oocyte expression system, which has been shown to be a convenient system to study the function of Na,K-ATPase (Horisberger et al., 1991a).

The measurement of radioactive rubidium uptake (68Rb) allows to probe for K+ pump function when the other K+ pathways are blocked (Jaunin et al., 1992). We designed an experimental protocol (Fig. 3 A) which allows to minimize the contribution of the endogenous oocyte Na,K- pump by a short exposure to 10 μM ouabain. This maneuver has been previously shown to inhibit the Xenopus laevis Na,K- pump by more than 98% for at least 20 min (Jaisser et al., 1992). The Na,K-/H,K-ATPase family requires α/β subunit assembly for functional expression at the plasma membrane (Geering, 1991). In the present study, we selected a novel β subunit isoform (β2) which we have characterized from the same toad bladder epithelium cDNA library (Jaisser et al., 1993b). We have postulated that the β2 could be functionally associated with an α subunit of either Na,K- or H,K-ATPase. As shown in Fig. 3 B, the injection of α2 cRNA
Northern blot analysis were performed using 1.5 μg poly A(+) RNA obtained from various tissues from the toad *B. marinus* and from the TBM 18-23 clonal cell line, which derives from the urinary bladder. Autoradiograms were exposed for 3 d (Na, K-ATPase αq subunit) or 10 d (H,K-ATPase αb subunit).

alone (lane 2) or βa cRNA alone (lane 3) did not induce any significant increase of rubidium uptake compared to the water-injected oocytes (lane 1). When αa and βa were co-injected (lane 4), a more than 20-fold increase in rubidium uptake was observed with respect to oocytes injected with either subunit alone.

As shown in Fig. 4 A, rubidium uptake was activated in a dose-dependent manner by external K⁺, with a Kᵂ of 370 μM. This value can be compared with those observed for the amphibian Na,K- pump (~1 mM) (Jaisser et al., 1992) and those reported for the gastric H,K-ATPase (~750 μM) (Rabon et al., 1992). It is very close to the Kᵂ value of 320 μM reported for the K-ATPase of amphibian distal nephron (Planeües et al., 1991). We thus propose that this rubidium transport is mediated by a K⁺-activated ATPase.

**Pharmacological Profile**

Na,K- and H,K-ATPase bind important drugs such as the cardiotonic glycosides in the case of Na,K-ATPase (Forbush, 1983) and the SCH28080 compound for the gastric H,K-ATPase (Wallmark et al., 1987). The bladder K⁺ pump is inhibited by SCH28080 in a dose-dependent manner with a Kᵂ of 230 μM (Fig. 4 B). It is thus much less sensitive to this compound than the gastric H,K-ATPase (Wallmark et al., 1987), however, clearly more sensitive than the Na,K-

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**Figure 2.** Tissue distribution of the H,K-ATPase αb subunit and the Na,K-ATPase αq subunit. Northern blot analysis were performed using 1.5 μg poly A(+) RNA obtained from various tissues from the toad *B. marinus* and from the TBM 18-23 clonal cell line, which derives from the urinary bladder. Autoradiograms were exposed for 3 d (Na, K-ATPase αq subunit) or 10 d (H,K-ATPase αb subunit).

**Figure 3.** ⁸⁶Rb uptake in *Xenopus* oocytes mediated by the bladder H,K-ATPase. (A) Flow chart of the experimental protocol used to determine the ⁸⁶Rb uptake in *Xenopus* oocytes. (B) ⁸⁶Rb uptake in *Xenopus* oocytes injected with water (lane 1), αa alone (lane 2), βa alone (lane 3) or αa and βa together (lane 4). ⁸⁶Rb uptake was performed in the presence of 500 μM K⁺ and after preliminary inhibition of the endogenous, ouabain-sensitive, Na,K-ATPase with 10 μM ouabain. Results are expressed as mean ± SE, n = 10–24 from three independent experiments.

**Figure 4.** K⁺-dependent activation of ⁸⁶Rb uptake (A), dose-dependent inhibition of ⁸⁶Rb uptake by SCH28080 (B) and by ouabain (C) in *Xenopus* oocytes injected with αaβb subunit cRNAs. SCH28080 and ouabain effects were determined in the presence of 200 μM KCl in the incubating solution. The final concentration of DMSO (diluent) was identical in all experimental conditions. Results are expressed as mean ± SE, n = 9–11. The activation (Kᵂ) and inhibition Kᵂ were obtained by fitting the ⁸⁶Rb uptake data to a single site model (insets).
ATPase (Fig. 5). In addition, the bladder K- pump is also sensitive to ouabain with a K, of 25 μM. This level of ouabain sensitivity is similar to that of the moderately ouabain-resistant toad Na,K- pump α1 isoform, which has a K, of 50 μM (Jaissier et al., 1992), when measured in the presence of 10 mM K+, while ouabain-sensitive isoforms have a K, of the order of 50 nM (Canessa et al., 1992). As both ouabain and SCH28080 are potassium competitive inhibitors (Wallraark et al., 1987; Forbush, 1983), we tested the effect of extracellular potassium on SCH28080 and ouabain-mediated inhibition of 86Rb uptake. The inhibitory effect of 300 μM SCH28080 was antagonized by external K+ (mean ± SE) (200 μM K+: 56.3 ± 5.3%; 2.5 mM K+: 37.5 ± 3.5%, n = 11, P < 0.05), as well as the inhibitory effect of 1 mM ouabain (200 μM K+: 95.1 ± 0.5%; 2.5 mM K+: 85.5 ± 0.4%, n = 10, P < 0.001). We performed another set of experiments to compare the effects of SCH28080 and ouabain on both the toad Na,K-ATPase and bladder H,K-ATPase (Fig. 5). In the presence of 500 μM external potassium, the pharmacological profile of the two pumps is quite distinct. The Na,K- pump is not sensitive to 500 μM SCH28080 and is almost completely inhibited by 200 μM ouabain. In contrast, the bladder ATPase is partially inhibited by 500 μM SCH28080 and by 200 μM ouabain. Thus, the pharmacological profile of the bladder ATPase is quite unique and distinct from previously characterized Na,K- or H,K-ATPases.

The Expression of αm and βm Induces H+ Secretion

At this point, we do not know whether the bladder ATPase can exchange potassium ions against other cations. Evidence from SCH28080-sensitive rubidium uptake and K+ transport in the collecting tubule cells indicates that this process is not electrogenic (Okusa et al., 1992; Wingo and Armitage, 1992). Thus K+ ions are probably exchanged against an intracellular cation. One likely candidate for a counter ion is the proton. In this case the new ATPase would be a H,K-ATPase with transport functions similar to the gastric H,K-pump. Two sets of experiments indicate that this is the case. We measured intracellular pH in oocytes 2 or 3 d after injection with βm alone, αm/βm or αm/βm as described in Fig. 6 A. A significant alkalization of the oocyte was observed only in cells coinjected with αm and βm (Fig. 6 B). The most likely explanation for this observation is that the bladder ATPase exchanges extracellular potassium ions against intracellular protons. We have tested directly H+ secretion in oocytes two days after coinjection of αm/βm or αmNK/βm cRNAs shown in Fig. 7. Within 15 min of incubation, an important acidification of the external medium was clearly visualized by the color change of the pH indicator. In a second experiment, direct measurement of the pH in the external medium was carried out using liquid ion-exchanger pH-sensitive microelectrodes (Fig. 8). After a 15 to 20-min incubation, the pH of the external medium surrounding oocytes injected with the bladder ATPase cRNA was significantly more acid than those of oocytes injected with the Na,K-ATPase cRNAs. The acidification of the external medium was completely blocked by ouabain (1 mM) and partially by
Figure 8. *X. laevis* oocytes were injected with $\alpha_{bl}/\beta_{hl}$ or $\alpha_{Na,K}/\beta_{hl}$ cRNAs. Oocytes were incubated in a weakly buffered solution containing diluent (DMSO), SCH28080 (500 $\mu$M) or ouabain (1 mM). Extracellular pH were measured after 15–20 min. pH values are expressed as mean ± SE (n); * $P < 0.05$, *** $P < 0.005$, t-test.

Discussion

A New Member of the Na,K-/H,K-ATPase Gene Family

The primary structure of the new protein presented here clearly indicates that it is a new member of the large P-ATPase $\alpha$ subunit gene family. It is homologous with the gastric H,K-ATPase and any of the three known isoforms of the Na,K-ATPase, and slightly closer to another P-ATPase cloned from the rat colon, which function is not yet known. Both Na,K- and gastric H,K-ATPase are heterodimeric proteins, including a glycosylated $\beta$ subunit that is essential to the function of the enzyme. The requirement of coexpression of a $\beta$ subunit for expression of an active H,K-pump suggests that the novel ATPase is a new member of the Na,K-/H,K-ATPase subfamily.

The new H,K-ATPase is expressed specifically in urinary epithelia and could not be detected in colon. This suggests that the novel $\alpha$ subunit (which we term $\alpha_{bl}$) is an isofrom of the H,K-ATPase expressed specifically in the urinary tract, which was previously postulated to exist in several species (Doucet and Marcy, 1987; Garg and Narang, 1988; Cheval et al., 1991; Planellès et al., 1991; Okusa et al., 1992; Wingo and Armitage, 1992) and distinct from the putative H,K-ATPase identified in the rat colon (Crowson and Shull, 1992; Jaisser et al., 1993a). It is not expressed in TBM cells (Fig. 2) which are sodium transporting cells derived from the toad bladder epithelium (Asher et al., 1988) that have the characteristics of the granular cells, the equivalent of the principal cells of the mammalian collecting tubule (CCT). The novel $\alpha$ subunit could therefore derive from any of the four other cell types composing the epithelium (Kraehenbuhl et al., 1979). Of special interest is the possibility that the $\alpha$ subunit is expressed in mitochondria rich cells. These cells are the amphibian counterpart of intercalated cells of CCT. Two types of intercalated cells have been described in mammal: $\alpha$ cells are believed to secrete protons while $\beta$ cells are believed to be involved in bicarbonate secretion (Alpern et al., 1991; Schuster, 1993). Proton secretion in $\alpha$ cells could be mediated by a H,K-ATPase and/or by a vacuolar V-type ion motive ATPase (Alpern et al., 1991; Schuster, 1993). An H,K-ATPase has also been involved in the basolateral extrusion of the $\beta$ intercalated cells (Schuster, 1993). Recently, SCH28080-sensitive proton transport has been described in intercalated cells of the CCT (Silver and Frindt, 1993).

Structure–Function Relationship

Na,K-ATPase and gastric H,K-ATPase are the receptors to important drugs such as the cardiotonic glycosides in the case of Na,K-ATPase (Forbush, 1983) and the SCH28080 compound for the H,K-ATPase (Wallmark et al., 1987). The
pharmacological profile of the bladder H,K-ATPase is of special interest in view of what is already known for the Na,K-ATPase and the gastric H,K-ATPase. In Fig. 9, the amino acid sequence of the \( \alpha \) subunit of the bladder H,K-ATPase is compared with those of the rat colon putative H,K-ATPase (lane 2) (Crowson and Shull, 1992), the rat gastric H,K-ATPase (lane 3) (Shull and Lingrel, 1987), and the \( \alpha \) subunit of the Bufo Na,K-ATPase (Jaisser et al., 1992). The ouabain-binding site of Na,K-ATPase is localized on the H1 transmembrane segment (Canessa et al., 1992), the HI-H2 ouabain-binding site of Na,K-ATPase is also critical in conferring ouabain resistance in rat and toad (Price et al., 1990; Jaisser et al., 1992). On the other hand, site specific chemical modification of gastric H,K-ATPase \( \alpha \) subunit by a photoactivable analogue of SCH28080 showed that the HI-H2 ectodomain was also involved in binding of this compound and modelling suggested that a phenylalanine (Phe124, pig gastric sequence) in the HI transmembrane segment (just at the interface with the ectoplasmic loop) and an aspartic acid (Asp316, Pig gastric sequence) in the ectoplasmic loop were participating in the docking of the drug (Munson et al., 1991). Inspection of the sequences shown in Fig. 9 reveals a striking diversity in this domain of the protein. In the bladder pump, a tyrosine residue (Tyr 133), similar to the Na,K-ATPase, is substituted by the phenylalanine (Phe124, pig gastric sequence) involved in SCH28080 binding. The extracytoplasmic loop itself is extremely divergent between the four sequences discussed here. Similar observations can be made for the H3-H4 ectodomain of a highly conserved tyrosine (Tyr313, X. laevis sequence) has been recently shown to be also involved in ouabain binding (Canessa et al., 1993). On the other hand, the tryptophane in the H3-H4 ectodomain which can be chemically labeled by an ouabain analogue (McParland et al., 1991) is substituted by different residues in the H,K-ATPase. Thus, the \( \alpha \) subunit shares sequences and residues with both Na,K- and H,K-ATPase. This mosaic at the primary structure level could well explain the pharmacological profile observed in this study. A more detailed analysis by chimeric-and site-directed mutagenesis approaches should allow to define the binding sites for ouabain and SCH28080 but also should help in designing specific drugs for the three types of pumps.

There are two other domains quite divergent between the sequences presented in Fig. 9 and of potential interest in the context of a discussion of function-structure relationships. First, the amino-terminal segment is strikingly divergent. This domain has been involved in controlling cation binding during the catalytic cycle of Na,K-ATPase by changing the activation of the pump by external potassium (Burgener-Kairuz et al., 1991), or by changing the potassium dependence of the current voltage relationship (Vasilets et al., 1991) or changing the nucleotide dependence of potassium deactivation (Wierzbiicki and Blostein, 1993). Second, the last hydrophobic segments (H7-H10) at the carboxy terminus of the molecule are also quite divergent. Omeprazole, another inhibitor of the gastric H,K-ATPase, is able to bind covalently with SH groups of two cysteines (Cys813 [or Cys822] and Cys892) predicted to be in the extracytoplasmic loops connecting the hydrophobic segment H5/H6 and H7/H8 (Besancon et al., 1993). These cysteine residues are not found in the bladder H,K-ATPase, the Na,K-ATPase or the rat colon putative H,K-ATPase.

It has been recently proposed that negatively charged amino acids, present in the putative transmembrane segments of Na,K-ATPase are involved in cation occlusion (Karlsh et al., 1992). The charge distribution within these last transmembrane domains is different for the four sequences compared in Fig. 9, suggesting that important functional differences in cation transport may be linked to these charges.

**Relationship with the Renal H, K-ATPase**

The relationship between the bladder H,K-ATPase described here and the H,K-ATPase studied in the mammalian cortical collecting tubule (Doucet and Marsy, 1987; Garg and Narang, 1988; Cheval et al., 1991; Wingo and Armitage, 1992) or the distal nephron of amphibia (Planelles et al., 1991) is not yet clear. In these studies, the K-ATPase activity was reported to be moderately sensitive to SCH28080 (K_x \text{M range}) but insensitive to ouabain (up to 1 mM) (Cheval et al., 1991; Planelles et al., 1991) whereas the bladder H,K-ATPase reported here is moderately sensitive to both drugs. It should be noticed that experiments designed to probe the activity of the kidney K- or H,K-ATPase were performed in the presence of high concentrations of ouabain to eliminate any Na,K-ATPase activity. These protocols might have overlooked the type of isoform described here.
On the other hand, it is conceivable that some ouabain-sensitive ATPase activity described in the cortical and medullary collecting duct that had been attributed to the Na,K-pumps (Hayashi and Katz, 1987; Feraillle et al., 1993) were in fact due to a moderately ouabain-resistant H,K-pump. An apical ouabain-sensitive K+ pump in the distal Na,K-pumps (Hayashi and Katz, 1987; Feraille et al., 1993) sensitive ATPase activity described in the cortical and were in fact due to a moderately ouabain-resistant H,K-ATPase. The gene is expressed in brain and kidney. The sequences of exon 5, 9, and 20 suggest that it could be another member of the Na,K/H,K-ATPase subfamily described here. The precise relationship between the human gene and the amphibian H,K-ATPase will require knowledge of the sequence of a full-length cDNA and its functional expression.

The renal H,K-ATPase of the CCT has been physiologically located at the apical membrane of α cells (Alpern et al., 1991, Schuster, 1993). Likewise gastric H,K-ATPase is functionally expressed at the apical membrane of parietal cells. Thus, H,K-ATPases are in principle targeted to the apical membrane of epithelial cells whereas Na,K-ATPases are generally routed to the basolateral membrane (Gottardi and Caplan, 1993). The specific targeting to each of the two plasma membrane domains appears to involve information encoded on both the α and β subunits (Gottardi and Caplan, 1993). The sequence of Otm and β2 (Jaissier et al., 1993b) should help in designing experiments addressing this important question.

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