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Sodium-Potassium-Adenosinetriphosphatase-Dependent Sodium Transport in the Kidney: Hormonal Control

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Féraille, Eric, and Alain Doucet. Sodium-Potassium-Adenosinetriphosphatase-Dependent Sodium Transport in the Kidney: Hormonal Control. *Physiol Rev* 81: 345–418, 2001.—Tubular reabsorption of filtered sodium is quantitatively the main contribution of kidneys to salt and water homeostasis. The transcellular reabsorption of sodium proceeds by a two-step mechanism: Na⁺-K⁺-ATPase-energized basolateral active extrusion of sodium permits passive apical entry through various sodium transport systems. In the past 15 years, most of the renal sodium transport systems (Na⁺-K⁺-ATPase, channels, cotransporters, and exchangers) have been characterized at a molecular level. Coupled to the methods developed during the 1965–1985 decades to circumvent kidney heterogeneity and analyze sodium transport at the level of single nephron segments, cloning of the transporters allowed us to move our understanding of hormone regulation of sodium transport from a cellular to a molecular level. The main purpose of this review is to analyze how molecular events at the transporter level account for the physiological changes in tubular handling of sodium promoted by hormones. In recent years, it also became obvious that intracellular signaling pathways interacted with each other, leading to synergisms or antagonisms. A second aim of this review is therefore to analyze the integrated network of signaling pathways underlying hormone action. Given

the central role of $\text{Na}^+\text{-K}^+\text{-ATPase}$ in sodium reabsorption, the first part of this review focuses on its structural and functional properties, with a special mention of the specificity of $\text{Na}^+\text{-K}^+\text{-ATPase}$ expressed in renal tubule. In a second part, the general mechanisms of hormone signaling are briefly introduced before a more detailed discussion of the nephron segment-specific expression of hormone receptors and signaling pathways. The three following parts integrate the molecular and physiological aspects of the hormonal regulation of sodium transport processes in three nephron segments: the proximal tubule, the thick ascending limb of Henle's loop, and the collecting duct.

I. INTRODUCTION

Mammalian kidneys play a major role in the homeostasis of extracellular compartment. Despite large qualitative and quantitative variations in dietary intake of solutes and water, the kidneys are able to maintain the composition and the volume of the extracellular compartment within very narrow margins. This homeostatic function of kidneys requires the presence of numbers of specific carriers able to transport a large variety of substrates and their fine control by specific factors and hormones.

Since the onset of modern renal physiology, tremendous efforts have been made to describe the transport properties of the kidney tubule and to analyze their regulatory factors. This led, in the mid 1980s, to an almost coherent cellular description of the transport properties of the successive segments constituting the nephron, as well as to the localization and characterization of hormonal regulation of these processes (566).

During the past 10–15 years, most efforts have permitted the evolution from this cellular level of understanding to a molecular one. This evolution mainly results from 1) the molecular cloning of membrane transporters and hormone receptors involved in solute and water transport and its regulation, 2) the characterization of new extracellular regulatory factors and deciphering of new intracellular signaling pathways, 3) the acknowledgement that intracellular signaling pathways should not be considered as linear and parallel chains of interactions, but as intricate and interactive networks. Such combinatorial organization markedly increases the diversity of signaling. 4) Lastly, the idea has slowly emerged that the cornerstone of kidney transport machinery, $\text{Na}^+\text{-K}^+\text{-ATPase}$, is not a house-keeping protein that does not participate actively to rapid adaptations of kidney function but is an important molecular target of hormonal regulation. For this last reason, we have chosen to take $\text{Na}^+\text{-K}^+\text{-ATPase}$ as a leading thread in the analysis of the hormonal control of sodium transport in the kidney.

This review has been focused on the regulatory pathways of sodium transport that share the following criteria: 1) mechanisms are deciphered, at least partially, at the molecular level; 2) transport is dependent on $\text{Na}^+\text{-K}^+\text{-ATPase}$; and 3) transport mechanism has a functional relevance with sodium homeostasis.

In the two first sections of this review, we summarize the general properties and the renal specificities of $\text{Na}^+\text{-K}^+\text{-ATPase}$ and of intracellular signaling pathways.

The three following parts are devoted to the hormonal regulation of cation transport in proximal tubule, thick ascending limb of Henle's loop, and collecting duct. For each structure, the cellular and molecular mechanisms of sodium transport are analyzed before discussing the actions of the main hormones. For each hormone, the general physiological response is first described, and then the regulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ and other transporters is analyzed in terms of intrinsic changes in properties and of signaling mechanisms.

II. SODIUM-POTASSIUM-ADENOSINETRIPHOSPHATASE IN SODIUM TRANSPORT ALONG THE RENAL TUBULE

Epithelial cell layers separate compartments of distinct compositions and ensure transfer of water and solutes between them. The serosal compartment, in equilibrium with blood plasma, is characterized by the constancy of its composition. In contrast, the composition of the mucosal compartment varies greatly from one epithelium to another and with time. Epithelial cells are characterized by their functional polarization, since their apical membrane facing the mucosal compartment has receptors as well as transport and permeability properties distinct from their basolateral membrane bathed by the serosal compartment. This polarity is maintained by targeting to and/or withdrawal of newly synthesized proteins from a specific cell pole, and by prevention of planar diffusion of membrane constituents between the apical and basolateral domains by specific proteins located at the intercellular junctional complexes (115, 131).

In renal tubular cells, as in all sodium-reabsorbing epithelia, $\text{Na}^+\text{-K}^+\text{-ATPase}$ is exclusively located in the basolateral membrane (723), the infoldings of which are closely surrounded by mitochondria. In contrast, the sodium gradient generated by $\text{Na}^+\text{-K}^+\text{-ATPase}$ between intra- and extracellular compartments is mainly dissipated across the apical membrane. A net transfer of sodium from mucosal toward serosal compartment results from this architectural organization. Quantitatively, net sodium reabsorption is the major function of renal $\text{Na}^+\text{-K}^+\text{-ATPase}$, and a close relationship exists between the abundance of $\text{Na}^+\text{-K}^+\text{-ATPase}$ and the sodium reabsorption capacity of the different segments of nephron (323). In humans, kidneys reabsorb over 600 g sodium/day and

utilize over 2 kg of ATP for this process. Accordingly, kidney cells are rich sources of Na⁺-K⁺-ATPase; they contain up to 50 million pumps per cell (248) compared with a few hundred to a few thousand pumps in nonpolarized cells.

Renal Na⁺-K⁺-ATPase energizes not only sodium reabsorption, but also the secondary active transport (reabsorption or secretion) of large amounts of a wide variety of substances, including other ions and uncharged solutes. Indeed, passive entry of sodium into the cell is often coupled to the transport of other solute(s) at the level of symport or antiport systems. In turn, transport of charged solutes generates transmembrane voltage and concentration gradients that serve as driving force for passive electrolyte movements through ion channels. Transcellular movements of solutes may also generate a transepithelial potential difference that drives ion movements along the paracellular pathway, especially in leaky epithelia.

In summary, Na⁺-K⁺-ATPase can be considered as an energetic transducer that converts metabolic energy into rapidly mobilizable ionic solute gradients. Despite its ubiquitousness and its quantitative prevalence in kidney epithelial cells, it is worth recalling that Na⁺-K⁺-ATPase and sodium and potassium gradients are not a universal source of energy. This function may also be achieved by H⁺-ATPase and proton gradient in most lower eukaryotes, but also in some cells of higher eukaryotes, such as the intercalated cells of the collecting duct.

A. General Properties of Na⁺-K⁺-ATPase

The main function of Na⁺-K⁺-ATPase is to pump intracellular sodium ions out of the cells and extracellular potassium ions within the cells, at the expense of ATP hydrolysis. Although it can be considered either as an ion transporter (the sodium pump) or as an enzyme (Na⁺-K⁺-ATPase), it is essential to remind that these are two aspects of a same function achieved by a single protein complex.

1. Enzymatic properties

Some 40 years ago, 1997 Nobel Prize winner J. C. Skou (748) first reported that microsomal membrane fractions from crab nerve contain an ATP-hydrolyzing activity stimulated by concentrations of sodium and potassium usually found in intracellular and extracellular fluids, respectively (747). This requirement for both sodium and potassium ions remains the fundamental characteristic of Na⁺-K⁺-ATPase.

Na⁺-K⁺-ATPase activity is stimulated by sodium (acting at the cytosolic face of the membrane) with an apparent mean affinity constant ($K_{0.5}$) in the 5–15 mM range in the presence of 5–10 mM K⁺, and under these conditions the maximum velocity (V_{\max}) is achieved with 60–100 mM

of sodium. Because intracellular sodium concentration is in the 5–20 mM range, Na⁺-K⁺-ATPase works well below its V_{\max} in intact cells. Thus any increase in intracellular sodium concentration stimulates Na⁺-K⁺-ATPase activity which, in turn, pumps more sodium out of the cell and thereby contributes to restore the initial intracellular sodium concentration. Conversely, any decrease in intracellular sodium concentration slows down the pump and participates in maintaining cellular homeostasis. This autoregulatory process is highly efficient because sodium activation of Na⁺-K⁺-ATPase displays a marked positive cooperativity; thus small variations of sodium concentration around the $K_{0.5}$ induce large variations of Na⁺-K⁺-ATPase activity. In addition, any regulatory process that alters the sodium affinity of Na⁺-K⁺-ATPase also alters the pump activity. From the extracellular side, Na⁺-K⁺-ATPase is stimulated by potassium with an apparent Michaelis constant (K_m) in the millimolar range (0.5–1.5 mM). Thus extracellular potassium is not rate limiting for ATPase activity, except in the case of severe hypokalemia.

The requirement for intracellular sodium is almost absolute except for lithium, which is transported (although at a slower rate than sodium) by human erythrocytes and kidney cells. This has no physiological relevance because lithium concentration in body fluids is very low. The selectivity for potassium is less strict since it can be replaced by rubidium and ammonium with almost similar affinities and efficiencies. Na⁺-K⁺-ATPase-mediated transport of ammonium instead of potassium into the cells has a physiological relevance in the kidney medulla since it participates to the recycling of ammonium. Transport of rubidium by Na⁺-K⁺-ATPase has no physiological significance, but use of rubidium as a potassium surrogate proved to be a precious tool for studying the sodium pump. Indeed, the radioactive isotope ⁸⁶Rb⁺ is much easier to handle in the laboratory than ⁴²K⁺ because it has a much longer radioactive half-life (≈18 days vs. 12 h).

The energy necessary to move sodium and potassium against their transmembrane electrochemical gradients is provided by the hydrolysis of the “energy-rich” ATP molecule, as other nucleotides triphosphate are hydrolyzed at much slower rates. The true substrate of Na⁺-K⁺-ATPase is the ATP-Mg complex, but the dependency on magnesium is not absolute because other divalent cations (manganese, cobalt) can substitute for magnesium. However, most divalent cations, in particular calcium, inhibit ATPase activity.

For each ATP molecule hydrolyzed, Na⁺-K⁺-ATPase moves two potassium ions into the cell and three sodium ions out of the cell. An important consequence of this 3Na⁺:2K⁺ stoichiometry is the electrogenicity of Na⁺-K⁺-ATPase and therefore its dependence on membrane potential (see below).

As with all P-type ATPases, $\text{Na}^+\text{-K}^+\text{-ATPase}$ is transiently phosphorylated during its activation. P-type ATPases are also called $\text{E}_1\text{-E}_2$ ATPases because they exhibit two main conformation states that can be either unphosphorylated (E_1 and E_2) or phosphorylated ($\text{E}_1\text{-P}$ and $\text{E}_2\text{-P}$). The two conformation states of $\text{Na}^+\text{-K}^+\text{-ATPase}$ are characterized by their respective affinities for sodium, potassium, and ATP and by the accessibility of the cationic sites at the intracellular or extracellular sides of the membrane: E_1 conformation confers a high affinity for ATP and sodium and a low affinity for potassium, both cation sites being accessible from the intracellular side, whereas under the E_2 conformation, the cation sites are accessible from the outside and display low affinity for sodium and high affinity for potassium. $\text{Na}^+\text{-K}^+\text{-ATPase}$ cycles through these different conformations according to the so-called Albers-Post model (Fig. 1). ATP, magnesium, and sodium bind to E_1 on the intracellular side of the pump, allowing phosphorylation of E_1 ($\text{E}_1\text{-P}$) and "occlusion" of sodium ions that are no longer accessible

from either side of the membrane. After release of ADP, the exergonic transconformation of $\text{E}_1\text{-P}$ to $\text{E}_2\text{-P}$ occurs and promotes the extracellular delivery of sodium and the binding of extracellular potassium. This latter process induces dephosphorylation of $\text{E}_2\text{-P}$ and potassium occlusion. Spontaneous reversion to E_1 releases potassium inside the cell, completing the reaction cycle (reviewed in Ref. 449).

2. Pharmacology and toxicology

A) VANADATE. Vanadate acts as a structure analog of phosphate to inhibit all P-type ATPases through binding to their phosphorylation site and blockade under their E_2 configuration (Fig. 1). Although vanadate was initially considered as a putative physiological modulator of $\text{Na}^+\text{-K}^+\text{-ATPase}$ (130), this now appears unlikely because the redox state prevailing within cells reduces vanadate to inactive vanadyl.

B) DIGITALIS GLYCOSIDES. Digitalis glycosides are natural and potent inhibitors of $\text{Na}^+\text{-K}^+\text{-ATPase}$ (710) used in therapy as well as in the laboratory. Ouabain (G-strophanthin) is generally used in vitro because of its better, although limited, water solubility, whereas digoxin is the most widely used digitalic in therapy. Ouabain binds to an extracellular domain of $\text{Na}^+\text{-K}^+\text{-ATPase}$ under its E_2 conformation and decreases its affinity for potassium, and vice versa, as a competitive inhibitor (Fig. 1). As a clinical counterpart, digitalic poisoning is more severe in hypokalemic patients. Through impediment of potassium binding, ouabain prevents the dephosphorylation of the enzyme and the associated transconformation from E_2 to E_1 . The affinity of $\text{Na}^+\text{-K}^+\text{-ATPase}$ for ouabain varies within a wide range of concentrations (from nM to mM) between species (rats, mice, and *Bufo marinus* are rather resistant to ouabain) and between organs or cells from a given species (kidneys being less sensitive to ouabain than brain and heart). These differences are accounted for in part by the molecular heterogeneity of $\text{Na}^+\text{-K}^+\text{-ATPase}$ (see below).

For over 40 years, ouabain has been considered as a highly specific inhibitor of $\text{Na}^+\text{-K}^+\text{-ATPase}$. In particular, despite its functional and structural similarities with $\text{Na}^+\text{-K}^+\text{-ATPase}$, gastric $\text{H}^+\text{-K}^+\text{-ATPase}$ is not sensitive to ouabain. However, it is now established that ouabain also inhibits several nongastric forms of $\text{H}^+\text{-K}^+\text{-ATPase}$ (431).

C) PALYTOXIN. Palytoxin, a nonprotein toxin produced by a marine coelenterate, not only inhibits $\text{Na}^+\text{-K}^+\text{-ATPase}$ but transforms it into a sodium channel (358). The tumor-promoting activity of palytoxin is related to its ability to increase intracellular sodium by this mechanism (482).

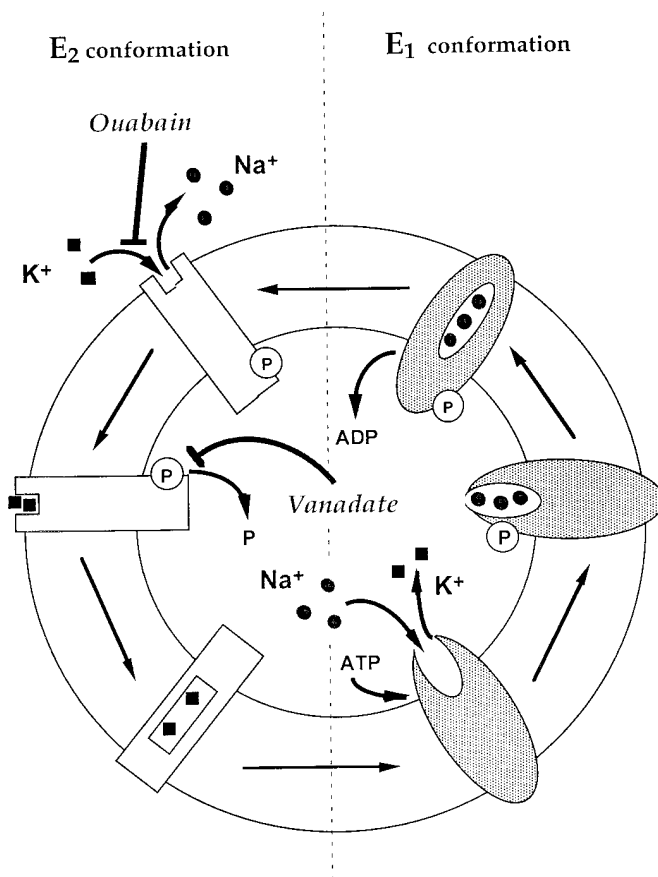


FIG. 1. Catalytic cycle of $\text{Na}^+\text{-K}^+\text{-ATPase}$. This model shows the transition between the main conformational forms of $\text{Na}^+\text{-K}^+\text{-ATPase}$ catalytic subunit (E_1 , $\text{E}_1\text{-P}$, $\text{E}_2\text{-P}$, and E_2) with either accessible or occluded cation binding sites. It also indicates the sites of action of $\text{Na}^+\text{-K}^+\text{-ATPase}$ inhibitors vanadate and ouabain.

3. Structure and structure-function relationship

Purification (438) and molecular cloning (456, 615, 730, 734, 735, 736) have shown that Na⁺-K⁺-ATPase consists of two main subunits (α and β) that are associated in a 1:1 molar ratio.

The α -subunit (~1,000 amino acid residues and 110 kDa) displays all the functional properties described above (binding sites for sodium and ATP and phosphorylation site on the cytoplasmic domain, and binding sites for potassium and ouabain on the extracellular domain) and is therefore considered as the catalytic subunit. It consists of 10 membrane-spanning domains (M_1 - M_{10}) with intracellular NH₂- and COOH-terminal domains and a long M_4 - M_5 intracytoplasmic loop (Fig. 2).

Site-directed mutagenesis of amino acid residues and covalent chemical modifications of the α -subunit have permitted the identification of functionally important amino acids and domains (reviewed in Ref. 396). The ATP binding domain and the phosphorylation site are located into the long M_4 - M_5 cytoplasmic loop; their highly conserved sequence is a molecular signature of P-ATPases. The M_4 , M_5 , and M_6 transmembrane domains likely constitute the cation occlusion site and the ion pore. The intracellular NH₂-terminal domain might play a role in cation gating. M_1 - M_2 as well as part of the M_3 - M_4 ectodomains are involved in ouabain binding. The M_7 - M_8 ectodomain is the main site of interaction with the β -subunit. Finally, several intracellular amino acid residues are phosphorylation sites for protein kinases (see below).

The β -subunit is smaller (~300 amino acids) and displays a single membrane-spanning domain and a large extracellular domain with several N-linked glycosylation sites. This ectodomain is responsible for the interaction with α -subunit. Although the β -subunit has no enzymatic or transport activity, its association with an α -subunit is an absolute requirement for ATPase and pump activities: it allows the folding of newly synthesized α -subunits and their targeting from the endoplasmic reticulum to the plasma membrane, as well as the stabilization of α -subunits within the membrane (328, 330, 828).

Na⁺-K⁺-ATPase may also contain a γ -subunit (53 amino acids, ~10 kDa), which was first recognized as copurifying with α - and β -subunits (296). More recently, this γ -subunit has been cloned (554); its mRNA is abundantly expressed in kidney and at lower level in other epithelia but is absent in other tissues. Thus, conversely to the α - and β -subunits, the γ -subunit is not an absolute requirement for functional Na⁺-K⁺-ATPase although, when present, it is an integral part of Na⁺-K⁺-ATPase. The γ -subunit contains a single transmembrane domain with an extracellular NH₂ terminus. Expression in *Xenopus* oocyte indicates that the γ -subunit reaches the cell membrane only when associated with the $\alpha\beta$ -complex (in a 1 α :1 β :1 γ stoichiometry) (69). Functionally, coexpression of γ -subunit with α - and β -subunits was described as modifying the voltage sensitivity of potassium activation (69), decreasing the affinity of the pump for ATP (805, 806) as well as for sodium and potassium (28).

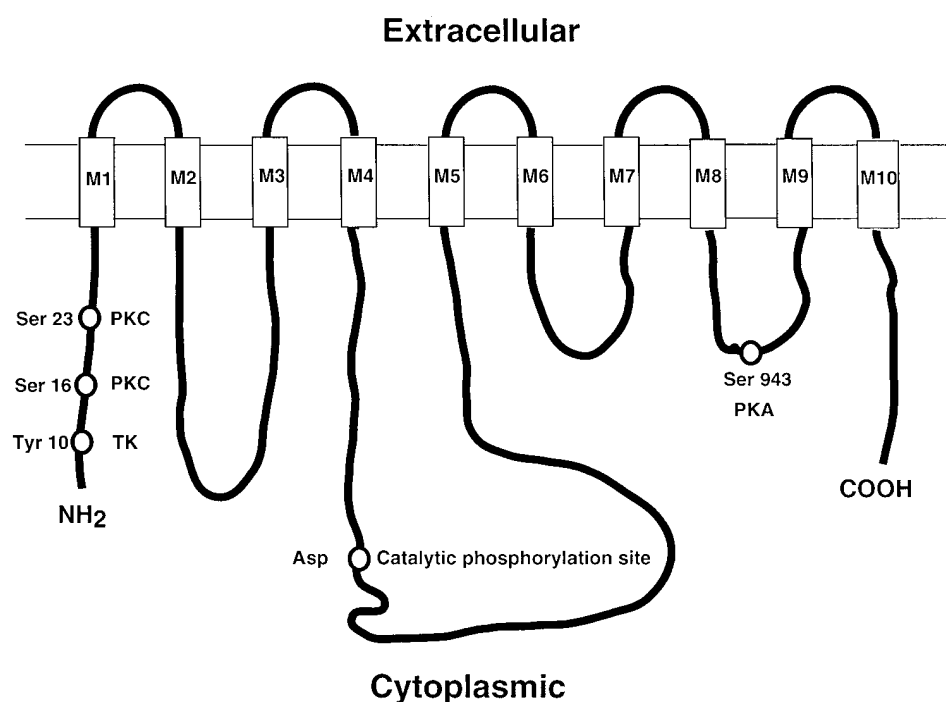


FIG. 2. Topology of the Na⁺-K⁺-ATPase α -subunit and localization of the phosphorylated amino acids. The Na⁺-K⁺-ATPase α -subunit displays 10 membrane-spanning domains with intracytoplasmic NH₂ and COOH termini. The currently identified amino acids phosphorylated by protein kinase C (PKC) and tyrosine kinases (TK) are located in the extreme NH₂ terminus of the α -subunit. Both Tyr-10 and Ser-16 are conserved in all cloned α_1 -subunits, whereas Ser-23 is specific of the rat α_1 -subunit. The protein kinase A (PKA) phosphorylation site is located at Ser-943 into the M_8 - M_9 intracellular loop. Also indicated is the Asp residue within the M_4 - M_5 large intracellular loop that is phosphorylated during the catalytic cycle of the pump.

4. Molecular and functional heterogeneity of $\text{Na}^+\text{-K}^+\text{-ATPases}$

Despite canonical characteristics, the $\text{Na}^+\text{-K}^+\text{-ATPase}$ is functionally highly heterogeneous. Molecular cloning and expression of several isoforms of $\text{Na}^+\text{-K}^+\text{-ATPase}$ catalytic subunits provided some molecular basis for this heterogeneity. As yet, four genes encoding $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunits and three genes encoding β -subunits have been cloned from mammals (reviewed in Ref. 396). In addition, two splice variants of the γ -subunit (γ_1 and γ_2) have been recently characterized in rat kidney (483). The γ_1 -subunit has the amino acid sequence predicted by the published cDNA sequence, whereas the γ_2 -subunit contains a different sequence of its 7 NH_2 -terminal amino acids and is acetylated on its first methionine. Experiments in which specific α - and β -isoforms were coexpressed in heterologous cellular systems indicate that all types of $\alpha\beta$ -dimers tested are functional. However, it remains to be demonstrated that all the combinations between different α - and β -isoforms are functionally expressed in normal cells. The following discussion on the properties of these different isoforms is focused around α -subunits because they condition the main properties of the holoenzyme.

Sequence comparison between the different α -isoforms in a given species reveals a very high degree of conservation, suggesting the existence of a common ancestor gene. The four isoforms of $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunit ($\alpha_1\text{-}\alpha_4$) are differentially expressed among tissues: the α_1 -isoform is ubiquitous and is the most abundant, if not the only, form in the kidney; the α_2 -isoform is predominantly expressed in heart, skeletal muscle, and brain; the α_3 is expressed in neural tissue and ovary; whereas expression of the α_4 -isoform is restricted to testis (786, 895).

In rat, it is well established that α -subunit isoforms endow different affinities for cardiac glycosides: α_3 [dissociation constant (K_D) ≈ 2 nM] $>$ α_2 ($K_D \approx 100$ nM) $>$ α_4 ($K_D \approx 300$ nM) $>$ α_1 ($K_D \approx 1$ mM) (602, 648, 895). The very low affinity of rat α_1 -isoform for ouabain mainly results from the presence of a positively charged arginine residue and a negatively charged aspartate residue at the two ends of the first ($\text{M}_1\text{-M}_2$) ectodomain of the α -subunit (649). Such differences in ouabain sensitivities are not found in all species; in humans, for example, the $\alpha_1\text{-}\alpha_3$ isoforms display similar affinities for ouabain (190).

Isoforms of $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunits may also differ by their voltage dependence. The equilibrium potential of $\text{Na}^+\text{-K}^+\text{-ATPase}$ (i.e., the membrane potential for which the energy necessary to move three sodium and two potassium ions across the cell membrane equals the free energy of hydrolysis of one molecule of ATP) is around -280 mV. From that membrane potential, at which the pump cannot work, the pumping rate of $\text{Na}^+\text{-K}^+\text{-ATPase}$ should theoretically increase as the membrane depolarizes to 0 mV and to positive potentials. Such relationships between membrane potential and $\text{Na}^+\text{-K}^+\text{-ATPase}$ pumping rate (as evaluated by the pump current) were experimentally observed within a wide range of membrane potentials (from -100 to $+50$ mV) in excitable cells (which mainly contain the α_1 - and α_3 -isoforms) such as axons (660) and myocytes (318). However, in renal epithelial cells (which mostly contain the α_1 -isoform), the pump current does increase with membrane potential within the -175 to -75 mV range, but reaches a plateau at higher physiological potentials (-75 to -25 mV) (397). Whether these distinct behaviors are intrinsic properties of the distinct isoforms originating in these two types of tissues or result from the specific cellular environment remains unknown. The marked voltage dependency of $\text{Na}^+\text{-K}^+\text{-ATPase}$ in excitable cells is teleologically sound, since stimulation of the pump during membrane depolarization facilitates the recovery of intracellular sodium concentration during action potential. Also physiologically sound is the absence of such regulation in epithelial cells since their membrane potential does not vary much.

Thus the expression of functionally distinct isoforms of the $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunit in specific tissues may have physiological consequences. In addition, these properties might be modulated by the association with different isoforms of β -subunit and/or the absence or presence of the different splice variants of the γ -subunit.

Thus the expression of functionally distinct isoforms of the $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunit in specific tissues may have physiological consequences. In addition, these properties might be modulated by the association with different isoforms of β -subunit and/or the absence or presence of the different splice variants of the γ -subunit.

5. Regulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ through phosphorylation of α -subunit

An emerging but important regulatory mechanism for $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity in intact cells is phosphorylation by protein kinases. Phosphorylation of the $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunit has been first recognized using purified preparations of $\text{Na}^+\text{-K}^+\text{-ATPase}$ incubated in the presence of protein kinase C (PKC) or protein kinase A (PKA) (83, 283, 522). PKA- and PKC-mediated phosphorylation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunit has been subsequently revealed in tissue homogenates (167) and in intact cells (66, 67, 86, 105, 134, 135, 295, 496, 529, 555, 616).

A single PKA phosphorylation site has been mapped to Ser-943 (Fig. 2) located in a typical PKA consensus site conserved in all cloned $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunits (66, 283, 294). In addition, two PKC phosphorylation sites are currently identified (Fig. 2). The first one, located at Ser-16, is conserved among all cloned α_1 -subunits and lies within an unusual PKC phosphorylation motif (66, 68). The second one, located at Ser-23, is found only in the rat α_1 -subunit and is comprised of a typical PKC consensus site within the lysine-rich cluster of the NH_2 -terminal domain of the α_1 -subunit (68, 73, 284). Finally, phosphorylation of the $\text{Na}^+\text{-K}^+\text{-ATPase}$ α_1 -subunit at Tyr-10 (Fig. 2) has been recently identified (276), similarly to the closely

related gastric H⁺-K⁺-ATPase α -subunit (809). It should be mentioned that phosphorylation of the identified sites does not account for the whole basal phosphorylation of the Na⁺-K⁺-ATPase α_1 -subunit (66, 68). These findings, together with the identification of threonine phosphorylation of rat α_1 -subunit in intact cells (276), indicate that an additional phosphorylation site(s) remains to be identified.

The functional effects of serine phosphorylation of the α -subunit are still highly debated. Results obtained in transfected COS-7 cells have suggested that PKA phosphorylation of the α -subunit has an inhibitory effect on Na⁺-K⁺-ATPase activity (294). However, in vitro PKA phosphorylation of shark rectal gland Na⁺-K⁺-ATPase stimulates its activity, whereas the activity of the pig kidney enzyme is unchanged under similar conditions (186). It should be mentioned that in native rat kidney epithelial cells, PKA phosphorylation of the Na⁺-K⁺-ATPase is associated with stimulation of its activity (135, 467).

Similarly, in response to PKC phosphorylation of its α -subunit, Na⁺-K⁺-ATPase activity was either stimulated (134, 628, 835), inhibited (73, 166, 168, 835), or unchanged (77, 285). These discrepancies observed in intact cells may be accounted for in part by the presence of both indirect effects of PKC phosphorylation such as internalization of active Na⁺-K⁺-ATPase units (165) and direct effects of phosphorylation such as an increase in apparent affinity for sodium (276). This later effect of phosphorylation of Na⁺-K⁺-ATPase α -subunit was recently demonstrated using COS-7 cells stably transfected with either wild-type or Ser-16 (the ubiquitous PKC phosphorylation site) mutant Na⁺-K⁺-ATPase α_1 -subunits: 1) phorbol esters increased the apparent sodium affinity of wild-type Na⁺-K⁺-ATPase; 2) when nonspecific increase in fluid-phase endocytosis was prevented, mutation of Ser-16 prevented the stimulatory effect of phorbol esters on the transport activity of Na⁺-K⁺-ATPase; and 3) mutant α_1 -subunits in which Ser-16 was substituted by an acidic residue (Asp or Glu) mimicking constitutive phosphorylation exhibited an increased apparent sodium affinity (276). This effect of Ser-16 phosphorylation on the apparent sodium affinity of Na⁺-K⁺-ATPase is in agreement with the results of Logvinenko et al. (515), who showed that in vitro phosphorylation of purified Na⁺-K⁺-ATPase by PKC shifts the conformational equilibrium of the Na⁺-K⁺-ATPase toward the E₁ conformation, i.e., the conformation displaying high affinity for sodium (see sect. II A1). These observations are also consistent with earlier studies showing that the α_1 -subunit NH₂-terminal domain is involved in conformational changes of the enzyme. Indeed, tryptic cleavage of the α_1 -subunit occurring between Lys-30 and Glu-31 (440), or truncation of the NH₂ terminus by site-directed mutagenesis (854, 880), displaces the E₁-E₂ conformational equilibrium toward the E₁ conformation through stimulation of potassium deoc-

clusion (880), and thereby may account for the increased apparent sodium affinity of Na⁺-K⁺-ATPase (440). This recent report (276) agrees with a growing number of studies documenting a stimulation of Na⁺-K⁺-ATPase activity in response to PKC activation (277, 356, 393, 530, 628), but contrasts with a few others (73, 285). It should be stressed, however, that these last two studies (73, 285) focused on the role of the additional rat-specific Ser-23 phosphorylation site and not on that of the ubiquitous Ser-16 phosphorylation site. These two phosphorylation sites might be targets for different PKC isozymes and/or produce different physiological effects. Indeed, phosphorylation of Ser-23 per se does not alter Na⁺-K⁺-ATPase activity (165, 285) but promotes endocytosis of the Na⁺-K⁺ pump in proximal tubule and in opossum kidney (OK) cells (165, 166). This hypothesis is supported by recent data indicating that 1) in OK cells, the opposite effects of phorbol esters and dopamine on the transport activity of Na⁺-K⁺-ATPase rely on classical PKC- β and atypical PKC- ζ activation, respectively (79); and 2) the transport activity of rat α_1 - β complexes expressed in *Xenopus* oocytes is inhibited while that of the endogenous *Xenopus* α_1 - β complexes, which were previously shown to be exclusively phosphorylated on Ser-16 (68), are stimulated by injection of purified rat PKC (835). In addition, secondary regulatory mechanisms that may be cell specific and/or brought about by experimental conditions, such as oxygen (81, 277) or calcium (161) availability, may also explain some discrepancies.

In response to the activation of receptor tyrosine kinases, i.e., insulin, insulin-like growth factor I (IGF-I), or epidermal growth factor (EGF) receptors, stimulation of Na⁺-K⁺-ATPase activity is almost always reported (178, 209, 266, 279, 280, 531, 544, 766). These observations are consistent with the recent identification of Tyr-10-dependent stimulation of Na⁺-K⁺-ATPase activity in native and cultured renal proximal tubule epithelial cells (278).

B. Na⁺-K⁺-ATPase Along the Nephron

1. Anatomic and topographic segmentation of the nephron

Figure 3 schematically depicts the topographical organization and the axial segmentation of the rat nephron and lists the abbreviations used in this review for the different nephron segments.

The proximal tubules extend from the glomeruli down to the thin segments, at the junction between the outer and inner stripes of the kidney outer medulla. Its apical cell border is characterized by a well-developed brush border made of densely packed microvilli. The basolateral plasma membrane forms deep infoldings that are in close contact with mitochondria. Both apical microvilli and basolateral membrane infoldings consider-

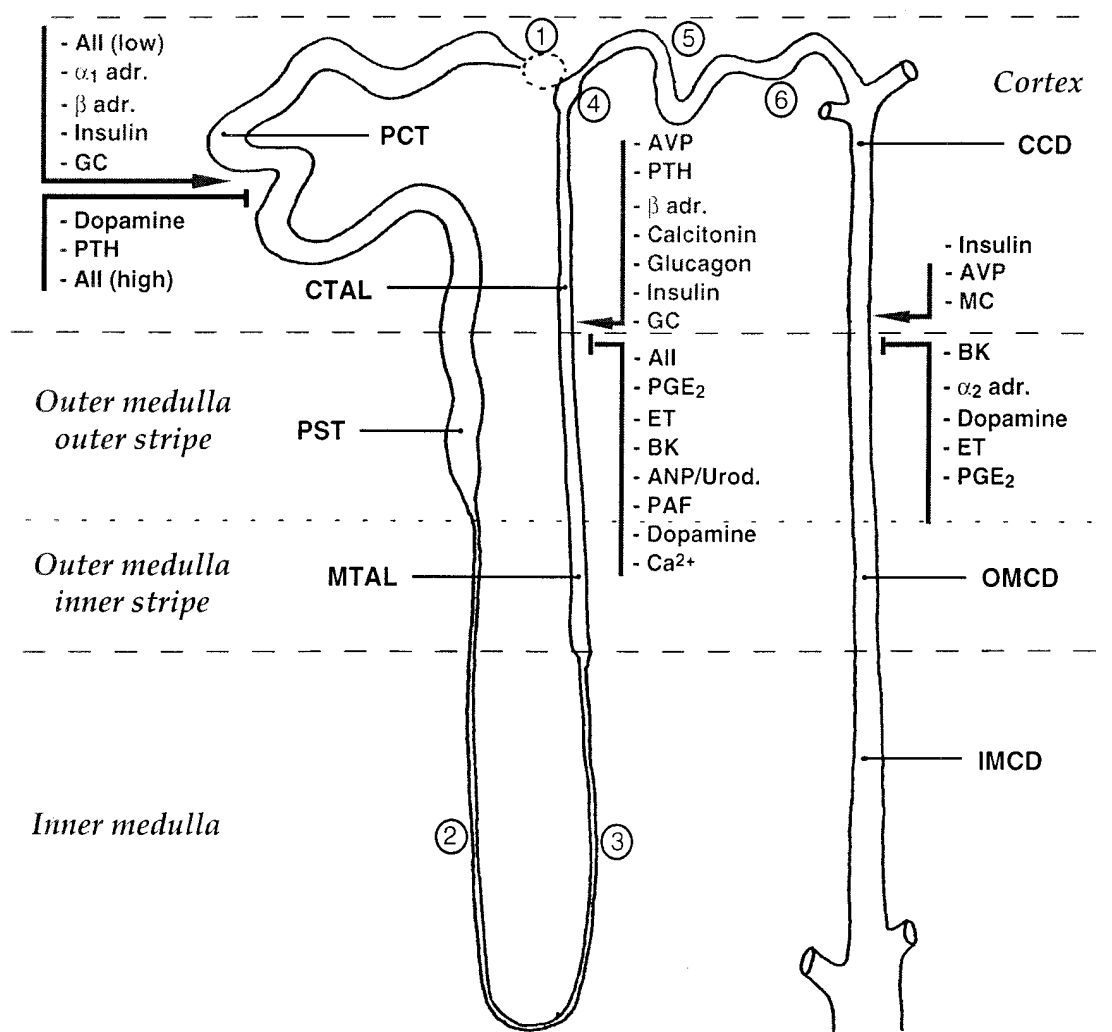


FIG. 3. Topology of the main nephron segments and sites of action of hormones controlling sodium transport. Schematic representation of a nephron with its successive portions: 1) glomerulus; PCT, proximal convoluted tubule; PST, proximal straight tubule; 2) thin descending limb of Henle's loop; 3) thin ascending limb; MTAL, medullary thick ascending limb of Henle's loop; CTAL, cortical thick ascending limb; 4) macula densa; 5) distal convoluted tubule; 6) connecting duct; CCD, cortical collecting duct; OMCD, outer medullary collecting duct; IMCD, inner medullary collecting duct. For the three structures analyzed in this review (proximal tubule, thick ascending limb of Henle's loop, and collecting duct), we mentioned the main hormones or factors that stimulate (→) and inhibit (—) sodium reabsorption: ANG II, angiotensin II (low and high referring to pico- and micromolar concentrations); adr, adrenergic agonists; AVP, arginine vasopressin; PTH, parathyroid hormone; GC, glucocorticoids; MC, mineralocorticoids; PGE_2 , prostaglandin E_2 ; ET, endothelin; ANP/Urod, atrial natriuretic peptide and urodilatin; PAF, platelet-activating factor; BK, bradykinin.

ably increase the membrane surface area available for transport. Intercellular cell junctions are shallow, and the epithelium is leaky. The proximal tubule is usually subdivided in three successive portions on a morphological basis: S_1 includes the initial and mid proximal convoluted tubule (PCT), S_2 includes the late PCT and the cortical portion of the proximal straight tubule (PST), and S_3 consists of the outer medullary PST. In most species but rat, the cell size, the density of apical microvilli, and the height of brush border and basolateral infoldings decrease from S_1 to S_3 , and along with these morphological

changes, the transport capacity of the proximal tubule also decreases from S_1 to S_3 .

The thin segments of the loop of Henle extend from the end of PST up to the junction with thick ascending limbs. Despite their importance for urine concentration by a countercurrent mechanism, they are exclusively the site of passive solute and fluid exchanges. Accordingly, their Na^+-K^+ -ATPase activity is very low (see below), and therefore, they are not considered in the following sections.

The thick ascending limb of Henle's loop (TAL) ex-

tends from the junction between the inner and outer medulla (where the thin segments end) up to the macula densa, or a few micrometers beyond, in the superficial cortex. It therefore includes a medullary and a cortical portion (MTAL and CTAL, respectively). On the basis of morphological criteria, TAL appears as made of a single type of cell that displays deep basolateral membrane infoldings surrounding numerous mitochondria. Apical membrane forms only few and short microvilli, and the junctional complexes are numerous and of the shallow type. Functionally these intercellular junctions are permeable to solutes but highly impermeable to water.

The distal convoluted and connecting tubules (DCT and CNT, respectively) complex, which extends from the macula densa to the first branching with another tubule, represents an heterogeneous portion from morphological, functional, and biochemical points of view. It consists of three cell types (DCT cells, connecting cells, and intercalated cells), the distribution of which along the DCT and CNT varies with species. In most species, however, the three cell types are present along most of the length of this nephron portion. Despite the functional and pharmacological importance of the DCT/CNT segments, in particular for calcium reabsorption and as the site of action of thiazide diuretics, their shortness and their cellular heterogeneity have precluded the determination of the molecular mechanism underlying the regulation of their transport properties. Therefore, this regulation is not discussed in the following sections.

Collecting ducts constitute the last segment of the nephron. They extend throughout the kidney, from the outermost cortex to the tip of the papilla, and therefore, they encounter surroundings of different compositions. On the basis of topographical criteria, the collecting duct is usually subdivided into three successive portions: the cortical collecting duct (CCD), the outer medullary collecting duct (OMCD), which is itself subdivided into outer stripe and inner stripe subsegments (OMCD_o and OMCD_i, respectively), and the inner medullary collecting duct (IMCD) also subdivided into three subsegments of equal length (IMCD₁, IMCD₂, and IMCD₃). The CCD and OMCD are made of two distinct cell types, namely principal, or light, cells (accounting for 60–65% of whole cells) and intercalated, or dark, cells (accounting for the remaining 35–40% cells). Intercalated cells are further subdivided into two subtypes called type A and type B intercalated cells (or α - and β -cells). Principal cells are characterized by a deeply invaginated basolateral membrane, the infoldings of which are closely associated with mitochondria, and a rather smooth apical membrane with few blunt microvilli and a single central cilium. Intercalated cells are characterized by a great number of mitochondria. Type A cells display extensive apical microvillae, numerous subapical tubulovesicular structures, and a rather nonextensive basolateral membrane. In contrast, type B

cells display fewer apical microvillae, the tubulovesicular structures are scattered throughout the cell, and the basolateral membrane is extensive. In fact, these are archetypal descriptions of types A and B intercalated cells, as one can distinguish intermediate subtypes of intercalated cells featuring only a few of those structural properties: intercalated cells can evolve from one phenotype to the other in response to different stimuli, and intermediate subtypes may correspond to evolving cells (8). Under normal conditions, there is an axial gradient in the relative proportion of the two subtypes of intercalated cells along the CCD and OMCD: type B cells are preponderant in the most cortical portion of the collecting duct (25–28% B cells vs. 10–12% A cells), whereas they almost disappear at the transition between OMCD_o and OMCD_i.

The OMCD_i and IMCD₁ consist of principal cells and type A intercalated cells. The proportions of intercalated cells decrease from 35–40% at the transition between OMCD_o and OMCD_i to 10% at the IMCD₁-IMCD₂ transition. The morphology of principal cells also varies from the most cortical regions of CCD down to the innermost region of IMCD₁. The most prominent aspect of axial changes is the decrease in size of the basolateral membrane and in the density of intracellular organelles, which correlates with a decrease in transport capacity.

IMCD₂ and IMCD₃ are made of IMCD cells that appear structurally homogeneous, even though there might be several functionally distinct subtypes of IMCD cells.

2. Methods used to study Na⁺-K⁺-ATPase in kidney tubules

Given this axial heterogeneity of nephrons, understanding the precise contribution of Na⁺-K⁺-ATPase to tubular cation transport has required the development of techniques allowing its study at the level of well-characterized nephron segments. Because this approach has obvious limitations, we thought it of interest to briefly discuss the advantages and limits of the methods presently available.

Although early approaches were based on isolation of well-defined portions of renal tubule from freeze-dried kidney sections (718), all the techniques presently used apply to nephron segments microdissected from fresh tissue. Moderate hydrolysis of kidney interstitium with collagenase allows the isolation of large numbers of samples from all the nephron subsegments. The main limitation of this approach results from the small size of microdissected samples: a 1-mm-long nephron segment accounts for ~300–400 cells, 100–250 ng of proteins, 3–5 ng RNAs, and 60–100 pg poly(A) RNAs. Nonetheless, techniques are now available for quantifying the enzymatic and transport activity of Na⁺-K⁺-ATPase, the number of catalytic units, as well as the amount of protein and

of mRNA coding its different subunits at the level of single or homogeneous populations of nephron segments.

The enzymatic (ATP-hydrolytic) activity of $\text{Na}^+\text{-K}^+$ -ATPase can be measured at the level of single nephron segments by monitoring the rate of hydrolysis of exogenous ATP. The amplification factor required by the small size of the sample is provided either by using radioactive ATP (224) or by enzymatically coupling the production of ADP to the generation of a fluorescent metabolite (323, 633). Whatever the method used, the assay needs to be carried out on broken or permeabilized cells to permit the access of exogenous ATP to intracellular catalytic sites. The $\text{Na}^+\text{-K}^+$ -ATPase activity should be discriminated from other ATPase activities present in the nephron segments on the basis of its sodium and potassium dependence rather than its sensitivity to ouabain, since this drug may inhibit other ATPases (nongastric $\text{H}^+\text{-K}^+$ -ATPase) potentially present in the tubular sample. Alternatively, it is possible to use specific inhibitors of these ouabain-sensitive $\text{H}^+\text{-K}^+$ -ATPases (such as Sch 28080) to circumvent this contamination. Measurement of $\text{Na}^+\text{-K}^+$ -ATPase activity allows us to define and control the concentration of substrates during the assay, and thereby to determine the kinetical parameters of the enzyme, in particular its V_{\max} and $K_{0.5}$ for cations. As a counterpart, permeabilization of cell membranes entails the loss of regulatory parameters such as the transmembrane voltage, the membrane limitation to potassium recycling, or intracellular diffusible regulatory molecules. Also, $\text{Na}^+\text{-K}^+$ -ATPase activity does not inform about the *in vivo* pumping activity of $\text{Na}^+\text{-K}^+$ -ATPase, as the latter is highly dependent on intracellular sodium concentration.

In nonpermeabilized nephron segments, the activity of $\text{Na}^+\text{-K}^+$ -ATPase can be determined through its pumping capacity by measuring ouabain-sensitive rubidium uptake under initial rate conditions (163). Although this method is widely used in a great variety of tissues, it has two main pitfalls. The first one, which results from the nonspecificity of ouabain (see above), can be easily circumvented by using Sch 28080 in the assay to abolish the activity of ouabain-sensitive $\text{H}^+\text{-K}^+$ -ATPases. More importantly, ouabain-sensitive rubidium uptake is calculated as the difference between the rates of intracellular accumulation of rubidium measured in the absence and presence of saturating concentrations of ouabain, respectively. Such a calculation implies that $\text{Na}^+\text{-K}^+$ -ATPase-independent rubidium intake is similar in the absence and presence of ouabain. This is very unlikely, since inhibition of $\text{Na}^+\text{-K}^+$ -ATPase by ouabain abolishes the concentration gradient of rubidium across cell membranes and may thus increase the driving force for passive, $\text{Na}^+\text{-K}^+$ -ATPase-independent rubidium movements. Thus ouabain-insensitive rubidium uptake probably overestimates $\text{Na}^+\text{-K}^+$ -ATPase-independent rubidium uptake, and therefore, ouabain-sensitive rubidium uptake underestimates Na^+

K^+ -ATPase activity. However, because ouabain-insensitive rubidium uptake in renal tubule cells represents a minute fraction of the total rubidium uptake (163), this underestimation might be limited. An additional technical difficulty of this measurement in isolated nephron segments results from their huge $\text{Na}^+\text{-K}^+$ -ATPase activity: the kinetics of rubidium uptake is fast, and measurement under initial rate conditions must be performed within 0.5–1 min. Changes in rubidium uptake reflect alterations of the V_{\max} of the pump and/or changes of its efficiency brought about by changes in intracellular concentration of sodium and/or in affinity for sodium.

Despite its importance, the regulation of the pump affinity for intracellular sodium concentration remains very difficult to evaluate in intact nephron segments, since this requires the precise clamping and monitoring of intracellular sodium concentration. An elegant method has been proposed (97) in which the rate of sodium efflux is monitored as a function of time in nephron segments initially loaded with $^{22}\text{Na}^+$ by cold exposure in a potassium-free medium. Because the apical entry of sodium is blocked during the efflux study, i.e., the specific radioactivity of $^{22}\text{Na}^+$ remains constant, at any time one can calculate the sodium pumping rate of $\text{Na}^+\text{-K}^+$ -ATPase from the rate of appearance of $^{22}\text{Na}^+$ in the superfusate and the intracellular concentration of sodium from the remaining quantity of $^{22}\text{Na}^+$. This allows the correlation of $\text{Na}^+\text{-K}^+$ -ATPase functional activity in intact cells to intracellular sodium concentration. Unfortunately, this method has not been given the large use it deserves.

To elucidate whether changes in $\text{Na}^+\text{-K}^+$ -ATPase activity are due to activation of preexisting units or induction of new ones, it is possible to quantify these units as well as the mRNAs encoding them. Quantification of $\text{Na}^+\text{-K}^+$ -ATPase units is feasible on single nephron segments by measuring the specific binding of [^3H]ouabain under saturating conditions (248). Contamination by ouabain-sensitive $\text{H}^+\text{-K}^+$ -ATPase can be prevented by Sch 28080, which is a competitor of ouabain (119). Unfortunately, this method is hardly applicable to the rat because its kidney $\text{Na}^+\text{-K}^+$ -ATPase displays a low affinity for ouabain. Alternatively, relative quantification can be made by Western analysis with specific antibodies against the different subunits of $\text{Na}^+\text{-K}^+$ -ATPase (547). Although it requires pooling several tens of nephron segments in each sample, this approach is now routinely used. It is even possible to discriminate between plasma membrane pump and intracellular pools by biotinylation of membrane proteins and streptavidin precipitation before Western blotting analysis (136).

Finally, the transcripts of $\text{Na}^+\text{-K}^+$ -ATPase subunits can be quantitated by quantitative RT-PCR (118, 818). Given the sensitivity of PCR and the abundance of renal $\text{Na}^+\text{-K}^+$ -ATPase, this is feasible on very short portions of nephron (0.1 mm).

3. Distribution and properties of Na⁺-K⁺-ATPase along the nephron

Measurements of Na⁺-K⁺-ATPase activity in microdissected segments of nephrons from different mammalian species have revealed the heterogeneity of distribution of this pump along the nephron (323, 454). In all species studied as yet, Na⁺-K⁺-ATPase activity is high in the TAL and DCT, intermediate in the proximal tubule (PCT and PST), relatively low in the collecting duct, and vanishingly low in the thin segments of Henle's loop. This distribution profile is paralleled by the number of Na⁺-K⁺-ATPase units determined either by [³H]ouabain binding ($\alpha\beta$ -complexes) (248) or by Western blotting (α - and β -subunits) (547).

From the number of specific [³H]ouabain binding sites and the V_{\max} of Na⁺-K⁺-ATPase catalytic activity, one can calculate a molecular activity of $\sim 2,000$ cycles \cdot ouabain binding sites⁻¹ \cdot min⁻¹ in all the nephron segments (248). This molecular activity is much lower than the 10,000 cycles \cdot ouabain binding sites⁻¹ \cdot min⁻¹ reported for the Na⁺-K⁺-ATPase purified from kidney (439), suggesting the presence of cellular components that downregulate the enzyme activity in the cell.

With the assumption of a 1 ATP:2 K⁺ stoichiometry (see sect. II A1), comparison of Na⁺-K⁺-ATPase activity and ouabain-sensitive rubidium uptake indicates that in intact tubular cells the pump is working at 20–30% of its maximum rate, which is consistent with measurements of intracellular sodium concentration and sodium affinity (163).

Despite technique availability, only one report, on rat OMCD, provides absolute quantification of Na⁺-K⁺-ATPase subunits mRNA expression (118). In this study, mRNAs for the β_1 -subunit were greater than threefold more abundant than those coding for α_1 -subunit, suggesting that the transcription of α_1 -subunit mRNAs is the rate-limiting step in the regulation of Na⁺-K⁺-ATPase expression. Absolute quantification of mRNAs and of [³H]ouabain binding sites indicated that there are 24,000 Na⁺-K⁺-ATPase units per α_1 -subunit mRNA, which suggests either a high efficiency of translation or a slow turnover rate of the protein.

The functional properties of Na⁺-K⁺-ATPase vary along the rabbit nephron: compared with proximal tubules and TAL, the collecting ducts display a higher affinity for ouabain (220) and for sodium (48). In addition, Na⁺-K⁺-ATPase activity is inhibited by a specific anti- α_3 -isoform monoclonal antibody in collecting ducts and by an anti- α_1 -isoform monoclonal antibody in proximal tubules and thick ascending limbs (46). In the rat nephron, two functional forms of Na⁺-K⁺-ATPase displaying different sensitivities to ouabain and to the anti- α_1 - and anti- α_3 -antibodies are coexpressed in each nephron segment (275).

However, despite some controversy (6, 176), most studies (162, 821) failed to demonstrate the presence of α_2 - or α_3 -isoforms in the rat nephron (α_4 has not been looked but seems restricted to testis). The $\alpha_1\beta_1$ heterodimer is likely the exclusive Na⁺-K⁺-ATPase complex expressed in kidney tubules, and the functional axial heterogeneity of kidney Na⁺-K⁺-ATPase might result from cell-specific regulation. An interesting possibility would be that coexpression of the γ -subunits might be responsible for the observed differences (at least for sodium affinity).

III. HORMONE SIGNALING ALONG THE NEPHRON

A. General Mechanisms of Hormone Signaling

1. Receptors coupled to G proteins and adenylyl cyclase

Many peptide hormones, catecholamines, eicosanoids, nucleotides, and calcium ions act through binding to plasma membrane receptors coupled with specific multimeric G proteins. These G proteins are constituted by the association of a $G\alpha$ -subunit with a $G\beta$ - and a $G\gamma$ -subunit. Binding of a ligand to its cognate receptor induces a conformational change that is transmitted to the G protein, causing GDP release and GTP binding by the $G\alpha$ -subunit, and promoting its dissociation from $G\beta\gamma$ -subunit complex. The free $G\alpha$ -subunit and $G\beta\gamma$ -heterodimer each activate target effectors. The reaction is turned off by GTP hydrolysis and reassociation of the G protein subunits. Among the multiple targets of G protein subunits, adenylyl cyclase and phospholipase C- β couple the binding of an agonist to its receptor with the modulation of PKA and PKC activity, respectively.

In the kidney, peptide hormones, e.g., parathyroid hormone and vasopressin, and catecholamines, e.g., epinephrine and dopamine, bind to G protein-coupled receptors and lead to the activation of adenylyl cyclases. Adenylyl cyclases are stimulated by $G\alpha_s$ (795) but are either further stimulated (322, 793) or inhibited by $G\beta\gamma$ (453, 753, 796) according to their subtypes (Fig. 4). Other mediators such as angiotensin II or norepinephrine can decrease the generation of cellular cAMP through an inhibition of adenylyl cyclases by $G\alpha_i$ subunits (Fig. 4).

Stimulation of adenylyl cyclase increases the intracellular concentration of cAMP leading to the activation of cAMP-dependent protein kinase (PKA) (Fig. 4). PKA is a heterotetramer consisting of a dimer of regulatory (R) subunits that maintains two catalytic (C) subunits in an inactive state. Upon binding of cAMP to the R subunits, active C subunits are released and can phosphorylate substrates. PKA phosphorylates serine or threonine resi-

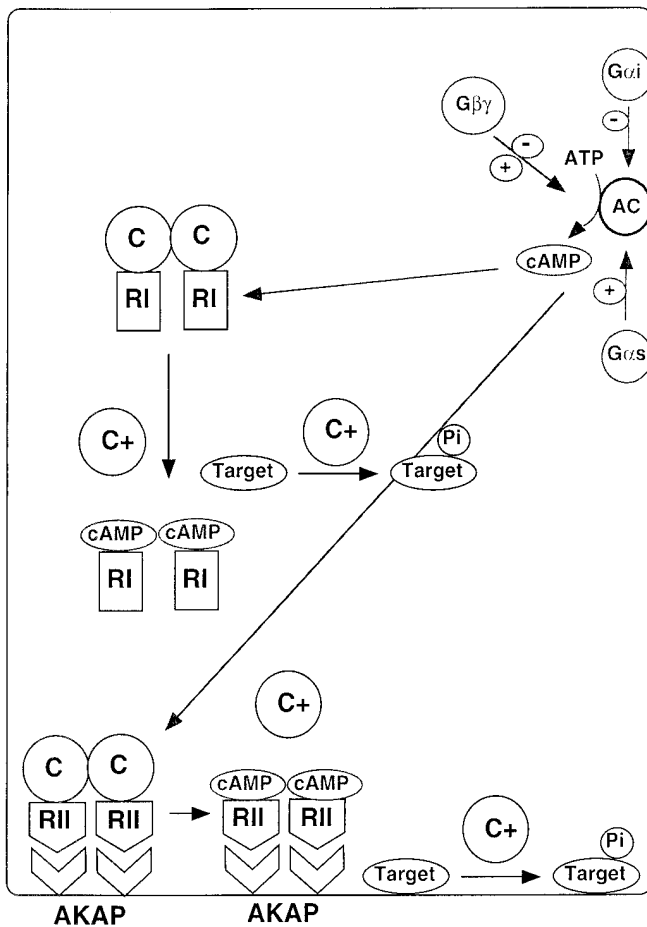


FIG. 4. Schematic overview of the cAMP-PKA signaling pathway. Activation of cell-surface serpentine receptors (not shown) induces the dissociation of heterotrimeric G proteins into free α -subunits and $\beta\gamma$ -subunits that may either activate or inhibit adenylyl cyclases (AC). The cAMP generated by adenylyl cyclases binds to the regulatory subunits (RI or RII) of PKA, allowing the dissociation of the catalytic subunits (C). The free catalytic subunits (C+) phosphorylate target membrane or cytosolic proteins. Subcellular targeting of PKA is mediated by interactions between A-kinase anchoring proteins (AKAPs) and the RII isoform of the regulatory subunit. Arrows indicate the direction of the signaling cascade and the resulting stimulatory (+) or inhibitory (-) effect on their targets.

dues located in consensus sites exhibiting the Arg-Arg-Xaa-Ser/Thr or Lys-Arg-Xaa-Xaa-Ser/Thr motifs. To date, three isoforms of C subunit (α , β , and γ) and two isoforms of R subunits (RI and RII) have been identified in mammals. Some level of specificity of the PKA signal relies on the different affinities for substrates of C subunit isoforms as well as their binding properties to regulatory subunits (320). In addition, the RI and RII subunits exhibit different cAMP binding affinities and differential subcellular localization (203, 797). The type I PKA holoenzyme (containing RI) is predominantly cytoplasmic, whereas the type II PKA holoenzyme (containing RII) is mostly targeted to several subcellular compartments through binding to A-kinase anchoring proteins (AKAP) (203), conferring a fur-

ther level of specificity. It is interesting to mention that some AKAP, e.g., AKAP79, can act as scaffolding proteins and also bind PKC isozymes (469) and protein phosphatase 2B (179).

Recent pieces of evidence suggest the presence of alternate PKA-independent cAMP signaling pathways. Two intracellular cAMP-binding proteins were cloned and shown to act as guanine nucleotide exchange factors for the small G protein Rap-1 (207, 457). Thus cAMP can activate the Rap-1 pathway independently of PKA activation. Interestingly, one of these two cAMP binding proteins (Epac or cAMP-GEF-I) is expressed at very high levels in the kidney (207, 457). Further studies are needed to identify the functional targets of the cAMP/Epac/Rap-1 pathway, in particular in kidney.

Termination of the signal is accounted for by activation of compartmentalized phosphodiesterases (169, 729) and desensitization of adenylyl cyclases and receptors (225, 354, 434, 516, 863).

2. Receptors coupled to G proteins and phospholipase C

In addition to the modulation of adenylyl cyclase activity, peptide hormones, e.g., parathyroid hormone and angiotensin II, and catecholamines, e.g., norepinephrine and dopamine, may trigger G protein-mediated activation of phospholipase C (PLC)- β and subsequent PKC activation.

PKCs constitute a superfamily of protein kinases comprising 11 isoforms. These isoforms are currently grouped into three families (Fig. 5) according to their sensitivities to physiological and pharmacological activators (511, 553). The most studied group is the conventional PKCs, which includes the α -, β I-, β II-, and γ -isoforms. PKC- β I and - β II isoforms are generated by alternative splicing of the same gene. Conventional PKCs are activated by phosphatidylserine (PS) in a diacylglycerol (DAG)/phorbol esters and calcium-dependent manner. DAG and phorbol esters decrease the calcium concentration required for activation and dramatically increase PKC sensitivity to PS. PKCs δ , ϵ , η , and θ are members of the novel PKC family. These isoforms are calcium insensitive but remain activated by DAG and phorbol esters in the presence of PS. Finally, the members of the atypical PKC family, PKC- λ and PKC- ζ , are insensitive to calcium, DAG, and phorbol esters, and their mode of activation is not clearly established. PKCs phosphorylate serine or threonine residues located in consensus sites exhibiting the Ser/Thr-Xaa-Lys/Arg motif. A first level of specificity is conferred by the cell-specific expression of PKC isoforms. For instance, the kidney expresses high levels of the classical PKC- α but, in contrast to brain, β - and γ -isoforms are undetectable (451, 612). The novel PKC- δ and - ϵ as well as the atypical PKC- ζ are also ex-

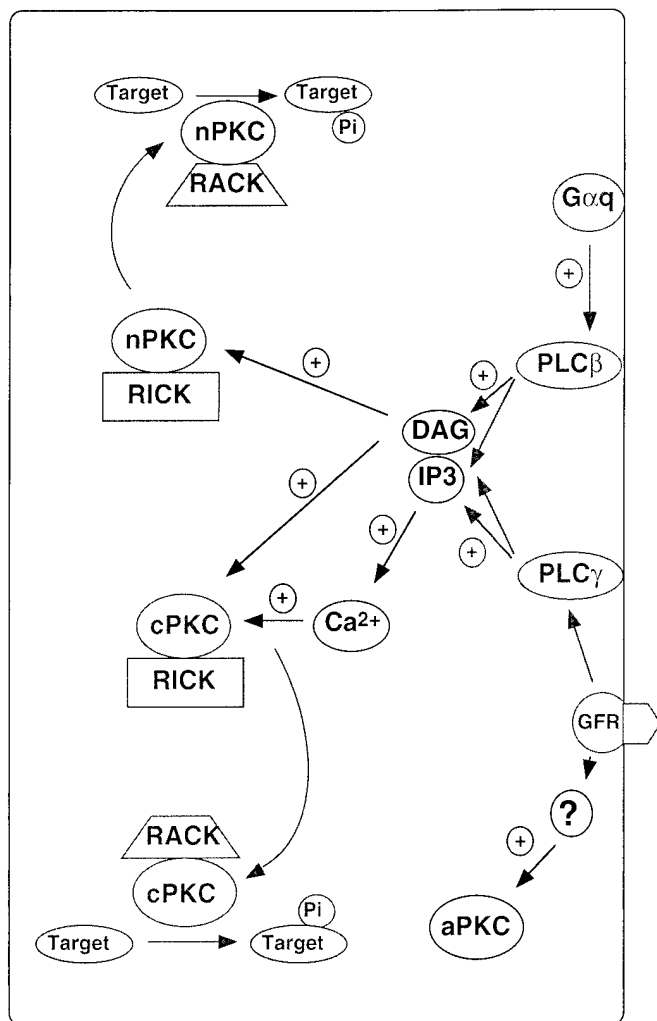


FIG. 5. Schematic overview of the PKC signaling pathway. Activation of cell-surface serpentine receptors (not shown) induces the dissociation of heterotrimeric G proteins into free α -subunits and $\beta\gamma$ -subunits that may activate phospholipase C- β (PLC- β). Alternatively, growth factor receptors (GFRs) may be coupled to the PLC- γ isoform. PLCs generate diacylglycerols (DAG) and inositol trisphosphate (IP₃) that increases cytosolic calcium. The classical isoforms of PKC (cPKC) are activated by calcium and DAG, the novel isoforms of PKC (nPKC) are calcium insensitive but DAG activated, whereas the atypical PKC (aPKC) are both calcium and DAG insensitive. The current model for PKC targeting to specific subcellular compartments assumes that once activated, PKC isozymes translocate from receptors for inactive C-kinase (RICK) to receptors for activated C-kinase (RACK). Arrows indicate the direction of the signaling cascade and the resulting stimulatory (+) effect on their targets.

pressed in the kidney cortex and medulla (451, 612). A second level of specificity is conferred by the differential pattern of PKC isoform activation in response to an agonist. In the kidney PCT, PKC- α , - δ , and - ϵ are activated in response to phorbol esters, whereas only PKC- α and - ϵ are activated in response to angiotensin II (451). The identification of PKC isozyme-specific anchoring proteins provides further specificity to the signal by targeting ei-

ther active or inactive PKC to various subcellular compartments (505, 558).

3. Tyrosine kinase receptors

Insulin and many growth factors, e.g., IGF-I, EGF, and platelet-derived growth factor (PDGF), share the property to bind to receptors exhibiting an intrinsic tyrosine kinase activity (Fig. 6). Binding of the ligand to the receptor activates its tyrosine kinase activity and induces receptor autophosphorylation as well as phosphorylation of substrate proteins on tyrosine residues (458). It is generally admitted that growth factor receptors form homodimers either in the absence of ligand, e.g., PDGF

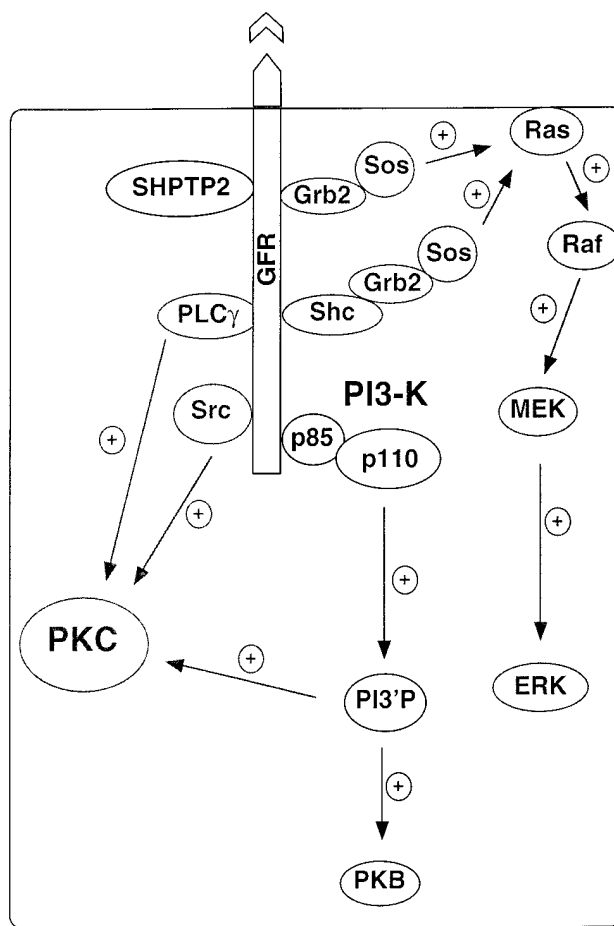


FIG. 6. Schematic overview of growth factor receptor signaling. Once activated by ligand binding, GFRs dimerize and undergo autophosphorylation on specific tyrosine residues. Phosphotyrosines generate binding sites for SH2 and PTB domains. For instance, phosphorylated receptors can bind PLC- γ , the nonreceptor tyrosine kinase Src, the tyrosine phosphatase SHPTP2, the p85 subunit of the phosphatidylinositol 3-kinase (PI 3-K), and the adaptor proteins Grb2 and Shc. PLC- γ , Src, and PI 3-K link GFR to the PKC pathway, PI 3-K links GFR to the protein kinase B (PKB) pathway, and Grb2 links GFR, directly or through Shc binding, to Sos which activates Ras leading to Raf, MEK, and ERK activation. Arrows indicate the direction of the signaling cascade and the resulting stimulatory (+) effect on their targets.

receptor, or after ligand binding, e.g., EGF receptor, and that autophosphorylation results from the phosphorylation of one receptor monomer by the other (382). Because it is well established for EGF and PDGF receptors, tyrosine phosphorylation of the receptor creates specific binding sites for SH2 or PTB domains contained in many proteins involved in the subsequent steps of the signaling cascade (180, 455, 458, 499). These interactions, together with growth factor receptor aggregation, induce the focal formation of signaling complexes. In the insulin signaling pathway, tyrosine phosphorylation of insulin receptor substrate 1 (IRS-1) instead of the insulin receptor itself mediates the binding of signaling intermediates (875, 876). Receptor tyrosine kinases and IRS-1 can be associated with nonreceptor tyrosine kinases of the Src family (783, 824), phospholipase C- γ (474, 913), the regulatory p85 subunit of phosphatidylinositol 3-kinase (PIK) (35, 258, 452, 474), the adaptor proteins Grb2 (582, 857) or Shc (93, 357), and the tyrosine phosphatase SHPTP-2 (74, 488, 905). These protein-protein interactions may link receptor protein kinases to 1) a second round of tyrosine phosphorylation of specific target proteins by nonreceptor tyrosine kinases, e.g., c-Src (458, 614, 761); 2) PKC activation through activation of PLC- γ and PIK (205, 458, 568), as well as isoform-specific tyrosine phosphorylation, e.g., PKC- δ (205, 477) and PKC- θ (677); 3) PIK-dependent generation of phosphatidylinositol 3-products (132, 661) and activation of protein kinase B (297); and 4) Ras-dependent activation of extracellular regulated kinases (ERK) secondary to the binding of Sos (a guanine nucleotide exchange factor for Ras) to Grb2 and Shc (521, 650, 666) and activation of Raf-1 kinase by active Ras (877).

Several mechanisms participate in the termination of the signal: dephosphorylation of receptors and signaling complexes by tyrosine phosphatases (174, 263, 777, 858), serine-threonine phosphorylation of receptors (265, 569, 807) and docking proteins, e.g., IRS-1 (626, 794), and internalization of activated receptors through clathrin-coated pits (133, 437, 754, 763, 883).

4. Nuclear receptors

Traditionally, steroids, thyroid hormone, vitamins A- and D-derived hormones, and some fatty acids are thought to primarily alter the transcription of specific mRNAs and protein synthesis. This mechanism of action was initially proposed on the basis of the sensitivity of the functional actions of these agents to inhibitors of transcription and translation such as actinomycin D and cycloheximide (644). It also accounts for the latency and slow development of the cells responses to these agents. Later, this hypothesis was confirmed by cloning the cDNAs encoding intracellular receptors for these factors (61, 256, 312). Indeed, steroids and related agents bind to a superfamily of intracellular receptors that interact with

regulatory elements of DNA, and thereby control the transcription of specific genes.

Steroid-thyroid-retinoid receptors consist of three major distinct domains: an immunogenic domain, a DNA binding domain, and a hormone binding domain. The DNA binding domain, which is the best conserved among different steroid receptors, consists of ~ 70 amino acids and contains two zinc finger structures (in which cysteines are coordinated by zinc), each followed by an α -helix domain. These structures are important for recognition and binding to DNA and for dimerization of the receptor (256). The DNA binding domain recognizes specific target sequences on the DNA, called hormone response elements (HREs), which are very similar for the different receptors. For example, glucocorticoid, progesterone, androgen, and mineralocorticoid receptors recognize the same glucocorticoid response elements (GREs) with the consensus sequence 5'-NGGTACANNNTGT-TCTN-3'. The hormone binding domain, a well-conserved region among distinct steroid receptors, consists of 250 amino acids forming an hydrophobic pocket that participates not only to hormone binding but also to the dimerization of the receptor, its nuclear translocation, and the resulting activation of the transcription (264). This region contains also the binding site for the 90-kDa heat shock protein (HSP90), a chaperone associated with the unbound receptor that facilitates the hormone response (636). The NH₂-terminal domain is highly variable between steroids and species. Its varies from 25 to 602 amino acids for the vitamin D and the mineralocorticoid receptors, respectively. This hypervariable region contains the epitopes of most antireceptor antibodies and is therefore called the immunogenic domain. Along with the hormone binding domain, it displays transactivation activity.

Circulating steroids are supposed to reach their intracellular receptors by passive diffusion across the cell membrane, although active or facilitated transport mechanisms have been proposed (12, 106, 827). Hormone binding activates the receptor and confers it the ability to interact with DNA. In case of the mineralocorticoid receptor, activation is associated with the release of HSP90 (658). Finally, receptor/DNA interaction induces the activation/repression of several genes whose protein products modify the functional properties of target cells. From a kinetic point of view, functional alterations are usually classified as early and late responses, but the overall response should better be considered as a continuous cascade of induction/repression of several genes encoding proteins, with various maturation and life span, acting either as transcription factors or as peripheral effectors accounting for the phenotypic changes.

In addition to this traditional mode of action of steroids, several other mechanisms may be involved. First, genomic effect via a direct interaction between the ste-

roids and nuclear DNA has been described (385, 825). Second, several pieces of evidence suggest nongenomic response via transduction through membrane receptors (reviewed in Ref. 862). This would account, for example, for very rapid responses such as the quasi-immediate inhibition of corticotropin release induced by abrupt increase in the blood concentration of cortisol. This mechanism is supported by ligand-binding experiments that revealed high-affinity membrane binding sites for several steroids (610, 861). However, the molecular characterization of these receptors is not yet available. Finally, steroid receptors may trigger cell response by protein-protein interaction (548), without binding to DNA. For example, glucocorticoid receptors have been shown to modulate AP-1- and NF κ B-induced transcription by direct protein-protein interaction (313, 634). In support of this mechanism, it was recently shown that transgenesis expression of a mutant glucocorticoid receptor unable to bind DNA allows survival of the mice, whereas the deletion of glucocorticoid gene is lethal (665).

B. Hormone Receptors and Signaling Pathways Along the Nephron

The following discussion on hormone receptors and cognate signaling pathways is restricted to the three renal target selected, i.e., the proximal tubule, TAL, and collecting duct principal cell.

1. Parathyroid hormone

In the late 1960s, the pioneering work of Chase and Aurbach showed that *in vivo* infusion of parathyroid hormone (PTH) increases urinary excretion of cAMP (154) and that *in vitro* addition of PTH stimulates adenylyl cyclase activity in kidney cortex homogenates (155). A few years later, the precise mapping of PTH-responsive nephron segments was obtained by measuring the *in vitro* effect of PTH on adenylyl cyclase activity in microdissected nephron segments (416). PTH-sensitive adenylyl cyclase was evidenced in PCT, PST, and CTAL from rat, rabbit, and human kidney (142, 143, 566) and in MTAL from some but not all species (143).

Although PTH receptors may be coupled to transducers other than adenylyl cyclase (see below), further attempts to localize renal PTH receptors that were not based on stimulation of adenylyl cyclase confirmed this distribution profile. The presence of PTH receptors in proximal tubules and CTAL was found by ligand binding (311, 682) and by localization of the mRNAs encoding the cloned PTH/PTH-related peptide (PTHrP) receptor (490, 674, 914). In contrast, the PTH-2 receptor cloned from brain is not expressed in the kidney (70, 833).

In rat proximal tubules, PTH receptors are expressed at both the apical and basolateral plasma membrane (311,

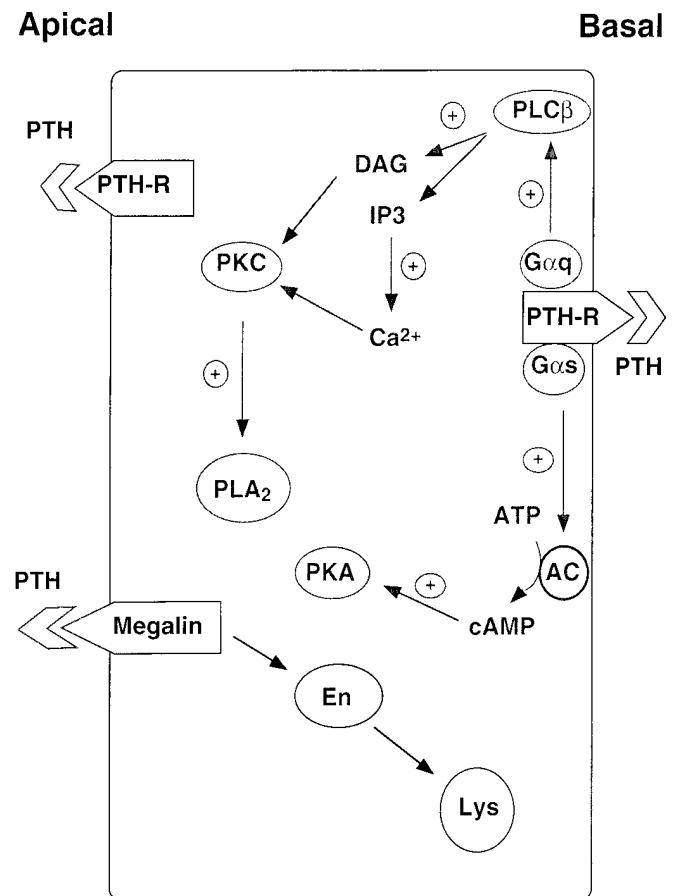


FIG. 7. PTH signaling in proximal tubule cells. Binding of PTH to basolateral PTH receptor (PTH-R) activates G α_s and G α_q that couple to adenylyl cyclase (AC) and PLC- β , respectively. Activated PLC generates DAG and IP $_3$, which increases cytosolic calcium. Calcium and/or DAG activate PKC isozymes which in turn may activate phospholipase A $_2$ (PLA $_2$). AC generates cAMP, which activates PKA. On the apical side, PTH may also bind PTH-R but might preferentially bind megalin, which undergoes endocytosis (En) leading to PTH degradation in lysosomes (Ly). Arrows indicate the direction of the signaling cascade and the resulting stimulatory (+) effect on their targets.

388) (Fig. 7). However, adenylyl cyclase is much better stimulated by basolateral than apical PTH (311), in agreement with *in situ* microperfusion study of the rat PCT showing a small effect of luminal with respect to basolateral PTH (59). Poorly efficient coupling between apical PTH binding and adenylyl cyclase is consistent with the recent demonstration of specific binding of full-length PTH and its biologically active NH $_2$ -terminal fragments to megalin (388). Megalin is a proximal tubule multifunctional endocytic receptor (172) that likely accounts for the largest part of specific PTH binding to apical membranes of proximal tubule cells (388). Thus biological effects of PTH on the proximal tubule are essentially mediated by basolateral PTH/PTHrP receptors (59), whereas apical megalin (Fig. 7) may account for the cel-

lular uptake and subsequent lysosomal degradation of filtered PTH (388).

In proximal tubules, PTH not only activates adenylyl cyclase but also PLC and PKC (229) (Fig. 7). Indeed, PTH dose-dependently stimulated inositol trisphosphate (IP_3) and DAG production and/or increased cytosolic calcium in rat PCT suspensions (288, 642, 792) as well as in primary cultures of dog proximal tubules and OK cells (400, 401).

The coupling of the PTH/PTHrP receptor to both adenylyl cyclase and PLC is further attested by its link with both $G\alpha_s$ (that activates adenylyl cyclase) and $G\alpha_{q/11}$ (that activates PLC) in osteoblast-like cells and transfected human embryonic kidney cells (724). This dual coupling of PTH/PTHrP receptor is dependent on different structural determinants of PTH, since various NH_2 -terminal fragments of PTH activate PKC either alone or together with PKA in transfected AP-1 cells (34).

In addition to PKA and PKC, PTH also activates phospholipase A_2 (PLA_2) in rat PCT (208, 608, 672). The presence of a PTH-mediated control of mitogen-activated protein (MAP) kinases remains controversial (837, 838).

2. Dopamine

Dopamine binds to two pharmacologically distinct groups of receptors (556): D_1 -like receptors (formerly central D_1 and peripheral DA_1 receptors) and D_2 -like receptors (formerly central D_2 and peripheral DA_2 receptors). Each of these groups consists of molecularly distinct isoforms: two forms of D_1 -like receptors (called D_1 and D_5 receptors, or D_{1A} and D_{1B} receptors in rodents) and three forms of D_2 -like receptors (D_2 , D_3 , and D_4 receptors) have been cloned. Both D_1 -like and D_2 -like receptors are expressed in kidneys.

Expression of D_1 -like receptors was first demonstrated in PCT, PST, MTAL, CTAL, and CCD by autoradiography using specific ligands (271, 406, 462, 675, 790). Expression of the D_{1A} - D_1 receptor isoform was confirmed at mRNA and protein levels in rat proximal tubules (603, 604, 912), as well as in OK and LLC-PK₁ cells (448, 589), and in human CCD (603, 604, 617), whereas it was hardly detected in human and rat medulla (603, 604, 617). Expression of D_{1B} - D_5 receptor isoform remains to be demonstrated. D_1 -like receptors are expressed on both apical and basolateral membranes (271, 604) (Fig. 8).

D_2 -like binding sites (Fig. 8) were demonstrated in proximal tubules (271) and attributed to the D_2 and D_3 receptor isoforms (321, 605, 760). D_2 and D_3 receptor mRNAs were also detected in the rat outer medulla (321), but the D_3 receptor protein was not detected in the rat TAL (605). D_3 and D_4 receptors were also evidenced both at mRNA and protein levels in rat CCD (605, 782). In summary, the renal expression level of dopamine recep-

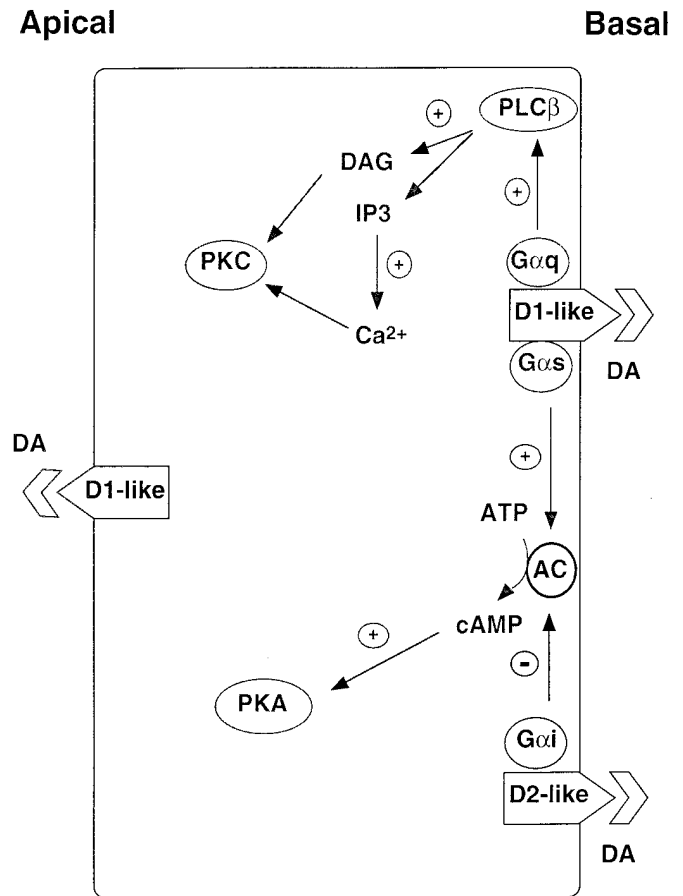


FIG. 8. Dopamine (DA) signaling in proximal tubule cells. Binding of DA to D_1 -like receptors expressed in both apical and basolateral membrane domains activates $G\alpha_s$ and $G\alpha_q$ that couple to AC and PLC- β , respectively. Activated PLC generates DAG and IP_3 , which increases cytosolic calcium. Calcium and/or DAG activate PKC isozymes. AC generates cAMP which activates protein kinase A (PKA). Binding of DA to D_2 -like receptors activates $G\alpha_i$ which inhibits AC. Arrows indicate the direction of the signaling cascade and the resulting stimulatory (+) or inhibitory (-) effect on their targets.

tors is high in proximal tubules, intermediate in CCD, and low in TAL.

It is generally assumed that dopamine D_1 -like and D_2 -like receptors are coupled to adenylyl cyclase activation through $G\alpha_s$ and inhibition through $G\alpha_i$, respectively (409, 441, 556). However, the D_1 receptor was shown to coprecipitate with $G\alpha_q$ (271), and its dual coupling to both $G\alpha_s$ and $G\alpha_{q/11}$ was demonstrated in basolateral membranes from rat proximal tubules (408). In this preparation, the dopamine D_1 receptor agonist fenoldopam induced a dose- and time-dependent binding of equivalent amounts of [35 S]GTP γ S to $G\alpha_s$ and to $G\alpha_{q/11}$. Coupling of D_1 -like receptors to $G\alpha_q$ may account for the reported activations of PLC- β , phosphoinositide breakdown, and PKC activation (448, 846, 921, 922) in suspensions of rat proximal tubules (Fig. 8). Activation of PLC and PKC likely accounts for dopamine-induced generation of ara-

chidonic acid reported in isolated rat PCTs (608). Fenoldopam also reduced the proportion of membrane-associated growth factor-activated PLC- γ in rat kidney cortex, but not in kidney medulla (921), suggesting that activation of D₁-like receptors reduced PLC- γ activity.

The membrane recruitment of various PKC subtypes in response to D₁-like agonists was studied in suspensions of rat proximal tubules obtained after *in vivo* infusion of drugs into the renal artery (915). Under these conditions, D₁-like agonists did not alter the cellular distribution of the classical PKC- α and atypical PKC- λ , whereas they increased the membrane abundance of the new PKC- θ and decreased that of the new PKC- δ and atypical PKC- ζ . In contrast to this latter finding, stimulation of PKC- ζ was suggested on the basis of its requirement for dopamine effect on sodium transport in OK cells (236). This discrepancy may rely on that dopamine binds to both D₁-like and D₂-like receptors and that activation of PKC- ζ might be dependent on the activation of both receptors subtypes, as shown previously for the effect of dopamine on Na⁺-K⁺-ATPase activity in guinea pig neostriatal neurons (84) and rat PCT (82).

Coupling between MAP kinases and dopamine receptors has been described in nonrenal tissues (525, 874, 930). However, this coupling remains to be established in renal epithelial cells.

3. Adrenergic receptors

Epinephrine, mainly synthesized by adrenal glands, reaches its renal targets through the blood circulation, whereas norepinephrine is mainly released locally by renal nerve endings. Epinephrine and norepinephrine bind to several classes of receptors that differ by their pharmacological and biological properties. These receptors, members of the G protein-coupled receptor superfamily, are classified as α_1 -, α_2 -, and β -receptors.

A) α_1 -ADRENERGIC RECEPTORS. Based on pharmacological properties, α_1 -adrenergic receptors were subdivided into α_{1A} - and α_{1B} -subtypes. Later, three molecular species of α_1 -adrenergic receptors were cloned (α_{1A} , α_{1B} , and α_{1D}) (216).

The presence of α_1 -adrenergic receptors in rat and human kidney cortex and outer medulla as well as in proximal tubules (Fig. 9) and MTALs was first evidenced by ligand binding studies (273, 274, 435, 545, 574, 831). Although the three α_1 -isoforms are expressed in proximal tubules (273, 506a, 830), the α_{1A} predominates (65%) in rat PCT (273), whereas in TAL, only the α_{1B} - and α_{1D} -isoforms are expressed (273, 830). The presence of α_1 -adrenergic receptors in collecting duct is more controversial: they were not detected in an initial study (830), whereas all three isoforms (α_{1A} , α_{1B} , and α_{1D}) were later found in rat CCDs (881).

α_1 -Adrenergic receptors couple predominantly to pertussis toxin-insensitive G $\alpha_{q/11}$ proteins (903) that, in

Apical

Basal

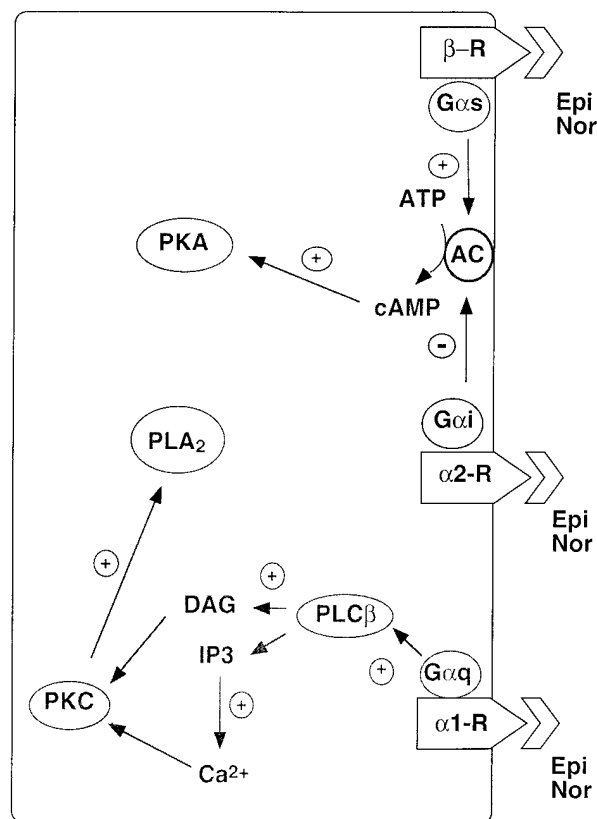


FIG. 9. Adrenergic agonists signaling in proximal tubule cells. Binding of norepinephrine (Nor) or epinephrine (Epi) to α_1 -adrenergic receptors (α_1 -R) leads to the activation of G α_q that couples PLC- β . Activated PLC generates DAG and IP₃, which increases cytosolic calcium. Calcium and/or DAG activate PKC isozymes, which in turn may activate PLA₂. α_2 -Adrenergic receptors (α_2 -R) are coupled to G α_i , which inhibits AC. β -Adrenergic receptors (β -R) are coupled to G α_s , which activates AC. The generation of cAMP by AC activates PKA. Arrows indicate the direction of the signaling cascade and the resulting stimulatory (+) or inhibitory (-) effect on their targets.

association with G $\beta\gamma$ (904), activate PLC- β (749, 921) and trigger the IP₃/DAG/PKC cascade (42, 907) (Fig. 9). In nonrenal cells, α_1 -adrenergic receptors can be coupled to 1) phospholipase D and phosphatidylcholine hydrolysis (42, 750), 2) PLA₂ activation and arachidonate generation (629, 873, 907), and 3) ERK activation (191, 204, 528), but there is currently no evidence for such coupling in renal epithelial cells.

B) α_2 -ADRENERGIC RECEPTORS. At least three isoforms of α_2 -adrenergic receptors (α_{2A} , α_{2B} , and α_{2C}) account for the pharmacologically defined α_2 -adrenergic receptors (216). The presence of α_2 -adrenergic receptor was first suggested in kidney cortex and PCT on the basis of the ability of epinephrine and of specific α_2 -receptor agonists to inhibit PTH-stimulated adenylyl cyclase *in vitro* and *in vivo* (829, 897, 898). Ligand binding studies confirmed this hypothesis in rat, guinea pig, and human kidney cortex

(575, 831, 919) and in rat proximal tubules (435, 473, 545, 784) (Fig. 9) and further demonstrated expression of α_2 -adrenergic receptors in rat and human kidney medulla (575, 831) as well as in rabbit MTAL (561). In proximal tubules, α_2 -adrenergic receptors are twice more abundant than α_1 -adrenergic receptors (435, 831) and are mainly accounted for by the α_{2B} -isoform (473, 545, 550) present at the basolateral cell border (403). In contrast, the α_{2AC} -receptor isoform accounts for α_2 -adrenergic receptors expressed in OMCD (550) where the α_{2B} is not detected (403, 550).

The negative coupling of α_2 -adrenergic receptors to adenylyl cyclase via pertussis toxin-sensitive $G\alpha_i$ protein was recognized first (518, 897, 898) (Fig. 9). In nonrenal cells, α_2 -adrenergic receptors coupling to $G\alpha_q$ and PLC- β activation (147, 332) and to activation of ERK pathway (10, 204) has been described.

C) β -ADRENERGIC RECEPTORS. The β -adrenergic receptors are subdivided into three molecular subtypes called β_1 , β_2 , and β_3 (214, 301, 581). β -Adrenergic receptors were first revealed by radioligand binding studies in rat proximal tubules (Fig. 9), although at a much lesser density than α -adrenergic receptors (784). Further functional characterization of β -adrenergic receptors, based on increased cAMP production in response to the preferential β_2 -agonist isoproterenol, indicated marked species differences in the proximal tubule expression of β -adrenergic receptors; in rat they are expressed in native and cultured proximal tubules (365, 429); in mouse, guinea pig, and dog kidney they are only found in PST but not in PCT (39, 494, 577), whereas they are not detected in either PCT or PST from rabbit kidney (39, 244) although functional effects were described (71). In primary cultures of rat proximal tubule cells grown on semi-permeable filters, β -adrenergic receptors are found on both apical and basolateral membrane domains (365). However, such a distribution needs to be confirmed in native tissue, since cell dedifferentiation, with loss of membrane polarity, occurs very rapidly in primary cultures of renal epithelial cells.

β -Adrenergic receptors are also found in mouse MTAL (39) and in rat outer medulla (550). Both β_1 - and β_2 -adrenergic receptors are expressed in the rat CCD and OMCD (535), most likely in intercalated cells (374), and therefore do not participate to the control of sodium transport.

The classical positive coupling of β_2 -adrenergic receptors to the $G\alpha_s$ /adenylyl cyclase/PKA cascade is also found in proximal tubule cells (365, 429, 577) (Fig. 9). In nonrenal cells, β_2 -adrenergic receptors also activate MAP kinases of the ERK family through $\beta\gamma$ -subunits of pertussis toxin-sensitive G protein and activation of Ras (7, 193, 204, 526, 527).

4. Angiotensin II

Two pharmacologically distinct subtypes of angiotensin II (ANG II) receptors have been cloned: AT₁ recep-

tors (580) mediate hemodynamic (426, 607, 778, 817) and sodium-retaining effects (139, 442) of ANG II, whereas AT₂ receptors (446, 573) appear to counteract the effects of AT₁ receptors on hemodynamics and sodium balance (381, 746). Conversely to humans who exhibit a single AT₁ gene, rodents display duplicated AT₁ receptor genes encoding for AT_{1A} and AT_{1B} subtypes (692, 916).

Binding studies demonstrated the presence of ANG II receptors in rat PCT and to a lesser extent in PST (572), and this was later confirmed in humans (911). AT₁ receptors were demonstrated in rat and rabbit proximal tubules at mRNA and/or protein levels (108, 123, 368, 557, 625, 802). Both AT_{1A} and AT_{1B} isoforms of ANG II receptors are expressed in rat proximal tubules (although the AT_{1A} isoform predominates) (108) and are functionally undistinguishable (108, 160, 426, 692, 817). AT₁ receptors are expressed at the apical and basolateral poles of proximal tubule (58, 368, 498, 564, 653, 655). Expression of AT₁ receptor mRNAs (predominantly AT_{1A}) was also found in rat TAL and collecting duct (108) and was functionally confirmed in rat TAL (108) and CCD (108, 715). Functional (513, 745) and biochemical (175) evidence indicate that AT₂ receptors are expressed in the kidney, and a recent study has demonstrated the presence of AT₂ receptor mRNA and protein in proximal tubules (557) (Fig. 10).

As in other cell types (711), proximal tubule AT₁ receptors are coupled to activation of PLC- β through $G\alpha_q$ protein (712), IP₃ generation, increased intracellular calcium concentration (108, 218, 443, 641), and activation of the classical PKC- α and novel PKC- ϵ (451). In proximal tubule cells, ANG II is also linked to the classical $G\alpha_i$ -mediated inhibition of adenylyl cyclase (509, 641, 804, 896) (Fig. 10). ANG II-induced inhibition of cAMP production in PCT may also result from increased intracellular calcium concentration because calcium-inhibited type 6 adenylyl cyclase is expressed in this tissue (141).

In addition to positive coupling with PLC and negative coupling with adenylyl cyclase, increasing pieces of evidence indicate that angiotensin receptors may trigger PLA₂ and MAP kinases. In primary cultures of rabbit proximal tubule cells, ANG II dose-dependently stimulated an apical membrane-associated PLA₂ activity (64, 370, 428) and thereby increased arachidonic acid release (428). ANG II-induced generation of arachidonic acid was also observed in LLC-PK₁ cells (64). Stimulation of PLA₂ by ANG II is mediated by AT₂ receptors (Fig. 10), since it is prevented by the specific AT₂ antagonist PD123319, whereas the specific AT₁ antagonist losartan is ineffective (228).

Another potentially important signaling pathway triggered by ANG II, in particular in proximal tubule cells (228, 801), is the ERK pathway (562, 719, 920). MAP kinases ERK1–2 (877) are activated by ANG II through at least two independent pathways: a PKC-dependent and

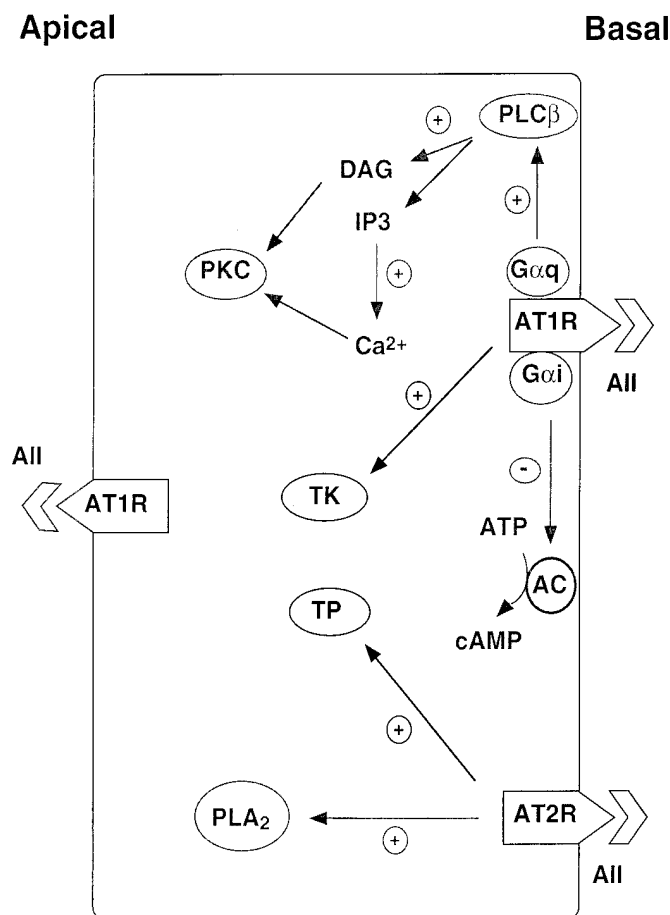


FIG. 10. Angiotensin II (ANG II) signaling in proximal tubule cells. Binding of ANG II to AT₁ receptors (AT₁R) expressed at both apical and basolateral membrane domains activates G_{α_i} and G_{α_q} that couple negatively to AC and positively to PLC-β, respectively. Activated PLC generates DAG and IP₃, which increases cytosolic calcium. Calcium and/or DAG activate PKC isozymes. AT₁ receptors may also couple to several tyrosine kinases (TK). Binding of ANG II to AT₂ receptors (AT₂R) activates PLA₂. In addition, AT₂ receptors might be coupled to the activation of tyrosine phosphatases (TP). Arrows indicate the direction of the signaling cascade and the resulting stimulatory (+) or inhibitory (-) effect on their targets.

Ras-independent pathway (501, 787, 933), and a tyrosine-kinase and Ras-dependent pathway (238, 421, 691, 713). The latter pathway is likely mediated through Src-dependent (421, 713) transactivation of EGF receptors (237, 239, 576). Intriguingly, activation of AT₂ receptors leads to ERK1-2 inhibition in neurons (402), whereas ERKs are activated through an AT₂ receptor-mediated activation of PLA₂ and subsequent generation of arachidonic acid in cultured renal proximal tubule cells (228).

In nonrenal cells, ANG II activates several tyrosine kinases (Fig. 10) through AT₁ receptors (689), including 1) Pyk-2, a calcium-regulated tyrosine kinase (114, 237, 689); 2) the Janus kinase Jak-2, which phosphorylates transcription factors of the STAT family (500, 536, 836); 3) c-Src (237, 500, 689, 705); and 4) the EGF receptor, which

is transactivated by c-Src (239, 576). Activation of AT₂ receptors exert opposite actions through the stimulation of tyrosine phosphatase(s) (120, 227, 584). The AT₁-mediated activation of tyrosine kinases remains to be demonstrated in renal epithelial cells.

5. Vasopressin

Two pharmacologically defined subtypes of vasopressin receptors found in the kidney have been cloned: the V₂ receptor (517) classically coupled with the activation of adenylyl cyclase and the V_{1a} receptor (565) coupled with the activation of PLC and the release of intracellular calcium stores (Fig. 11).

The pioneering work of Chase and Aurbach (155) showed that in vitro addition of vasopressin stimulated adenylyl cyclase activity in kidney medulla homogenates. Several years later, the precise mapping along the nephron of vasopressin response was determined by measuring the in vitro effect of vasopressin on adenylyl cyclase activity in microdissected nephron segments (417). Vasopressin-sensi-

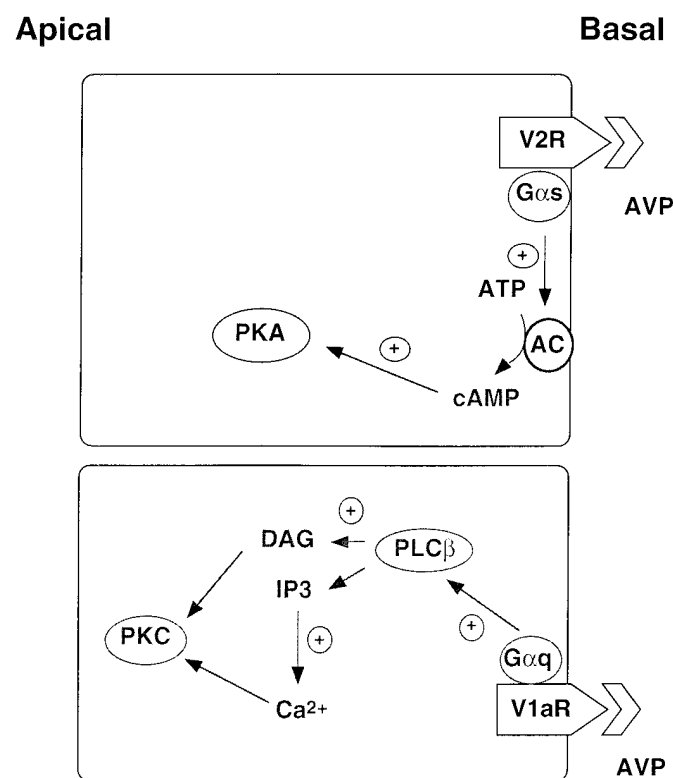


FIG. 11. Vasopressin (VP) signaling in principal cells of the collecting duct. Binding of VP to V₂ receptors (V₂R) activates G_{α_s} that couples to AC. The generation of cAMP by AC activates PKA. Conversely, binding of VP to V_{1a} receptors (V_{1a}R) coupled to PLC-β generates diacylglycerols (DAG) and IP₃, which increases cytosolic calcium. Calcium and/or DAG activate PKC isozymes. V₂R and V_{1a}R might be expressed either by the same cell type or by different cell types. Arrows indicate the direction of the signaling cascade and the resulting stimulatory (+) or inhibitory (-) effect on their targets.

tive adenylyl cyclase was evidenced in CTAL and MTAL from rat and rabbit (417, 418, 815), but not human kidney (142), whereas CCD and OMCD from all three species responded to vasopressin (142, 417, 418). These results are consistent with the expression of the cloned V_2 receptor (517) in these nephron segments. The expression of V_2 receptor in TAL and along the collecting duct was confirmed at the mRNA level by RT-PCR on microdissected rat nephron segments (293, 613, 803) and at the protein level by immunohistochemistry on rat kidney sections (597). In addition to the basolateral expression of V_2 receptors in all vasopressin-responsive segments, a significant level of apical expression was observed in the terminal IMCD (597).

The presence of V_{1a} receptors in vasopressin-responsive nephron segments was suspected on the basis of a vasopressin-induced increase in intracellular calcium (194, 414, 422, 769) and phosphoinositide breakdown (171, 798). Pharmacological studies with specific inhibitors of either V_1 or V_2 receptors have indicated that in rat and rabbit CCD and OMCD, the vasopressin-induced increase in intracellular calcium relies on V_{1a} receptors (17, 122, 918), whereas in rat IMCD the transient increase in intracellular calcium is mediated by V_2 receptor (150, 231, 737) and/or oxytocin receptors (532). In addition, the presence of functional V_{1a} receptors has been demonstrated in rabbit CTAL (595). The presence of V_{1a} receptor in rat CCD and OMCD was subsequently confirmed by ligand binding (16), detection of mRNAs in microdissected nephron segments (293, 803), and by immunolocalization (339). In agreement with pharmacological studies, V_{1a} receptor expression was not detected in the rat terminal IMCD (339, 293).

In addition to its classical positive coupling to adenylyl cyclase, activation of the V_2 receptor (517) also induces transient increases in intracellular calcium (150, 231) independently of cAMP production (737). The cloned V_{1a} receptor (565) is classically linked to activation of PLC, generation of IP_3 , increase in intracellular calcium, and activation of PKC. In nonrenal cells, V_{1a} receptors are also linked to tyrosine kinase (927) and Ras-dependent activation of MAP kinases (5, 376, 894).

6. Corticosteroids

Early [3H]aldosterone binding experiments in kidney preparations revealed two high-affinity receptors, called type I (higher affinity, 1–2 nM) and type II (lower affinity, 80 nM), which were later characterized as the physiological mineralocorticoid and glucocorticoid receptors (MR and GR), respectively (272, 314, 541). Both MR and GR were cloned in the mid 1980s (27, 390).

GRs are ubiquitous, and accordingly, they were found along the whole nephron by ligand binding experiments (102, 491) and localization of mRNAs (254, 808). However, immunolocalization experiments failed to detect GR in proximal tubule (261). This intriguing result

together with the absence of nuclear ligand binding in proximal tubule (102) may suggest that proximal tubules express a specific form of GR. Conversely, MRs are specifically expressed in tight epithelia. In the nephron, they were initially localized by binding experiments in the distal segments of the nephron, from DCT to IMCD, with a maximal binding capacity in CCD and OMCD (223, 262). This localization was confirmed at the mRNA level (254, 808) and by immunolocalization (479, 519, 688). In the rabbit CCD, mineralocorticoid staining is absent in 15–20% of the cells, suggesting that intercalated cells are devoid of MR, or at least that MRs are expressed at a much lower level in intercalated cells than in principal cells (519).

The colocalization of MR and GR in the distal segments of the nephron raises the problem of the specificity of corticosteroid action (259). Specifically, the question of how aldosterone may exert specific actions in the distal nephron is set by two types of observations: 1) the MR displays a similar intrinsic affinity for physiological mineralo- and glucocorticoids, but blood glucocorticoid concentration are ~100-fold higher than aldosterone concentration so that MRs should be permanently saturated by glucocorticoids *in vivo*. 2) If MRs and GRs recognize the same responsive elements (GREs) at the nuclear level, they should promote the same physiological responses.

There is no specific renal answer to the second point, but it is generally admitted that hormone-receptor complexes can interact with DNA sequences other than archetypal responsive elements, and therefore, MR and GR may have both common and different nuclear targets (313). For example, MRs and GRs were shown to have the same efficiency in GREs but to induce distinct actions on *plfG*, a low-affinity responsive element that binds the AP-1 transcription factor. GR repressed AP-1-induced transcription, whereas MR was inactive (627). In addition, some effects of steroids may not be mediated by receptor/DNA interaction (see sect. IIIA4).

With regard to the first point, there is clear evidence that renal mineralocorticoid target cells degrade glucocorticoids into compounds of low affinity for MRs, and thereby prevent continuous MR saturation by heterologous ligand. 11 β -Hydroxysteroid dehydrogenase (11 β -OHSD) catalyzes the oxidation of 11-hydroxysteroids into 11-ketosteroids, e.g., cortisol and corticosterone into cortisone and 11 β -dehydrocorticosterone, respectively, two compounds displaying low affinity for the MR (315). Aldosterone target tissues only contain the type 2 11 β -OHSD which, in contrast to the type 1 11 β -OHSD, displays a high affinity for 11-hydroxysteroids, and is therefore the most likely candidate to endow specificity on the MR (478). Type 2 11 β -OHSD activity is high in rabbit CCD and OMCD and low in aldosterone-insensitive segments (103). After cloning of type 2 11 β -OHSD (9), its expression in

aldosterone-sensitive nephron segments was confirmed at the mRNA and protein levels (585).

IV. HORMONAL CONTROL OF SODIUM TRANSPORT ALONG THE PROXIMAL TUBULE

A. General Transport and Regulatory Properties of Proximal Tubules

1. Transport properties

The proximal tubule reabsorbs over 70% of the filtered sodium, potassium, chloride, bicarbonate, phosphate, and water and virtually all the filtered glucose and amino acids. The rates of reabsorption of water and of many solutes decrease from S₁ to S₃, but the cellular and molecular mechanisms underlying these transports re-

main mostly similar in the successive subsegments of the proximal tubule.

Luminal sodium-dependent cotransport systems (nomenclature given in parentheses) account for the active uptake of glucose (SGLT), phosphate (NaPi-2, NPT-1, and Npt-1 in rabbit, human, and mouse, respectively), sulfate (NaSi-1), amino acids, and several organic acids in the proximal tubule (Fig. 12A). However, most luminal sodium entry within proximal tubule cells (>80%) is directly coupled to active proton extrusion, and secondarily to bicarbonate or chloride reabsorption. Thus regulation of sodium transport in the proximal tubule is discussed only with regard to bicarbonate and chloride reabsorption processes, although other transports may be important, especially for glucose and phosphate balance.

Apical proton extrusion is mediated by Na⁺/H⁺ exchange (Fig. 12A), and to a much lesser extent by V-type H⁺-ATPase. Na⁺/H⁺ exchangers constitute a family of

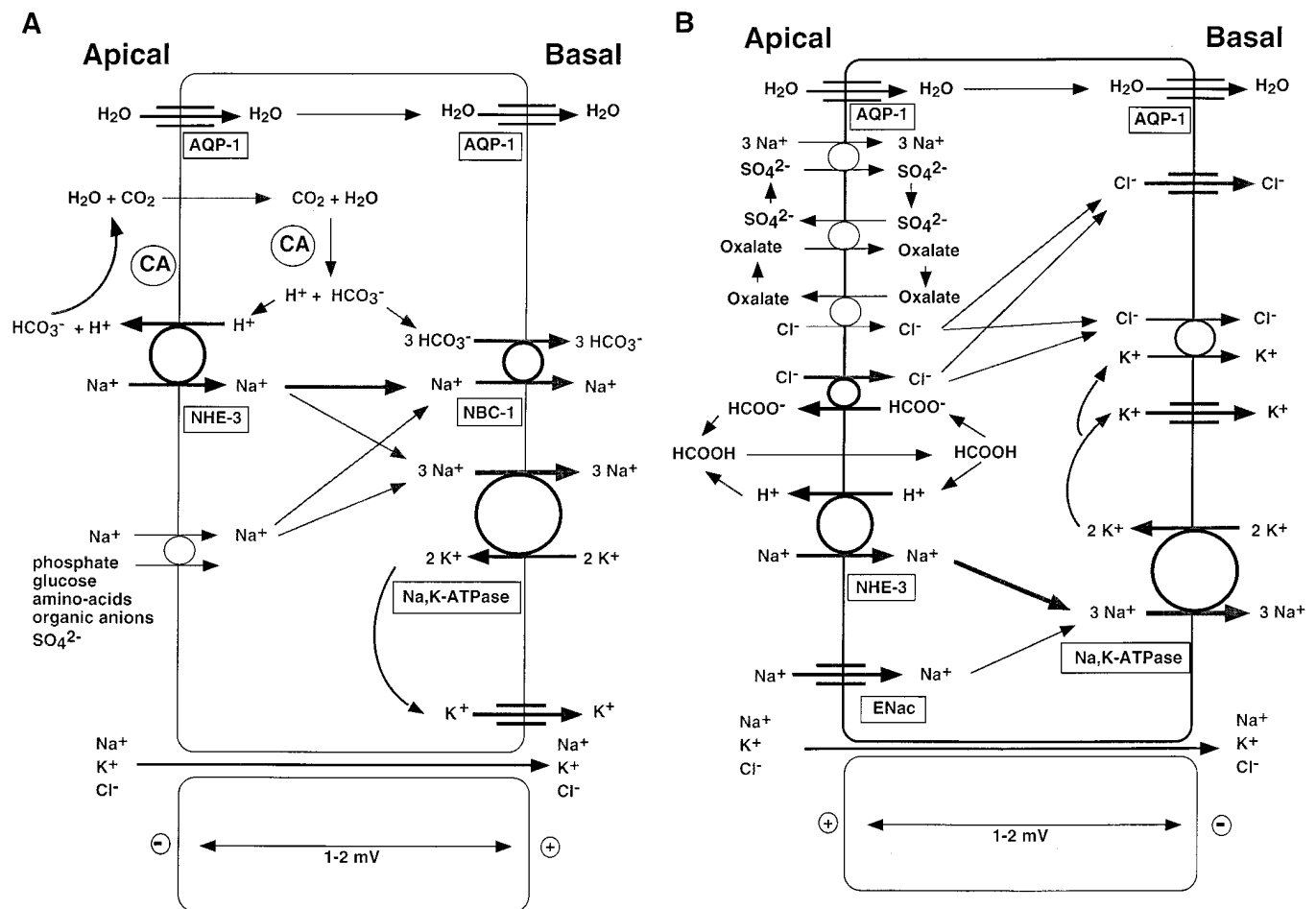


FIG. 12. Cellular mechanism of sodium, potassium, anion, and water transport in proximal convoluted tubules. The situations prevailing in early and late proximal tubule are depicted in A and B, respectively. Arrows indicate net fluxes of water and solutes. The names of the currently cloned transporters are mentioned into rectangular boxes. CA, carbonic anhydrase; AQP-1, aquaporin-1.

electroneutral antiporters that physiologically couple the downhill entry of sodium into the cell to the active extrusion of proton. Four isoforms of Na^+/H^+ exchangers (NHE-1 to -4) have been cloned and found in the kidney. Functionally, these isoforms mainly differ by their affinity for sodium (K_m from 4–18 mM for rat NHE-1 and NHE-3 to 40 mM for rat NHE-2), their sensitivity to amiloride and its derivative ethylisopropylamiloride (EIPA) (NHE-3 is less sensitive to amiloride and EIPA than other isoforms), their tissue distribution (NHE-1 is ubiquitous), and their polarity in epithelial cells (NHE-1 and NHE-4 are basolateral, whereas NHE-2 and NHE-3 are apical) (596, 620, 926). In the proximal tubule, apical proton extrusion is mainly mediated by NHE-3 (902), although the NHE-2 isoform might be also present (392).

The sequence of events ultimately resulting in net bicarbonate reabsorption is summarized by Figure 12A. Despite the impermeability of the luminal membrane of proximal cells to bicarbonate, proton secretion results in an equivalent bicarbonate reabsorption: the brush border contains an ecto carbonic anhydrase that allows the rapid dehydration of the carbonic acid formed from filtered bicarbonate and secreted proton. Carbon dioxide diffuses into the cellular compartment by nonionic diffusion, or possibly through the water channel aquaporin 1 (AQP-1) (182). In the intracellular compartment, where the pH is higher than in the lumen, bicarbonate is regenerated by the reverse sequence of reactions, catalyzed by intracellular carbonic anhydrase. Bicarbonate regenerated in the cells crosses passively the basolateral membrane through an electrogenic $\text{Na}^+/\text{HCO}_3^-$ cotransport system (NBC-1) (676). This electrogenic $\text{Na}^+/\text{HCO}_3^-$ cotransport system, which is inhibited by the stilbene derivative DIDS, couples the downhill extrusion of three bicarbonate ions to the active extrusion of one sodium ion. This improves the overall energetic efficiency of the system. For nine bicarbonate ions reabsorbed, nine sodium ions enter the cell via the apical Na^+/H^+ exchanger, six of which leave the cell through Na^+/K^+ -ATPase (at the expense of the hydrolysis of 2 molecules of ATP), whereas the remaining three are transported along the $\text{Na}^+/\text{HCO}_3^-$ transport system. Thus 4.5 sodium ions, instead of 3, are reabsorbed through the transcellular pathway for each ATP molecule hydrolyzed.

As tubular fluid flows along the proximal tubule, its pH and bicarbonate concentration decrease, whereas chloride concentration increases, because this mechanism of proton secretion favors the reabsorption of NaHCO_3 over that of NaCl . Luminal fluid acidification reduces the efficiency of the Na^+/H^+ exchanger by increasing the proton gradient. In the mid and terminal proximal tubule, this is palliated in part by indirect coupling of proton secretion to chloride reabsorption rather than to bicarbonate reabsorption. Two mechanisms account for this coupling (Fig. 12B): 1) apical chloride/

formate exchange with recycling of formate by nonionic cellular diffusion of the formic acid generated by the protonation of formate in the lumen, and 2) apical chloride/oxalate exchange with recycling of luminal oxalate through oxalate/sulfate exchange coupled to Na^+ -sulfate cotransport (25, 26). Given the presence of basolateral exit pathways for chloride (both chloride channels and K^+/Cl^- cotransporters), sodium reabsorption drives chloride reabsorption. In addition, increased luminal concentration of chloride above that in the interstitium generates a driving force for its passive reabsorption via the intercellular route. In turn, this generates a lumen-positive voltage in the mid-terminal proximal tubule, which serves as driving force for intercellular cation reabsorption (Fig. 12B). Because the ionic conductance of the shunt pathway is high for both sodium and chloride, paracellular reabsorption fluxes of both ions are high, whereas the transepithelial voltage remains in the millivolt range.

In addition to apical sodium-coupled transporters, a recent study (885) suggested the participation of the epithelial sodium channels (ENaC) (see sect. viA for properties of ENaC) in apical sodium entry in rat PCT (Fig. 12B). This conclusion is based on the following: 1) micromolar concentrations of luminal amiloride (that inhibit ENaC but not NHE-3) hyperpolarized the apical membrane of in vitro microperfused rat PCT, and 2) mRNAs encoding the three subunits of ENaC were detected by RT-PCR in rat PCT.

Because luminal and basolateral membranes of proximal tubules cells are made freely permeable to water through the expression of AQP-1 (594), net water reabsorption is passively driven by the overall osmotic balance of solute fluxes.

2. Regulatory properties

Sodium and fluid reabsorption by the proximal tubule is controlled by many hormones and neurotransmitters including PTH, dopamine, epinephrine and norepinephrine, angiotensin II, insulin, and glucocorticoids. PTH is the main regulator of phosphate transport and an important modulator of bicarbonate reabsorption in proximal tubule. However, PTH most likely plays an accessory role in the overall sodium and fluid balance. The bulk of sodium and water reabsorption by the proximal tubule is controlled positively mainly by ANG II and epinephrine/norepinephrine and negatively by dopamine. Insulin may play a physiological role in postprandial periods. Glucocorticoids play a role in the day-to-day control of the reabsorption process through transcriptional regulation of sodium transporters. In addition to this stricto sensu hormonal control, local factors, including endothelins and nitric oxide, may modulate the proximal tubule reabsorption process, and the reader may refer to recent reviews on that topic (476, 537).

Because hormones trigger different signaling pathways in a same cell (see sect. III B), we first present data obtained through unique activation of either cAMP/PKA pathway by forskolin and/or permeant analogs of cAMP, or of phorbol ester-sensitive PKC pathway.

B. cAMP/PKA Signaling Pathway

Both in vivo and in vitro microperfusion studies demonstrated that luminal cAMP and cell-permeant cAMP analogs inhibit the proximal tubule reabsorption of fluid, sodium, and bicarbonate (59, 549, 725). This inhibitory effect was observed in tubules microperfused with an ultrafiltrate-like solution containing ~25 mM bicarbonate. In contrast, when the perfusate contained 5 mM bicarbonate, which mimicks the situation prevailing in the late proximal tubule, cAMP analogs and forskolin stimulated fluid and NaCl reabsorption (848). This stimulation was dependent on transcellular chloride transport through apical chloride/anion exchangers and basolateral chloride channels and required the presence of a chloride gradient. This suggests that cAMP might both 1) inhibit bicarbonate transporters, e.g., apical Na⁺/H⁺ exchanger and/or basolateral Na⁺-HCO₃⁻ cotransporter, and consequently inhibit the fraction of sodium and fluid transport coupled to bicarbonate reabsorption, and 2) stimulate sodium and chloride transporters not coupled to bicarbonate transport, e.g., apical sodium channels and basolateral chloride channels and K⁺-Cl⁻ cotransporter.

1. Stimulation of Na⁺-K⁺-ATPase

A large body of evidence indicates that cAMP-PKA modulates the activity of Na⁺-K⁺-ATPase in proximal tubules. Most studies concluded to a stimulatory effect of cAMP on proximal tubule Na⁺-K⁺-ATPase measured either in intact cells by 1) ouabain-sensitive oxygen consumption (63), 2) Na⁺-K⁺-ATPase-dependent basolateral membrane potential variation (110), and 3) ouabain-sensitive rubidium uptake (135, 136), or in permeabilized isolated PCTs (80, 136) and kidney cortex homogenate (337) by the Na⁺-K⁺-ATPase hydrolytic activity. In one study, inhibition of ouabain-sensitive oxygen consumption was reported in response to a cAMP analog (673). However, this inhibitory effect likely resulted from insufficient supply of aerobic metabolic substrates leading to the activation of cell protective mechanisms. Such mechanisms include PLA₂ activation (121, 170, 645) and generation of inhibitors of Na⁺-K⁺-ATPase through cytochrome P-450-monoxygenase arachidonate metabolism (11) (this inhibitory pathway has been well established in TAL and is further discussed in sect. VB1). Indeed, incubation solution used in this study did not contain lactate, a major metabolic substrate in PCT cells (444, 826), which is mandatory to support active sodium transport (163).

Finally, in two other reports, incubation of isolated rat PCTs at room temperature with exogenous or endogenous cAMP did not alter Na⁺-K⁺-ATPase activity, revealing the temperature dependence of the stimulatory effect of cAMP (82, 702). This latter observation is consistent with membrane redistribution events. Indeed, the stimulation of Na⁺-K⁺-ATPase activity by cAMP analogs was observed at V_{max} and was associated with increased number of pump units at the plasma membrane at the expense of early endosomes (136). This suggests that latent intracellular Na⁺-K⁺-ATPase units located in an early endosomal compartment can be translocated to the basolateral membrane in response to PKA activation in PCT cells, although a PKA-induced inhibition of Na⁺-K⁺-ATPase endocytosis cannot be excluded (Fig. 13).

Because the effects of cAMP are mainly mediated by PKA, phosphorylation of the Na⁺-K⁺-ATPase α-subunit might be implicated in the redistribution of Na⁺-K⁺-

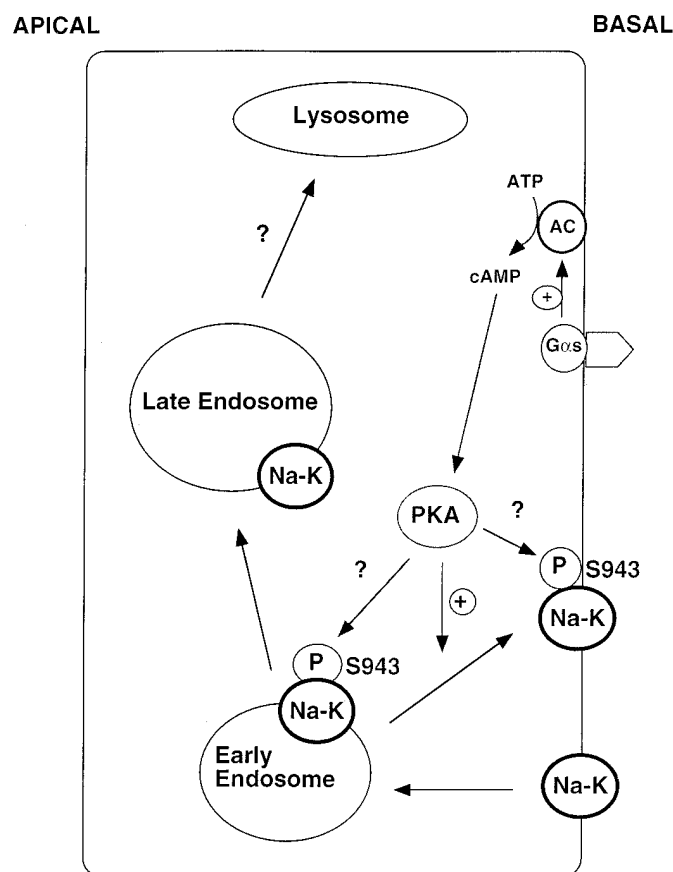


FIG. 13. Mechanism of stimulation of Na⁺-K⁺-ATPase by cAMP in proximal convoluted tubule. Activation of AC through Gα_s increases cellular cAMP levels and activates PKA. Activation of PKA induces translocation of Na⁺-K⁺-ATPase units from early endosomes to the basolateral plasma membrane domain. Whether PKA phosphorylates (P S943) Na⁺-K⁺-ATPase units located at the plasma membrane or in early endosomes remains to be determined. Arrows indicate the direction of the signaling cascade.

ATPase observed in proximal tubule. Phosphorylation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunit by PKA was evidenced in vitro (83, 167) and in intact cells (66, 135, 294). The PKA phosphorylation site was mapped at the well-conserved Ser-943 of the α_1 -subunit (66, 283, 294). cAMP-mediated phosphorylation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ and stimulation of ouabain-sensitive rubidium uptake occurred with the same time course in intact cells of rat kidney cortex (135), suggesting that both events are linked. However, the definite relationship between cAMP-stimulated phosphorylation and stimulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity remains to be established.

2. Inhibition of Na^+/H^+ exchanger and $\text{Na}^+\text{-HCO}_3^-$ cotransporter

The inhibitory effect of cAMP on sodium and bicarbonate reabsorption is mediated at least in part by coordinate inhibition of the apical Na^+/H^+ exchange (869) and of the basolateral $\text{Na}^+\text{-HCO}_3^-$ cotransport (685). cAMP-induced inhibition of Na^+/H^+ exchange is also observed in OK cells (128, 384, 643). Reconstitution studies in proteoliposomes demonstrated that cAMP-induced inhibition of the brush-border Na^+/H^+ exchanger NHE-3 was dependent on active PKA (866, 870) and required a dissociable phosphoprotein cofactor (870, 871). This cofactor, called NHE-RF, was recently cloned from a rabbit renal cDNA library (872), and soon after, an analogous cofactor (E3KARP) was cloned from a human fibroblast cDNA library (924). Both NHE-RF and E3KARP directly bind to the cytoplasmic tail of NHE-3 (924) through their PDZ domains (923). Phosphorylation of NHE-3 by PKA was also demonstrated in transfected AP-1 fibroblasts (559, 929, 932) and in OK cells (929). The cAMP-induced inhibition of NHE-3 requires its PKA phosphorylation, since a dominant-negative PKA-regulatory subunit, as well as mutation of the two serine residues (Ser-552 and Ser-605) of the rat NHE-3 which are phosphorylated in response to PKA activation in intact cells, abolished the effect of cAMP on NHE-3 activity (929). Conversely, phosphorylation of NHE-RF and E3KARP is not necessary for the inhibition of NHE-3 by cAMP (484, 932). A direct interaction between E3KARP and the cytoskeletal protein ezrin has been recently demonstrated (484, 923), and because ezrin plays the anchoring role of AKAP for type II PKA (484), the following model has been proposed. The ezrin-E3KARP/NHE-RF complex would bring in close vicinity type II PKA and NHE-3 so as to facilitate the preferential PKA phosphorylation of NHE-3 in response to cAMP binding. This phosphorylation would reduce the intracellular pH dependence of the Na^+/H^+ exchanger (484). It is interesting to mention that NHE-RF also interacts with the proximal tubule basolateral $\text{Na}^+\text{-HCO}_3^-$ cotransporter, and reconstitution assays have shown that NHE-RF is required for its PKA-dependent inhibition (76). These ob-

servations illustrate the complexity of the regulation of ion transporters through a network of interactions with cytoskeleton, adaptor proteins, and protein kinases (Fig. 14).

3. Stimulation of bicarbonate-independent transporters

cAMP-induced stimulation of sodium chloride and fluid reabsorption observed in the absence of luminal bicarbonate likely results from the coordinated regulation of several transporters at the apical and basolateral pole of the cell. At the basolateral border, stimulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity 1) increases basolateral sodium exit; 2) hyperpolarizes the basolateral membrane (110), and thereby increases chloride exit via basolateral chloride channels (785); and 3) increases the driving force for paracellular chloride reabsorption. At the apical border, epithelial sodium channels (885) are good candidates, since they might be activated when sodium entry through apical Na^+/H^+ exchanger is decreased. Indeed, ENaC activity is closely related to the sodium availability and is upregulated by a decreased rate of sodium entry (307, 885). Furthermore, cAMP increases ENaC activity in the collecting duct (305), therefore inferring that similar regulation may occur in PCT.

In summary, cAMP promotes a shift from sodium-bicarbonate toward sodium-chloride reabsorption in PCT through inhibition of apical Na^+/H^+ exchanger and basolateral $\text{Na}^+\text{-HCO}_3^-$ cotransporter. In this context, the stim-

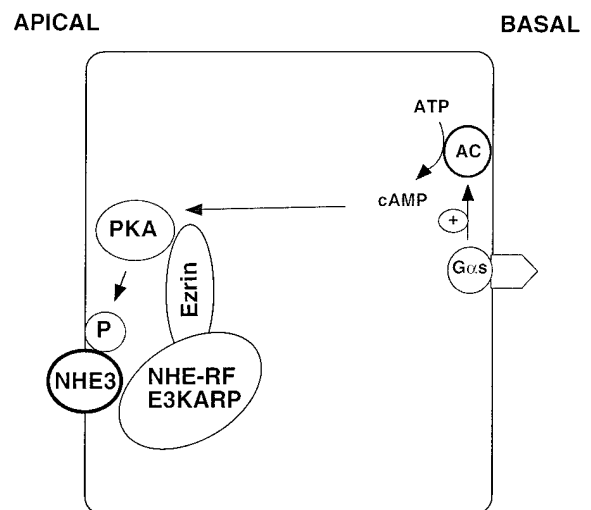


FIG. 14. Mechanism of inhibition of the apical Na^+/H^+ exchanger NHE3 by cAMP in proximal convoluted tubule. Activation of AC through $\text{G}\alpha_s$ increases cellular cAMP level and activates PKA which phosphorylates NHE3. Ezrin, a cytoskeletal protein, binds both the regulatory (RII) subunit of PKA and E3KARP-NHE-RF. E3KARP and NHE-RF bind to the cytoplasmic tail of NHE3. The E3KARP-ezrin complex brings type II PKA and NHE3 in close vicinity, thus favoring the phosphorylation of NHE3. Arrows indicate the direction of the signaling cascade.

ulation of Na⁺-K⁺-ATPase by cAMP could play a key role in the enhanced sodium chloride reabsorption by maintaining or increasing the electrochemical gradients necessary for sodium and chloride reabsorption independently of the apical Na⁺/H⁺ exchanger and basolateral Na⁺-HCO₃⁻ cotransporter activities.

C. PKC Signaling Pathway

In the in situ microperfused rat PCT, phorbol esters and dioctanoylglycerol stimulated water and solute reabsorption, whereas inhibition of PKC decreased them (510). In an other study, in contrast, an inhibitory effect of phorbol esters and dioctanoylglycerol was reported in the in vitro microperfused rabbit PCT (54). However, this inhibition likely resulted from the lack of pyruvate and lactate in bathing solution which, as discussed above, may lead to the activation of cell protective mechanisms that downregulate active sodium transport (for further discussion see below and sect. vB1). Finally, a third study in the in situ microperfused rat PCT reported an initial stimulation of fluid reabsorption by phorbol esters lasting 10 min, followed by an inhibitory effect (847). This finding may result from 1) sequential activation of different isoforms of PKC by phorbol esters, 2) downregulation of PKCs after prolonged exposure to phorbol esters, or 3) activation of the above-mentioned cell protective mechanisms in response to toxic effects of phorbol esters.

1. Stimulation of Na⁺-K⁺-ATPase

Primary modulation of Na⁺-K⁺-ATPase activity most likely plays a key role in the effect of phorbol esters on sodium transport in the proximal tubule. The studies of Bertorello et al. (79, 81) and Satoh et al. (702) concluded that direct in vitro activation of PKCs by phorbol 12,13-dibutyrate (PDBu) decreased the V_{\max} of Na⁺-K⁺-ATPase activity through an activation of PLA₂ and of arachidonic acid metabolism (608, 702), but this effect was no longer observed in well-oxygenated isolated rat PCTs incubated in the presence of oxidative metabolic substrates (277). Thus phorbol esters inhibit proximal tubule Na⁺-K⁺-ATPase and sodium transport as a result of poor metabolic status that triggers cell protective mechanisms, whereas under adequate metabolic conditions, phorbol esters stimulate both sodium transport and Na⁺-K⁺-ATPase activity.

In well-oxygenated rat PCTs, PDBu did not alter the V_{\max} of Na⁺-K⁺-ATPase activity but increased ouabain-sensitive rubidium uptake, as a result of increased Na⁺-K⁺-ATPase apparent affinity for sodium (277). In suspensions of rat proximal tubules, the stimulatory effect of phorbol ester on the transport activity of Na⁺-K⁺-ATPase was correlated and cosaturated with an increase in the phosphorylation level of Na⁺-K⁺-ATPase α -subunit (134).

This suggested a causal relationship between PKC-dependent phosphorylation and increased sodium affinity of Na⁺-K⁺-ATPase (277). This hypothesis was recently confirmed by the demonstration that phosphorylation of the Na⁺-K⁺-ATPase α_1 -subunit at Ser-16 increases the apparent sodium affinity of the enzyme in COS-7 cells (276) (see sect. II A5).

2. Stimulation of Na⁺/H⁺ exchanger and Na⁺-HCO₃⁻ cotransporter

In addition to modulating Na⁺-K⁺-ATPase activity, phorbol esters may also alter sodium-dependent transporters in proximal tubule. Stimulation of the proximal tubule apical Na⁺/H⁺ exchanger by purified phorbol ester-sensitive PKC has been documented in isolated rabbit brush-border membranes (868). Similar findings were obtained with brush-border Na⁺/H⁺ exchangers incorporated into artificial proteoliposomes (865), suggesting that PKC-dependent phosphorylation of the Na⁺/H⁺ exchanger mediates the observed stimulation of Na⁺/H⁺ exchange. This stimulatory effect of PKC-dependent phosphorylation was questioned by several studies on fibroblast-like cells and in epithelial-like Caco-2 cells transfected with NHE-3, which reported a phosphorylation-associated inhibition of Na⁺/H⁺ exchange activity by phorbol esters (493, 816, 917, 925). In addition, Na⁺/H⁺ exchange was acutely inhibited by phorbol esters in OK cells (384), which express exclusively the NHE-3 isoform (33). However, a recent study has demonstrated that individual clones of Na⁺/H⁺ exchanger-deficient AP-1 cells stably transfected with the rat NHE-3 may exhibit opposite responses to phorbol esters (879). Indeed, clones with stimulatory, inhibitory, or no response were observed despite a similar pattern of phorbol ester-induced phosphorylation analyzed by phosphopeptide mapping. Therefore, the effect of PKC-dependent phosphorylation of NHE-3 is indirect and largely dependent on cell-specific factors that may determine the stimulatory effect observed in proximal tubule brush-border membranes.

The activity of the basolateral Na⁺-HCO₃⁻ cotransporter is also increased in response to phorbol esters in isolated rabbit proximal tubule cells (910). In addition, the activity of the cotransporter is increased by phosphorylation by purified PKC of basolateral membranes isolated from rabbit proximal tubules (685). Altogether, these effects are consistent with the phorbol ester-induced alkalinization of dog proximal tubules cells (552).

In summary, activation of phorbol ester-sensitive PKCs stimulates the activity of sodium-coupled acid-base transporters in PCT which, together with the stimulation of Na⁺-K⁺-ATPase, may increase bicarbonate reabsorption in this segment. The pleiotropic coordi-

nated stimulation by phorbol esters of both apical sodium entry and basolateral sodium exit allows the increase of net transepithelial reabsorption of sodium without altering its intracellular concentration. This whole process most likely requires phosphorylation of the $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunit, of NHE-3, and of the $\text{Na}^+\text{-HCO}_3^-$ cotransporter.

D. ANG II

1. ANG II is locally produced

Several studies indicated that luminal proximal tubule concentrations of ANG II are 1,000-fold (nM range) (109, 591, 931) to 100-fold (0.1 nM range) (99, 590) higher than plasma concentrations (pM range), indicating that PCTs secrete either circulating or locally generated ANG II. Several lines of evidence suggest that the major part of luminal ANG II derives from local synthesis: 1) proximal tubule cells express angiotensinogen (218, 420), renin (560), and angiotensin I converting enzyme (116, 137, 911); 2) both angiotensin I (591) and angiotensin I converting enzyme (137) are secreted into the PCT lumen; and 3) circulating and proximal tubule luminal ANG II concentrations may vary independently (99). Only a very small fraction of luminal ANG II is excreted in the urine, since it is almost entirely reabsorbed and degraded by proximal tubules (631, 651). In contrast to PTH, the role of the multifunctional endocytic receptor megalin (172) has not been evaluated in the clearance of ANG II from the proximal tubule luminal fluid.

2. Solute and fluid transport

A biphasic effect of ANG II on sodium reabsorption by the PCT has been recognized in the late 1970s. By *in vivo* microperfusion of rat PCT and peritubular capillaries, Harris and Young (366, 367) demonstrated that low concentrations of ANG II (10^{-12} to 10^{-10} M) stimulated sodium and fluid reabsorption, whereas high concentrations of ANG II (3×10^{-7} to 3×10^{-6} M) inhibited sodium and water transport. This early observation was subsequently confirmed using either the same technique in rat (156, 507) or the *in vitro* microperfusion of rabbit PCT (218, 720). In rats, the stimulatory effect of low concentrations of ANG II was observed along the whole proximal tubule (326, 507), but ANG II was less potent in PST than in PCT (507). ANG II exerted its dose-dependent effects on PCT fluid and solute reabsorption at both the basolateral (367, 508, 720) and the apical side of the tubule (58, 498, 508), but it was more potent when applied to the lumen of rabbit PCT (498). In addition, the action of luminal ANG II can be modulated by basolateral ANG II (498). Indeed, the concomitant application of a high concentration of luminal ANG II (inhibitory) and a low con-

centration of basolateral ANG II (stimulatory) stimulated fluid reabsorption. It is important to mention, however, that the micromolar concentrations of ANG II that inhibit fluid reabsorption in proximal tubule are never observed under physiological conditions, even at the luminal border of PCTs.

In tubules perfused with an ultrafiltrate-like solution (containing more than 20 mM bicarbonate), the stimulatory effect of ANG II on sodium and fluid reabsorption was associated with increased bicarbonate reabsorption (507). However, in contrast to the inhibitory effect of PTH (206, 549), ANG II increased sodium chloride reabsorption even when tubules were perfused with bicarbonate-free solutions (890).

Micropuncture and clearance studies have shown that under basal conditions, ANG II may exert a tonic control on sodium transport by PCT (931). This was confirmed using the *in vitro* microperfused rabbit PCT in which perfusion with an inhibitor of the angiotensin converting enzyme or an AT_1 receptor antagonist decreased fluid reabsorption (653). Similar observations were obtained by *in vivo* microperfusion of rat PCT (752, 906). In addition, regulation of proximal tubule ANG II secretion by extracellular volume may account in part for the homeostatic adaptation of proximal tubule fluid reabsorption to volume changes (654). Indeed, in volume-depleted rats, *in vivo* luminal perfusion of ANG II had no effect on fluid reabsorption, whereas administration of an AT_1 receptor antagonist inhibited it, suggesting a high basal concentration of luminal ANG II sufficient for maximal activation of fluid transport. Conversely, in volume-expanded rats, the AT_1 receptor antagonist was ineffective, whereas the fluid reabsorption was stimulated by luminal exogenous ANG II, suggesting a basal luminal ANG II concentration below the stimulation threshold.

On the basis of pharmacological studies using non-peptidic antagonists, the stimulatory and inhibitory effects of ANG II on sodium and fluid transport were attributed to AT_1 receptors (654, 893).

3. Sodium-dependent transporters

Consistent with its effects on sodium, bicarbonate, and fluid reabsorption, ANG II modulates $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity in a biphasic manner (88). At low concentrations, the stimulatory action of ANG II on $\text{Na}^+\text{-K}^+\text{-ATPase}$ results from either a V_{max} effect (327) or from increased apparent affinity for sodium (22). The precise mechanism of control of $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity by ANG II as well as the signaling pathway mediating these effects remain to be investigated.

The effect of ANG II on the apical Na^+/H^+ exchange has been investigated more extensively. Stimulation of the apical Na^+/H^+ exchange in response to low concentrations of ANG II was first suggested on the basis of the

abolition by amiloride of the increase in sodium and bicarbonate transport in rat PCT microperfused in situ (508). Stimulation of the apical Na⁺/H⁺ exchanger was directly demonstrated in the in vitro microperfused rabbit PCT where low concentration of ANG II increased the rate of EIPA-sensitive intracellular alkalinization (331). This observation was confirmed by measurement of the activity of the Na⁺/H⁺ exchanger taken as 1) the initial rate of amiloride-sensitive sodium uptake in freshly isolated rabbit (690) and rat proximal tubule cells (335) or 2) the initial rate of sodium-dependent intracellular pH recovery after acid loading in suspensions of rat PCT (398). Similarly, in brush-border membrane vesicles (BBMVs) isolated after exposure of rabbit proximal tubule cells to low concentration of ANG II, the activity of the Na⁺/H⁺ exchanger was stimulated (95, 690). Conversely, the activity of the Na⁺/H⁺ exchanger, measured as the initial rate of sodium-dependent intracellular pH recovery after an acid load, was decreased by high concentrations of ANG II in suspensions of rat PCT (398). The precise mechanism of Na⁺/H⁺ exchanger stimulation by ANG II remains to be established. In some studies, ANG II was reported to increase the V_{\max} of proton efflux (95, 690), raising the possibility that ANG II might increase the expression of NHE-3 at the apical membrane.

Studies in rat proximal tubule suggested that the stimulatory effect of low concentration of ANG II relies in part on decreased cAMP cell content (398, 509). In the in situ microperfused rat PCT, ANG II decreased cAMP content in luminal fluid, and its effect on fluid transport was partially prevented through inhibition of G α_i by pertussis toxin and was abolished by a cell-permeant cAMP analog (509). These results suggest that ANG II may act in part through the G α_i -mediated inhibition of adenylyl cyclase, and thus by reversing the inhibitory effect of cAMP on NHE-3. Alternately, studies with PKC inhibitors (398) or activators (510) suggested that activation of the phorbol ester-sensitive PKC- α and PKC- ϵ by low concentration of ANG II (451) participates to the stimulation of Na⁺/H⁺ exchange. It is most likely that the stimulation of the apical Na⁺/H⁺ exchanger by low concentration of ANG II results from complex interactions between multiple signaling pathways, since PLA₂ (498, 564) and c-Src (819) may also participate to this effect. The inhibitory effect of high concentration of ANG II on Na⁺/H⁺ activity likely relies on PLA₂-mediated generation of arachidonic acid and subsequent synthesis of active metabolites through the cytochrome P-450-monooxygenase pathway (398, 498).

Stimulation of the basolateral Na⁺-HCO₃⁻ cotransport also participates to increase bicarbonate reabsorption in response to low concentration of ANG II. Using the in vitro microperfused rabbit PCT, Giebel et al. (331) have shown that ANG II stimulated the rate of basolateral Na⁺-HCO₃⁻ cotransport, measured as the rate of DIDS-sensitive sodium-dependent intracellular pH recovery in

tubules loaded with the fluorescent probe 2',7'-bis(carboxyethyl)-5,6-carboxyfluorescein (BCECF). This was confirmed by electrophysiological measurement of the Na⁺-HCO₃⁻ cotransport rate in the same preparation (183) and by measurement of the bicarbonate-sensitive sodium uptake in basolateral membrane vesicles from rabbit kidney cortex (240, 686). This stimulatory effect of low concentration of ANG II is likely mediated by an activation of PKC and by a decrease in intracellular cAMP, since it was prevented by inactivation of G α_i by pertussis toxin and by inhibition of PKC by calphostin C (686). In contrast, high concentrations of ANG II inhibited the Na⁺-HCO₃⁻ cotransport measured in the in vitro microperfused rabbit PCT by bicarbonate-dependent changes in basolateral membrane potential (184).

In conclusion, ANG II controls sodium and fluid reabsorption by the proximal tubule through a coordinated modulation of the sodium transporters present at apical and basolateral membrane domains. However, ANG II appears to alter apical and basolateral sodium transporters within a different time frame, since it exerts a transient biphasic effect on intracellular sodium concentration (669, 892). The apical sodium transport step, mediated by Na⁺/H⁺ exchange, might be altered first since the intracellular sodium concentration initially increased or decreased in response to low or high concentrations of ANG II, respectively.

E. Epinephrine and Norepinephrine

1. Stimulatory effect of α -adrenergic agonists

The direct α -adrenergic control of fluid and solute reabsorption in the PCT has been demonstrated in the 1980s. In the in situ perfused rat kidney, infusion of norepinephrine or epinephrine increased fluid reabsorption (152, 867), and this effect was reversed by the α -adrenergic antagonists phenoxybenzamine (152) and phenolamine (867). In agreement with the lack of luminal binding sites, luminal norepinephrine had no effect on fluid reabsorption by PCT (152). At the level of isolated PCTs, norepinephrine stimulated 1) sodium reabsorption in *Ambystoma* (3); 2) sodium, chloride, and bicarbonate reabsorption and ouabain-sensitive oxygen consumption in rabbit (60); and 3) ouabain-sensitive rubidium uptake in rat (39). The stimulatory effect of norepinephrine on proximal tubule reabsorption is mediated at least in part by α_1 -adrenergic receptors, since prazosin, a specific α_1 -antagonist, decreased chloride reabsorption by the in situ microperfused rat PCT (891) and antagonized the decrease in bicarbonate excretion induced by renal nerve stimulation in anesthetized dogs (611). In contrast to prazosin, specific α_2 -antagonists did not alter ion transport in these settings (611, 891). Moreover, an inhibition of fluid reabsorption has been reported in response to the

specific activation of α_2 -adrenergic receptors by clonidine in the isolated perfused rabbit PCT (683).

Stimulation of proximal tubule sodium transport in response to norepinephrine is largely mediated by a primary increase in $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity as shown by the decrease in intracellular sodium concentration in *Ambystoma* proximal tubule (3) and by direct measurement of the hydrolytic activity of $\text{Na}^+\text{-K}^+\text{-ATPase}$ in basolateral membranes isolated from norepinephrine-treated rabbit PCTs (60). These results were confirmed in isolated rat PCTs by measurements of the hydrolytic activity of $\text{Na}^+\text{-K}^+\text{-ATPase}$ in response to the α -adrenergic agonist oxymetazoline (23). Attempts to delineate the α -adrenergic receptor subtype involved in the stimulation of proximal tubule $\text{Na}^+\text{-K}^+\text{-ATPase}$ indicated that the specific α_1 -antagonist prazosin prevented the stimulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ in response to α -agonists (23, 340). Surprisingly, however, the stimulatory effect of the nonspecific α -agonist oxymetazoline was fully prevented by the α_2 -antagonist yohimbine (23). Further studies, using more specific tools, are therefore required to reach a definitive conclusion about the respective roles of α_1 - and α_2 -adrenergic receptors in this effect. The signaling pathway leading to the stimulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity in response to α -adrenergic agonists is far from being fully elucidated. It appears to be dependent on a diacylglycerol-insensitive and staurosporine-sensitive protein kinase (39, 340) and on the calcium/calmodulin-dependent protein phosphatase 2B (calcineurin) (23).

In addition to $\text{Na}^+\text{-K}^+\text{-ATPase}$, norepinephrine also modulates, directly or indirectly, sodium-coupled acid-base transporters in proximal tubule, since α -adrenergic agonists increased intracellular pH (334). In BCECF-loaded suspensions of rat proximal tubules, both α_1 - and α_2 -agonists increased intracellular pH through stimulation of Na^+/H^+ exchange, since this effect was dependent on extracellular sodium and fully prevented by EIPA. Stimulation of Na^+/H^+ exchange by both α_1 -adrenergic (333, 506a) and α_2 -adrenergic (177, 333, 599) agonists has been confirmed in isolated rat (333) and rabbit proximal tubules (599), as well as in primary and immortalized cultures of mouse proximal tubules (506a) and OK cells (177). Studies with antisense oligonucleotides and subtype-specific antagonists demonstrated that the stimulation of Na^+/H^+ exchange in mouse proximal tubule cells is mediated for half by α_{1A} -receptors and for the remaining half by α_{1B} -receptors, whereas α_{1D} -receptors are not involved in this regulatory pathway (506a). Because α -adrenergic control of the proximal tubule Na^+/H^+ exchange has been investigated only in intact cells, it is not possible to discriminate between a primary stimulation of Na^+/H^+ exchangers and a secondary activation driven by decreased intracellular sodium concentration brought about

by increased $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity. The signaling pathway responsible for Na^+/H^+ exchange stimulation remains to be determined. Specific agonists of α_1 - and α_2 -adrenergic receptors had synergistic effects in rat PCT (333), suggesting either that the number of receptors might be rate limiting or, more likely, that the two subtypes of receptors trigger different signaling pathways. In OK cells, the α_2 -adrenergic stimulation of Na^+/H^+ exchange is independent of the decrease in cellular cAMP concentration (177).

In conclusion, the antinatriuretic effect of α_1 -adrenergic agonists (40) is at least in part explained by an increase in sodium reabsorption in the proximal tubule mediated by stimulation of basolateral $\text{Na}^+\text{-K}^+\text{-ATPase}$ and apical Na^+/H^+ exchange, while the effect of α_2 -adrenergic agonists remains controversial.

2. Stimulatory effect of β -adrenergic agonists

Activation of the β -adrenergic receptors with isoproterenol increased sodium reabsorption in the in vitro microperfused rabbit PCT (71), and blockade of β -adrenergic receptors by propranolol inhibited fluid reabsorption in the in situ microperfused rat PCT (867). The mechanism of action of β -adrenergic agonists on sodium transport has been investigated in primary cultures of rat proximal tubule cells that maintained, at least in part, their functional polarity (743, 744). In this experimental system, β -adrenergic agonists stimulated the apical sodium transport, estimated by sodium uptake, and $\text{Na}^+\text{-K}^+\text{-ATPase}$ -mediated transport measured by ouabain-sensitive rubidium uptake. Whether β -agonists primarily stimulated the apical Na^+/H^+ exchanger and/or the basolateral $\text{Na}^+\text{-K}^+\text{-ATPase}$ remains to be determined.

A ligand-induced association of the COOH-terminal tail of the β_2 -adrenergic receptor with NHE-RF, the protein cofactor required for the cAMP-mediated inhibition of NHE-3 (924), has been recently demonstrated (361). In this study, Chinese hamster ovary cells expressing NHE-RF were stably transfected with both NHE-3 and wild-type or mutant β_2 -adrenergic receptors. Isoproterenol did not alter the activity of NHE-3 in the cells expressing the wild-type β_2 -receptor, whereas an inhibitory effect was observed in the cells expressing a mutant β_2 -receptor that did not bind NHE-RF. In addition, the inhibitory effect of recombinant NHE-RF on NHE-3 activity measured in the presence of active PKA and ATP in rabbit proximal tubule brush-border membranes was prevented by incubation with a GST fusion protein containing the COOH-terminal end of the β_2 -receptor. Altogether, these findings indicate that sequestration of NHE-RF by activated β_2 -adrenergic receptors may prevent the phosphorylation on NHE-3 by PKA and thereby impede its inhibition. This mechanism could antagonize the effect of a basal level of PKA activity and thereby could explain in part the stimulatory effect of

β -adrenergic agonists on sodium and fluid reabsorption by the proximal tubule.

F. Dopamine

1. Local production of dopamine and effect on sodium transport

Both neuronal and extraneuronal dopamine production occur in the kidney. The local synthesis of dopamine by proximal tubules is attested by 1) the presence of intracellular dopamine immunoreactivity (359), 2) the inhibition of sodium transport by precursors of dopamine such as L-dopa or glu-dopa and by inhibitors of dopamine degradation by COMT (241, 727), and 3) the release of dopamine by proximal tubule cells incubated with L-dopa (38, 855). Dopamine synthesis also takes place in OK cells and LLC-PK₁ cells (345, 758, 759). In kidney cortex (38, 489) as well as in LLC-PK₁ cells (759), uptake of L-dopa occurs at both apical and basolateral sides. In human and rat kidney cortex slices, dopamine synthesis from L-dopa is dependent on the presence of extracellular sodium and on Na⁺-K⁺-ATPase activity, suggesting a sodium-coupled mechanism of L-dopa uptake (756, 757). Locally synthesized dopamine is preferentially released into the tubular lumen (855, 856). The proximal tubule synthesis of dopamine is increased by high sodium intake and may therefore participate to the excretion of the sodium load (85, 856).

Indeed, dopamine is an important local regulator of sodium and fluid reabsorption by the proximal tubule. Dopamine decreases fluid and sodium reabsorption in the *in vitro* microperfused rabbit PCT (57) and PST (72). In isolated PCT, the effect of dopamine is detected only when sodium and fluid reabsorption is stimulated by norepinephrine (57). In this setting, dopamine acts from the luminal side but not from the basolateral side, in agreement with a physiological role of the luminal secretion of locally synthesized dopamine.

2. Inhibition of Na⁺-K⁺-ATPase

Effect of dopamine on proximal tubule Na⁺-K⁺-ATPase has been extensively studied. Inhibition of the hydrolytic activity of Na⁺-K⁺-ATPase by exogenously added (20, 82) and locally synthesized dopamine (20, 85) was evidenced in isolated rat PCTs in the late 1980s. These results were confirmed by subsequent studies on intact proximal tubule cells which showed that dopamine also inhibited ouabain-sensitive rubidium uptake (727, 751) and ouabain-sensitive oxygen consumption (727, 728). As in neostriatum neurons (84), inhibition of Na⁺-K⁺-ATPase activity in rat proximal tubule requires both D₁- and D₂-like receptor occupancy, since D₁- or D₂-like agonists alone had no effect (82). Conversely, other authors using

the D₂-like agonist bromocriptine reported pertussis toxin-sensitive stimulation of Na⁺-K⁺-ATPase activity in suspensions of rat proximal tubules (407).

In proximal tubules, the inhibitory effect of dopamine on Na⁺-K⁺-ATPase activity does not involve the PKA-dependent phosphorylation of the protein phosphatase 1 regulator DARPP-32 (21). Indeed, DARPP-32 was not detected by immunoblotting in rat kidney cortex (310), and protein phosphatase 1 activity was not altered by dopamine in suspensions of rat proximal tubule (751). Rather, dopamine-induced inhibition of Na⁺-K⁺-ATPase activity in rat PCT is primarily mediated by PKC (164, 168, 637), but also requires PLA₂ activation (168, 703) and the synthesis of arachidonic acid metabolites via cytochrome P-450-monooxygenase pathway (608).

A dopamine-induced decrease in Na⁺-K⁺-ATPase V_{\max} has been consistently reported in permeabilized (20, 82, 411) and intact rat proximal tubules (727, 728), as well as in OK cells (165). However, dopamine also alters the apparent affinity of the proximal tubule Na⁺-K⁺-ATPase for cations; it decreased the apparent affinity for potassium and increased that for sodium (20, 411). Thus dopamine-induced increase in the sodium affinity of Na⁺-K⁺-ATPase may antagonize functionally the effect of the decrease in V_{\max} of the enzyme, since sodium is rate limiting in intact cells. In intact cells, dopamine also inhibited the ouabain-sensitive rubidium uptake and oxygen consumption (727, 751), demonstrating an overall inhibition of Na⁺-K⁺-ATPase. This inhibition might be accounted for by a decrease in apical sodium entry secondary to the inhibition of the Na⁺/H⁺ exchanger (270, 335, 430, 732) and/or by a more pronounced effect of dopamine on V_{\max} than on sodium affinity, leading to a residual decrease in Na⁺-K⁺-ATPase activity in the presence of physiological intracellular sodium concentrations.

The mechanism of dopamine-induced decrease in V_{\max} of Na⁺-K⁺-ATPase has been extensively studied during the past few years. In suspensions of rat proximal tubule cells and in OK cells, dopamine induced a redistribution of Na⁺-K⁺-ATPase units from the basolateral plasma membrane to intracellular compartments. In these preparations, dopamine induced a rapid (within minutes) decrease in the number of Na⁺-K⁺-ATPase units expressed at basolateral membrane (166) and the sequential increase in Na⁺-K⁺-ATPase abundance in subcellular fractions corresponding to clathrin-coated pits (1 min), early endosomes (2.5 min), and late endosomes (5 min) (164, 166). This redistribution of Na⁺-K⁺-ATPase was associated with increased PIK activity and was prevented by wortmannin and LY-294002, two specific inhibitors of this kinase (168). This result further underlines the key role of PIK in vesicle trafficking between different subcellular compartments (117, 173, 480, 680, 820). The stimulation of PIK by dopamine was abolished by pretreatment with PKC or PLA₂ inhibitors, suggesting that both enzymes are

involved in this effect (168). Because $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunit can be phosphorylated by PKC in vitro (83, 167, 283) and in intact cells, including rat proximal tubule suspensions (66, 134, 295, 555), Chibalin and co-workers (165, 166) evaluated the role of PKC phosphorylation of the α -subunit in dopamine-induced inhibition of $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity. In suspensions of rat proximal tubules, dopamine induced a PKC-dependent phosphorylation of the α -subunit with the same time course as internalization of $\text{Na}^+\text{-K}^+\text{-ATPase}$ (166). The dopamine-induced internalization of $\text{Na}^+\text{-K}^+\text{-ATPase}$ was abolished in OK cells expressing a truncated rat α_1 -subunit lacking the first 31 amino acids, i.e., the two PKC phosphorylation sites (Ser-16 and Ser-23) (166), suggesting that phosphorylation of the α -subunit is an integral part of the signal leading to internalization of $\text{Na}^+\text{-K}^+\text{-ATPase}$ is further supported by the abolition of the dopamine-induced redistribution of $\text{Na}^+\text{-K}^+\text{-ATPase}$ units in OK cells stably expressing a mutant rat α_1 -subunit in which Ser-23 was substituted by alanine (165). Interestingly, despite its dopamine-induced phosphorylation, Ser-16 does not participate in $\text{Na}^+\text{-K}^+\text{-ATPase}$ internalization. Indeed, the dopamine-induced redistribution of $\text{Na}^+\text{-K}^+\text{-ATPase}$ was not altered in OK cells stably expressing a mutant rat α_1 -subunit in which Ser-16 was substituted by alanine (165). After endocytosis, the $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunit is dephosphorylated by protein phosphatase(s) in the late endosomal compartment (166). It remains to be determined whether $\text{Na}^+\text{-K}^+\text{-ATPase}$ units present in the late endosomal compartment are degraded in lysosomes or recycle back to the plasma membrane (Fig. 15).

3. Inhibition of Na^+/H^+ exchanger

Dopamine may also decrease proximal tubule sodium reabsorption through inhibition of the apical Na^+/H^+ exchanger. Dopamine-induced inhibition of proximal tubule Na^+/H^+ exchange, measured as the amiloride-sensitive sodium uptake, was observed in suspensions of intact rat proximal tubules (335) as well as in rat and rabbit brush-border membranes prepared after preincubation with dopaminergic agonists (270, 430, 732). The effect of dopamine on rat brush-border Na^+/H^+ exchanger is mediated by D_1 -like receptors (268, 270, 430), whereas in rabbit, both D_1 -like and D_2 -like receptors are involved (732). This latter finding is conflicting with the absence of effect of a specific D_2 -like antagonist on the inhibition of fluid reabsorption by the rabbit PCT in response to dopamine (57). The signaling pathway responsible for the inhibition of the brush-border Na^+/H^+ exchanger involves both cAMP- and PKA-mediated effects (270) and cAMP- and PKA-independent G protein-linked effects (268).

The dysfunction of the dopamine control of proximal

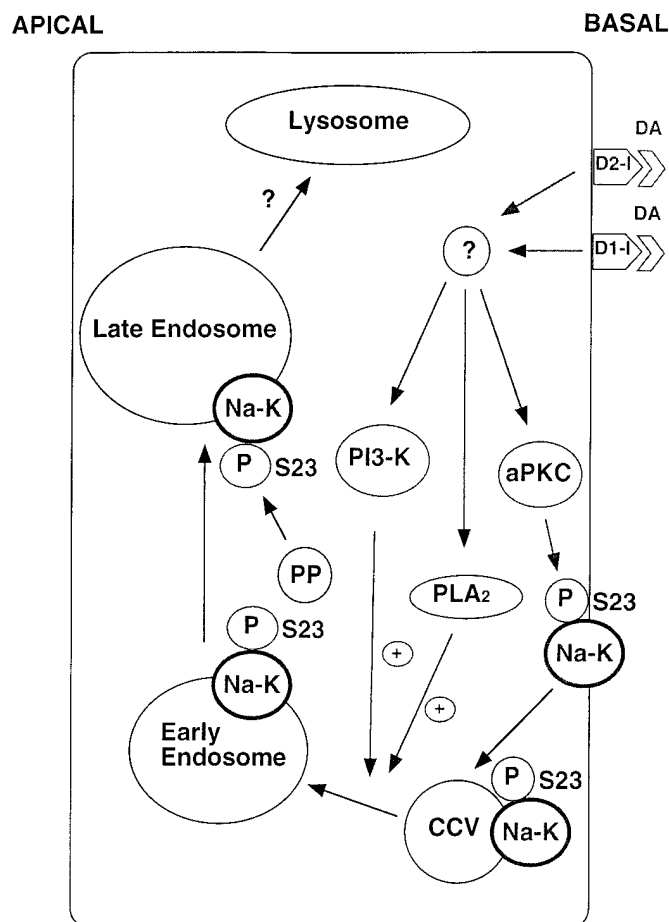


FIG. 15. Regulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ by dopamine in proximal convoluted tubule. Simultaneous binding of dopamine (DA) to D_1 -like ($\text{D}_1\text{-L}$) and D_2 -like ($\text{D}_2\text{-L}$) receptors activates the atypical PKC- ζ (aPKC), PI 3-K, and PLA_2 through yet undetermined signaling intermediate(s). PKC phosphorylates the $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunit on serine-23 (P S23), which triggers the endocytosis of $\text{Na}^+\text{-K}^+\text{-ATPase}$ through clathrin-coated pits (CCV) to early and late endosomes. Both PLA_2 and PI 3-K are required for endocytosis of $\text{Na}^+\text{-K}^+\text{-ATPase}$. The $\text{Na}^+\text{-K}^+\text{-ATPase}$ is then dephosphorylated in the late endosomal compartment by protein phosphatase(s) (PP). Arrows indicate the direction of the signaling cascade.

tubule active sodium reabsorption in the pathophysiology of hypertension is out of the scope of this article. The reader can refer to recent reviews focusing on this topic (409, 441).

G. PTH

The recently reviewed control of the sodium-coupled phosphate reabsorption by PTH in the proximal tubule (300, 579) is out of the scope of this article because it does not contribute significantly to sodium homeostasis.

1. Bicarbonate, sodium, and fluid transport

Acute inhibition of proximal tubule bicarbonate and fluid reabsorption by PTH has been demonstrated by in

vivo micropuncture experiments performed in thyroparathyroidectomized dogs (652) and rats (43). These results have been confirmed by *in vitro* microperfusion of the rabbit PCT (206, 363, 412, 549) and PST (206, 363, 549) and by *in situ* microperfusion of the rat PCT (59). Inhibition of fluid and sodium reabsorption by PTH was proportional to the decrease in bicarbonate reabsorption (43, 206, 412, 652). In addition, PTH had no effect on fluid and sodium reabsorption when proximal tubules were perfused with low bicarbonate solutions (206, 549). Altogether, these findings indicate that inhibition of fluid and sodium reabsorption by PTH is secondary to its effect on bicarbonate transport. Accordingly, the inhibitory effect of PTH is larger in the early PCT than in the late PCT and PST (206, 363). Inhibition of fluid and bicarbonate reabsorption was observed when PTH was applied to the basolateral but not the apical side of the tubule (59). It was mimicked by luminal cAMP (59) and by basolateral cell-permeant cAMP analogs (549). It should be mentioned that in the whole animal, acute PTH infusion did not decrease significantly acid excretion (43, 652), indicating compensatory mechanism in more distal nephron segments.

2. Inhibition of Na⁺-K⁺-ATPase

The effect of PTH on bicarbonate and fluid reabsorption is dependent on active transport, since it is abolished in tubules pretreated with ouabain (549). Several investigators have studied the effect of PTH on proximal tubule Na⁺-K⁺-ATPase. In suspensions of rabbit (217) and rat (673) proximal tubules, PTH decreased ouabain-sensitive oxygen consumption. These results were confirmed by the measurement of the hydrolytic activity of Na⁺-K⁺-ATPase in permeabilized isolated rat PCTs (608) and in basolateral membranes prepared from normal rat kidney cortices taken after acute intravenous infusion of PTH (928). PTH-induced inhibition of Na⁺-K⁺-ATPase is mediated by a PLC- and PKC-dependent activation of PLA₂ (208) and the subsequent metabolism of arachidonic by the cytochrome *P*-450-monooxygenase pathway (608, 672). Both PTH-(1–34) and PTH-(3–34) inhibited Na⁺-K⁺-ATPase activity (673, 928), and the effect was not reproduced by cAMP analogs (608). Conversely, PTH effect on Na⁺-K⁺-ATPase was mimicked by arachidonic acid and by its monooxygenase metabolites (608, 672) and was prevented by inhibitors of PLA₂ (208) and of cytochrome *P*-450 monooxygenase (608, 672).

Inhibition of Na⁺-K⁺-ATPase activity was observed at V_{\max} (608, 673, 928), indicating that PTH decreases either the number of active pumps or the turnover of each pump. PTH effect is unlikely accounted for by endocytosis of active Na⁺-K⁺-ATPase units, since no redistribution of Na⁺-K⁺-ATPase was observed by subcellular fractionation after *in vivo* PTH infusion (928).

However, the physiological relevance of the PTH-induced inhibition of Na⁺-K⁺-ATPase is not obvious. As already discussed for cAMP (see sect. IVB1), the inhibitory effect of PTH on fluid and sodium chloride reabsorption is entirely dependent on the inhibition of bicarbonate reabsorption (206, 549), which is consistent with inhibition of the apical Na⁺/H⁺ exchange and the basolateral Na⁺-HCO₃⁻ cotransport (see below). In contrast, inhibition of Na⁺-K⁺-ATPase should also decrease sodium chloride reabsorption in absence of luminal bicarbonate. Because it is mediated by the PLA₂/cytochrome *P*-450 monooxygenase pathway, it remains possible that the inhibitory effect of Na⁺-K⁺-ATPase observed *in vitro* is artefactual and results from limited metabolic availability, as the inhibitory effect of cAMP.

3. Inhibition of Na⁺/H⁺ exchanger

PTH controls the apical sodium entry step at the level of apical Na⁺/H⁺ exchangers. Monitoring intracellular pH with the fluorescent probe BCECF in the *in vitro* microperfused rabbit PCT (699) and PST (725) have shown that PTH inhibits the apical Na⁺/H⁺ exchanger. Indeed, in both PCT and PST, PTH reduced the initial rate of intracellular acidification after removal of sodium from bicarbonate-free perfusate, an index of Na⁺/H⁺ exchanger activity. This inhibitory effect of PTH on the Na⁺/H⁺ exchange was confirmed by measurement of the EIPA-sensitive sodium uptake in suspensions of rat PCT (335) and in BBMVs from rabbit proximal tubules (445). This inhibitory effect of PTH on the apical Na⁺/H⁺ exchange was reproduced in OK cells (383, 643) and in a simian virus 40-transformed cell line obtained from rabbit PCT (571). Studies on rat proximal tubules (257, 928), OK cells (33), and transfected nonrenal cells (34) demonstrated that PTH controls the activity of the NHE3 isoform of Na⁺/H⁺ exchanger.

As mentioned previously, PTH receptors are coupled to both adenylyl cyclase and PLC, leading to the activation of PKA and PKC, respectively. Several lines of evidence indicate that adenylyl cyclase activation is, at least in part, responsible for PTH-induced inhibition of apical Na⁺/H⁺ exchange in proximal tubule. First, the effect of PTH on the apical Na⁺/H⁺ exchange was mimicked by either cell-permeant cAMP analogs in suspensions of rabbit proximal tubules (445) and in OK cells (384, 643), or by direct activation of adenylyl cyclases by forskolin in OK cells (383, 384, 643). Second, decreasing cAMP generation by addition of 1,25-dihydroxyvitamin D₃ reduced PTH-induced inhibition of Na⁺/H⁺ exchange in OK cells (92). Finally, in the OK-P cell subclone, the biologically active NH₂-terminal fragments of PTH [PTH-(1–34)] and PTHrP [PTHrP-(1–34)] that increase cellular cAMP levels in the absence of PLC activation inhibited Na⁺/H⁺ exchange (533).

However, some studies on cell cultures also suggested a role of PKC in PTH-induced inhibition of proximal tubule Na^+/H^+ exchange. In OK cells, phorbol esters inhibited Na^+/H^+ exchange (383, 384). Biologically active fragments of PTH that activate both PKA and PKC [PTH-(1–34)] or PKC independently of PKA [PTH-(3–34); PTH-(28–42); PTH-(28–48)] inhibited Na^+/H^+ exchange in OK cells (33). Finally, in Na^+/H^+ exchanger-deficient AP-1 cells cotransfected with NHE-3 and PTH/PTHrP receptors, the effect of PTH-(1–34) was altered neither by the specific PKA inhibitor H-89 nor by the specific PKC inhibitor chelerythrine chloride, but it was prevented either by H-89 after downregulation of PKC by overnight incubation with phorbol esters (33) or by H-7 that inhibits both PKA and PKC (34). However, the involvement of PKC in PTH-induced inhibition of Na^+/H^+ exchange appears unlikely in native proximal tubules. Indeed, phorbol esters stimulated apical Na^+/H^+ exchange in suspensions of rabbit proximal tubules (866, 868), as did hormones and neurotransmitters coupled to PKC activation in suspensions of rat proximal tubules (335, 398). Similarly, in AP-1 cells stably transfected with NHE-3, phorbol esters stimulated Na^+/H^+ exchange activity (879). It remains possible that different isozymes of PKC be activated in response to phorbol esters and PTH; these isozymes might be coupled to either stimulatory or inhibitory pathways.

The mechanism of inhibition of proximal tubule Na^+/H^+ exchange by PTH was studied in normal rats (928) and in parathyroidectomized rats (257) given acute intravenous infusion of either PTH or its biologically active fragments. Subcellular fractionation in normal rat kidneys demonstrated a rapid (<1 h) redistribution of NHE-3 after infusion of PTH-(1–34), which activates adenylyl cyclase, PLC, and PLA_2 , but not after infusion of PTH-(3–34), which activates PLC and PLA_2 , but not adenylyl cyclase (928). These results confirmed the PTH-induced redistribution of Na^+/H^+ exchangers previously reported in suspensions of rat proximal tubules (386). In parathyroidectomized rats, PTH infusion inhibited apical membrane Na^+/H^+ exchange activity and increased NHE-3 phosphorylation after 30 min and decreased the apical membrane NHE-3 immunoreactivity without altering total cellular NHE-3 immunoreactivity after 4 h (257). This suggests that PTH first inhibited apical Na^+/H^+ exchanger through phosphorylation, and subsequently induced its endocytosis. Endocytosis of NHE-3 in response to PTH could explain the redistribution observed in normal rats. However, the decrease in apical membrane NHE-3 content was observed several hours after the redistribution of NHE-3 detected by subcellular fractionation studies. The early mobilization of NHE-3 to a specialized apical membrane subdomain in response to PTH or the coiso-

lation of apical membrane and subapical vesicles containing NHE-3 immunoreactivity (91) could explain this discrepancy.

4. Basolateral bicarbonate transporters

The effect of PTH on the basolateral base transport system is more controversial. Indeed, in the *in vitro* microperfused rabbit PCT, the activity of the basolateral $\text{Na}^+-\text{HCO}_3^-$ cotransporter, measured as the initial rate of change in intracellular pH after removal of bath sodium or lowering bath HCO_3^- from 25 to 5 mM, was either decreased (624) or unchanged (699) by PTH. In isolated basolateral membranes from rabbit proximal tubule, PTH inhibited in a cAMP- and PLA_2 -dependent manner the activity of $\text{Na}^+-\text{HCO}_3^-$ cotransporter, determined by bicarbonate-dependent sodium uptake (687). In contrast, in the *in vitro* microperfused rabbit PST, PTH and cAMP stimulated base exit through a $\text{Cl}^-/\text{HCO}_3^-$ exchanger (725). Taken together with the identification of a cAMP-stimulated basolateral chloride channels in the rabbit PST (726), these observations suggest that PTH promotes the shift from a NaHCO_3 to a NaCl reabsorption mode in the PST.

H. Insulin

De Fronzo et al. (198) first demonstrated that insulin exerts an antinatriuretic effect independently of the glycemic status in healthy human. A similar effect was later reported in dog (199) and rat (466). These results indicate that insulin may directly control renal sodium handling. Because insulin was shown to increase fluid and sodium reabsorption in *in vitro* microperfused rabbit PCT (51), the antinatriuretic effect of insulin is thought to originate in part in proximal tubules.

The stimulatory action of insulin is, at least in part, accounted for by an alteration of Na^+-K^+ -ATPase activity. Indeed, in isolated rat PCTs, physiological concentrations of insulin enhance the transport activity of Na^+-K^+ -ATPase independently of the apical sodium entry (279, 281). In this setting, insulin did not alter the V_{max} but increased the apparent sodium affinity of Na^+-K^+ -ATPase (279). This effect of insulin on rat proximal tubule Na^+-K^+ -ATPase activity was independent of PKC; it was prevented by tyrosine kinase inhibition and was mimicked by EGF and orthovanadate, an inhibitor of tyrosine phosphatases (280). These results indicate that insulin modulates Na^+-K^+ -ATPase activity through a tyrosine phosphorylation process, raising the possibility of a direct tyrosine phosphorylation of the Na^+-K^+ -ATPase.

This latter hypothesis was recently confirmed (278). Indeed, in rat proximal tubules, Na^+-K^+ -ATPase α -subunit was phosphorylated at Tyr-10, and insulin increased from 10 to 25% the proportion of tyrosine phosphorylated

Na⁺-K⁺-ATPase units. Several lines of evidence indicate that the stimulation of Na⁺-K⁺-ATPase activity by insulin in proximal tubule cells is most likely accounted for by tyrosine phosphorylation of its α -subunit: 1) substitution of Tyr-10 with Ala (Y10A) abolished the stimulation of ouabain-sensitive rubidium uptake by insulin in OK cells; 2) the basal exogenous Na⁺-K⁺-ATPase-mediated rubidium uptake is higher in OK cells expressing the Y10E mutant α_1 -subunit, a mutation that mimicks the effect of the negative charge introduced by phosphorylation; and 3) stimulation of ouabain-sensitive rubidium uptake and phosphorylation of Na⁺-K⁺-ATPase occurred with the same time course and within the same range of insulin concentrations and cosaturated in rat PCTs.

In addition, insulin may also stimulate directly the apical sodium entry through the Na⁺/H⁺ exchanger, as shown in suspensions of rat proximal tubule (336).

I. Glucocorticoids

Chronic corticosteroid excess increases whereas chronic corticosteroid deficiency reduces the urine excretion of ammonium, phosphate, and total and titratable acid (226, 404, 405). Effects on phosphate metabolism will not be discussed here because they do not contribute significantly to the sodium balance, and the reader is referred to recent reviews (299, 463). The increased excretion of acid results in part from increased proximal tubule proton secretion and bicarbonate reabsorption (56). Wilcox et al. (882) demonstrated that corticosteroid-induced changes in total and titratable acid urinary output and ammonium excretion are mediated by glucocorticoid receptors, in agreement with the proximal origin of these phenomena.

Glucocorticoids have little or no effect on proximal tubule Na⁺-K⁺-ATPase. In both rats and rabbits, adrenalectomy did not (or only slightly) reduce(d) Na⁺-K⁺-ATPase activity (246, 247), and long-term corticosteroid administration did not increase it (245, 323).

In contrast, studies in rat BBMVs demonstrated that glucocorticoid stimulated the apical Na⁺/H⁺ exchanger (298, 464, 465); although amiloride-sensitive sodium uptake in BBMVs was not altered in vesicles from adrenalectomized (ADX) rats, it was increased in BBMVs from normal or ADX rats treated for 2 days with dexamethasone. This stimulation was accounted for by an increased number of Na⁺/H⁺ exchangers in BBMVs since the exchanger affinities for sodium and proton were not altered by glucocorticoids. Because glucocorticoids stimulate endogenous production of acid (404, 405), and acidosis increases the V_{\max} of Na⁺/H⁺ exchanger in BBMVs (181), the question arose of establishing whether stimulation of Na⁺/H⁺ exchanger was a primary effect of glucocorticoid or was secondary to intracellular acidification. To answer

this question, the effect of glucocorticoids on Na⁺/H⁺ exchanger activity was determined in BBMVs from ADX rats either under normal acid/base balance or made acidotic by addition of NH₄Cl in the drinking solution. Results indicated that dexamethasone was equally efficient in stimulating Na⁺/H⁺ exchanger in normal and acidotic rats and that acidosis did not increase Na⁺/H⁺ exchanger activity in the absence of glucocorticoid treatment. This indicated that glucocorticoid effect was independent of acidosis, whereas the effect of acidosis was mediated by glucocorticoids.

Regulation of the number of Na⁺/H⁺ exchangers in rat brush-border membranes was recently confirmed directly by immunoblot and immunohistochemistry (514). Adrenalectomy did not alter the abundance of the NHE-3 isoform, whereas administration of dexamethasone for 2 days to either normal or ADX rats increased it in proximal tubules. This was a transcriptional effect of glucocorticoids since 1) the promoter of rat NHE-3 gene contains multiple DNA sequence elements recognized by the GR (127, 447); 2) in OK and LLC-PK₁ cells transiently transfected with a chimera made of the 5'-regulatory region of NHE-3 gene coupled to the luciferase gene, glucocorticoid treatment induced luciferase activity (447); and 3) NHE-3 mRNA abundance increased in proximal tubules from rabbits treated for 2 days with dexamethasone (55).

In addition to this long-term (2–3 days) *in vivo* effect of glucocorticoids, several studies indicate that dexamethasone can exert short-term (few hours) *in vitro* effects on proximal tubule Na⁺/H⁺ exchanger. *In vitro* addition of dexamethasone to microperfused rabbit PCT increased bicarbonate reabsorption (56) as well as Na⁺/H⁺ exchanger activity within 3 h (55). In rabbit proximal tubule cells, stimulation of Na⁺/H⁺ exchanger activity was observed as soon as 1 h after dexamethasone addition (90). Short-term stimulation of bicarbonate reabsorption in rabbit PCT resulted from a transcriptional effect of dexamethasone, since it was blocked by actinomycin D and cycloheximide (56). However, no change in NHE-3 mRNA level was observed (55), suggesting that dexamethasone might induce a protein regulating the activity and/or targeting of NHE-3 in brush-border membrane. These findings are at variance with results in OK-P cells in which dexamethasone increased within 4 h both the activity of Na⁺/H⁺ exchanger (53), the abundance NHE-3 mRNAs, and its transcription rate (52), suggesting a direct transcriptional effect of glucocorticoids on NHE-3.

J. Summary

Despite some discrepancies and missing data, a few general conclusions concerning the signaling pathways mediating hormone effects on proximal tubule function can be drawn (Fig. 16). The cAMP/PKA signaling pathway

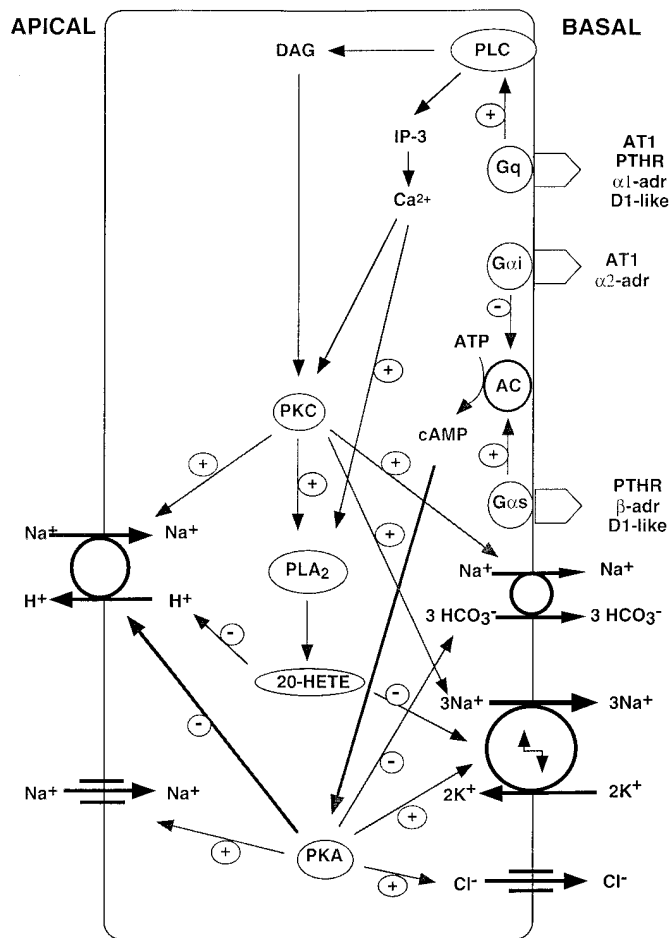


FIG. 16. Overview of the principal signaling pathways controlling sodium transport in proximal tubule cells. Arrows indicate the direction of the signaling cascade and the resulting stimulatory (+) or inhibitory (−) effect on their targets. AT₁, angiotensin II receptor; PTHR, parathormone receptor; α₁-adr, α₁-adrenergic receptor; α₂-adr, α₂-adrenergic receptor; β-adr, β-adrenergic receptor.

downregulates sodium-bicarbonate reabsorption and upregulates sodium-chloride reabsorption. This shift from a Na⁺-HCO₃[−] transport mode in proximal tubules to a Na⁺-Cl[−] one results from the differential regulation of proton/bicarbonate-coupled sodium transporters (the apical NHE-3 Na⁺/H⁺ exchanger and the basolateral NBC-1 Na⁺-HCO₃[−] cotransporter) which are inhibited, and of proton/bicarbonate-independent sodium transporters (the basolateral Na⁺-K⁺-ATPase and possibly the apical epithelial sodium channel ENaC) which are activated. cAMP/PKA-induced stimulation of Na⁺-K⁺-ATPase involves its phosphorylation and its redistribution toward the basolateral membrane, and therefore increases its V_{\max} . cAMP/PKA inhibition of NHE-3 (and probably NBC-1) also involves phosphorylation through a complex network of protein-protein interactions that requires NHE-RF and cytoskeletal components.

Phorbol ester-activated PKCs upregulate both bicar-

bonate-dependent and -independent transporters. Activation of Na⁺-K⁺-ATPase results from increased affinity for sodium brought about by its PKC phosphorylation on Ser-16 without change in its V_{\max} .

Finally, a PLA₂/arachidonate/cytochrome *P*-450-monooxygenase pathway downregulates the transport properties of proximal tubules, mainly through inhibition of Na⁺-K⁺-ATPase. This inhibitory pathway may be triggered by some types of PKCs and/or in response to metabolic stress. By inhibiting ATP consumption, it can be considered as a protective mechanism against the deleterious effects of cellular ischemia.

Phorbol ester-sensitive PKCs are the main mediators of the stimulatory effects of low concentrations of ANG II and of α-adrenergic agonists, even though decreased cAMP production may also participate to the upregulation of NHE-3. The cAMP/PKA pathway underlies the stimulatory effect of β-adrenergic agonists, with the inhibitory effect of cAMP/PKA on H⁺-HCO₃[−] transporters being likely prevented through functional inhibition of NHE-RF by direct interaction with activated β-receptors. Finally, the inhibitory effects of dopamine and PTH are mediated in part by the PLA₂/arachidonate/cytochrome *P*-450-monooxygenase pathway (inhibition of Na⁺-K⁺-ATPase) and in part through cAMP/PKA pathway (inhibition of H⁺-HCO₃[−] transporters).

In addition, tyrosine kinase phosphorylation of Na⁺-K⁺-ATPase on Tyr-10 appears as the main mechanism for the stimulatory effect of insulin. In contrast, the stimulatory effect of glucocorticoids mainly results from transcriptional activation of apical transporters.

V. HORMONAL CONTROL OF SODIUM TRANSPORT IN THE THICK ASCENDING LIMB

A. General Transport and Regulatory Properties of the TAL

1. Transport properties

TALs reabsorb ~15% of the filtered sodium and also reabsorb potassium, bicarbonate, and the divalent cations calcium and magnesium. In contrast, there is no net transport of either water, glucose, phosphate, or amino acids. The TAL is called the diluting segment with respect to this ability to reabsorb solutes in excess of water: the fluid delivered by the TAL to the distal convoluted tubule is hypotonic, and its sodium chloride concentration is ~30–40% of that in the glomerular ultrafiltrate. This function is very important for maintaining the water balance of the organism because it allows it to excrete water in excess of solutes in hypotonic states.

In TAL cells (Fig. 17), the sodium gradient generated

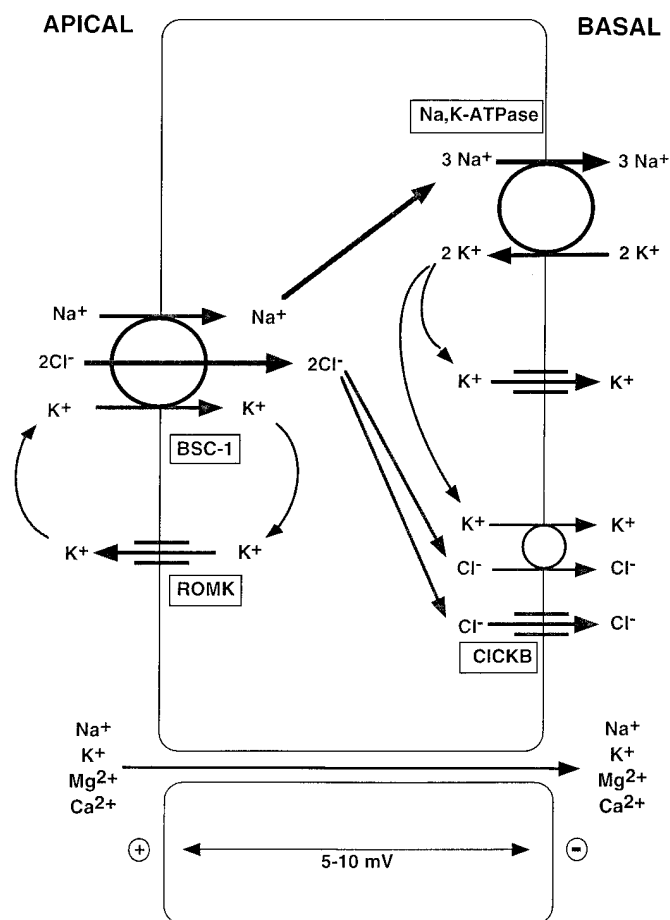


FIG. 17. Cellular mechanism of sodium, potassium, and anion transport in thick ascending limbs of Henle's loop. Arrows indicate net fluxes of solutes. The names of the currently cloned transporters are mentioned into rectangular boxes.

by basolateral Na⁺-K⁺-ATPase is mainly dissipated by an apical electroneutral Na⁺-K⁺-2Cl⁻ cotransport system (343) that couples the downhill entry of sodium to the uphill transport of potassium and chloride. This cotransport system displays a high affinity for both sodium (3–4 mM) and potassium (2 mM) and is specifically inhibited by the loop diuretics furosemide and bumetanide. This Na⁺-K⁺-2Cl⁻ cotransporter has been cloned (BSC1 or NKCC2) (319), and the cognate protein was found at the apical pole of TAL cells (450). Potassium ions accumulated by Na⁺-K⁺-2Cl⁻ cotransport above Nernst equilibrium are recycled across the apical membrane, allowing adequate potassium availability to the cotransporter, via inwardly rectifying, voltage-insensitive potassium channels (ROMK) (389, 908). Chloride ions leave the cells across the basolateral membrane via chloride channels (CICK2) (4) and electroneutral K⁺-Cl⁻ cotransport system (KCC1) (338, 344, 502). Conductive diffusion of chloride and potassium depolarizes the basolateral membrane and hyperpolarizes the apical one, respectively. These

two diffusion potentials in series combine to generate the lumen-positive transepithelial voltage characterizing the TAL. However, this transepithelial voltage is partly shunted by the electrical conductance of the paracellular pathway; because its conductance is higher for cations than for anions, the shunt current is mainly carried by net sodium reabsorption and to a lesser extent by chloride back flux. The lumen-positive voltage also serves as driving force for calcium and magnesium reabsorption (210, 889). The gene of paracellin-1, a protein accounting for the selective permeability of the shunt pathway to magnesium, was recently cloned, and mutations were shown to be responsible for renal magnesium wasting (742).

With the distal convoluted tubules, TALs display the highest sodium reabsorption capacity and Na⁺-K⁺-ATPase activity per tubular length unit. Under resting conditions, the quantity of sodium reabsorbed through TAL cells per minute approximately amounts to fourfold the intracellular pool of sodium. Thus maintenance of a constant intracellular sodium concentration requires a tight coordination of the activity of the different transporters involved in apical and basolateral ion movements. And, indeed, dysfunction of any of these transporters leads to dramatic impairment of sodium and water handling. Thus Bartter's syndrome may result from dysfunction of either the apical Na⁺-K⁺-2Cl⁻ cotransporter (740), the basolateral chloride channel (738), or the apical potassium channel (741).

TAL also constitutes an important site of fluid acidification and ammonia transport. Despite the presence of an apical V-type H⁺-ATPase, bicarbonate transport by TAL is primarily coupled to apical Na⁺/H⁺ exchanger, both NHE-2 and NHE-3 isoforms being present in apical membranes (149, 780). At the basolateral cell border, bicarbonate leaves the cell via Cl⁻/HCO₃⁻ exchange as well as K⁺-HCO₃⁻ and Na⁺-HCO₃⁻ cotransport (621). Ammonia reabsorption in TAL is active; at the apical cell border, ammonium ions enter mainly by competing with potassium for transport by the apical Na⁺-K⁺-2Cl⁻ cotransporter. Intracellularly regenerated ammonia leaves the cell by nonionic diffusion across the basolateral membrane, which displays a much higher permeability to ammonia than the apical membrane (460).

Although these cellular mechanisms of solute reabsorption are essentially similar in MTAL and CTAL, three distinct features characterize the two nephron segments: 1) compared with kidney cortex, blood supply to the renal medulla is restricted and oxygen can be rate limiting in the MTAL, especially in view of the large ATP requirement necessary for sodium chloride reabsorption in that portion of the nephron. Interestingly, MTALs, but not CTALs, display many feedback regulatory mechanisms that downregulate cation reabsorption and thereby limit anoxia. 2) In most species except rabbit, reabsorption of divalent cations along the TAL is restricted to the CTAL

(whether in these species paracellin-1 is expressed only in the CTAL remains to be determined). 3) The largest part of sodium chloride reabsorbed in the MTAL is recycled in the kidney medulla and contributes to generate the gradient of osmotic pressure, whereas salt reabsorbed along the CTAL is rapidly washed out of the kidney by cortical blood flow and therefore contributes to dilute the tubular fluid and to generate free water.

In summary, $\text{Na}^+\text{-K}^+\text{-ATPase}$ not only energizes sodium, potassium, ammonium, calcium, magnesium, chloride, and bicarbonate reabsorption in the TAL, but also serves as the motor for the generation of the corticopapillary osmotic gradient that drives water reabsorption along the collecting duct.

2. Regulatory properties

cAMP is the main stimulus of ion reabsorption in the TAL. Many hormones and mediators, e.g., vasopressin, PTH, glucagon, calcitonin, and β -adrenergic agonists, can be positively coupled to adenylyl cyclase in the TAL and stimulate sodium, potassium, chloride, and divalent cation reabsorption. A peculiarity of the hormonal control of TAL function through cAMP signaling is its redundancy. So many hormones activate a same pool of adenylyl cyclase in the TAL that in vivo the system is always stimulated maximally under normal physiological conditions. In other words, when the concentration of only one of the multiple hormones stimulating adenylyl cyclase in the TAL decreases, the remaining hormones suffice to fully sustain maximal TAL transport functions. This conclusion is based on the following: 1) characterization of the effects of adenylyl cyclase activating hormones on ion transport by in vivo micropuncture of rat TAL required the development of an hormone-deprived model in which plasma vasopressin, PTH, calcitonin, and glucagon were all four suppressed artificially beforehand (34, 242, 681). 2) Characterization of hormone action by in vitro microperfusion of TALs requires, before hormone application, a preequilibration period during which nephron segments recover from their in vivo stimulation; during this period, their transepithelial voltage decreases steadily down to a basal level, reflecting destimulation of solute transport. 3) Although human TALs lack vasopressin-sensitive adenylyl cyclase (142, 684), humans do not display any impairment of their ability to dilute urine, i.e., of their TAL function.

As a counterpart, the major physiological regulation of the cAMP/PKA signaling pathway in TALs may not be through its stimulation but through its inhibition. And, indeed, numerous factors oppose the stimulatory effects of adenylyl cyclase and are functionally important regulatory parameters.

The following discussion mainly focuses on the effects of the cAMP/PKA cascade and on its negative control by ANG II, PGE_2 , endothelin, cGMP, and extracellular calcium.

The effects of other hormones, including corticosteroids, dopamine, and insulin, are also discussed briefly.

B. cAMP/PKA Signaling Pathway and Related Hormones

As shown by micropuncture and by in vitro microperfusion studies, increased intracellular cAMP level is associated with increased sodium chloride reabsorption in the TAL (192, 211, 212, 243, 788, 887, 888). As expected from the presence of hormone-sensitive adenylyl cyclase in MTAL and/or CTAL of rat, rabbit, and mouse, the stimulatory effect of cAMP was mimicked by basolateral addition of either vasopressin (87, 360, 377, 379, 698, 888, 889), PTH (212, 243, 887), glucagon (211), calcitonin (242), or β -adrenergic agonists (36, 567) to in vitro microperfused CTAL and/or MTAL. The mechanism of the cAMP-dependent increase in sodium chloride transport was further analyzed at the molecular level.

1. Control of $\text{Na}^+\text{-K}^+\text{-ATPase}$

As already discussed, stimulation of transcellular sodium flux in TAL cells must imply the coordinated stimulation of both apical ($\text{Na}^+\text{-K}^+\text{-2Cl}^-$ cotransporter and potassium channel) and basolateral transporters ($\text{Na}^+\text{-K}^+\text{-ATPase}$ and chloride channel). However, the first study on isolated rat MTAL indicated that forskolin and cAMP analogs reduced $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity (702). Subsequently, this inhibitory effect was shown to result from limited oxygen and metabolic substrate supply that led to cellular ATP depletion and to the triggering of cell protective mechanisms (467). Indeed, in the presence of adequate oxygen supply and oxidative metabolic substrates that increased intracellular ATP level, both forskolin and cAMP analogs stimulated the transport and the hydrolytic activities of $\text{Na}^+\text{-K}^+\text{-ATPase}$ in isolated rat MTALs (467). Vasopressin also increased the V_{max} of $\text{Na}^+\text{-K}^+\text{-ATPase}$ (153, 638). The dependence of the regulation of sodium transport on oxidative metabolism has been observed in other nephron segments (see sect. III C1 for example), but it is exacerbated in MTAL cells because 1) cellular ATP is almost exclusively supplied by oxidative metabolism, as the contribution of anaerobic metabolism is very low (826), and 2) the ATP requirement for $\text{Na}^+\text{-K}^+\text{-ATPase}$ is very high and accounts for as much as 80% of total oxygen consumption (799). Thus oxygen availability may be rate limiting for ATP production and thereby for sodium transport by MTAL, as evidenced both in vitro and in vivo: 1) in vivo measurements with microelectrodes implanted in the kidney parenchyma indicate that Po_2 in kidney medulla was low (32, 492), and it increased markedly in response to transport inhibition by loop diuretics (113); and 2) in vitro measurements indicated that

basal cellular ATP content was 25% lower in nonoxygenated compared with oxygenated MTALs (467).

Stimulation of Na⁺-K⁺-ATPase by forskolin and cAMP observed in well-oxygenated MTALs likely resulted from PKA-mediated phosphorylation of its α -subunit. As discussed in section 14.5, PKA phosphorylates the α -subunit of Na⁺-K⁺-ATPase on Ser-943 in vitro and in intact cells (66, 83). In suspensions of rat MTALs, cAMP analogs increased the phosphorylation of Na⁺-K⁺-ATPase α -subunit (467). In addition, the stimulation of Na⁺-K⁺-ATPase activity was linearly related and cosaturated with the level of phosphorylation of its α -subunit (467), suggesting a causal relationship between the phosphorylation and the stimulation of Na⁺-K⁺-ATPase.

Inhibition of Na⁺-K⁺-ATPase activity observed in response to cAMP in hypoxic MTALs resulted from the stimulation of a PLA₂/cytochrome P-450-dependent monooxygenase pathway and the synthesis of arachidonic acid metabolites that directly inhibit the pump activity (702). Indeed, inhibition of Na⁺-K⁺-ATPase was mimicked by arachidonic acid (129, 702) and was prevented by inhibition of either PLA₂ with mepacrine (702) or cytochrome P-450-dependent monooxygenase with SKF525A (702). Triggering of this pathway in hypoxic MTALs may not result from a primary effect of cAMP/PKA but rather from decreased Po₂ brought about by an initial stimulation of sodium transport. Thus, whatever the oxygenation status of MTALs, activation of PKA would first stimulate sodium reabsorption, a process that increases oxygen and ATP consumption, as indicated by the decrease in cellular ATP content (467). In the absence of adequate oxygen supply, stimulation of sodium transport would rapidly provoke cellular hypoxia, insufficient ATP synthesis which, in turn, would stimulate the PLA₂/arachidonate/monooxygenase inhibitory pathway. Conversely, when oxygen supply is sufficient, cell metabolism would face the additional demand for ATP synthesis elicited by cAMP-induced increase in sodium transport, and the PLA₂/arachidonate/monooxygenase pathway would not be triggered.

In support to this hypothesis, it was found that 1) cAMP induced similar levels of phosphorylation of Na⁺-K⁺-ATPase α -subunit in hypoxic and in well-oxygenated MTALs, and 2) mepacrine abolished the inhibitory effect of cAMP on Na⁺-K⁺-ATPase activity in hypoxic MTALs but did not alter cAMP-induced phosphorylation of its α -subunit (467). Altogether, these findings indicate that the inhibitory mechanism triggered by PLA₂ stimulation applies to Na⁺-K⁺-ATPase units that had been phosphorylated through PKA stimulation beforehand.

2. Na⁺-K⁺-2Cl⁻ cotransporter

As expected, cAMP analogs also stimulated the Na⁺-K⁺-2Cl⁻ cotransport activity measured either as bumetanide-sensitive rubidium uptake (19) or bumetanide-sensi-

tive intracellular acidification in response to exposure to NH₄Cl (ammonium being transported by Na⁺-K⁺-2Cl⁻ cotransporter as a potassium substitute) (14) in suspensions of rat MTALs. This PKA-mediated functional effect relied on a primary activation of the cotransporter, since the stimulation of the Na⁺-K⁺-2Cl⁻ cotransporter was not prevented by the inhibition of either Na⁺-K⁺-ATPase, apical potassium channels, or basolateral chloride channels (14). In vitro treatment with vasopressin also stimulated apical sodium entry through the Na⁺-K⁺-2Cl⁻ cotransporter (563, 779).

In mouse MTALs, it had been proposed that vasopressin altered the mode of apical sodium entry from a Na⁺-Cl⁻ cotransport to the classical Na⁺-K⁺-2Cl⁻ cotransport (779), both modes being sensitive to furosemide. Very recently, a molecular basis has been proposed for this shift. Several alternatively spliced cDNAs encoding the murine apical furosemide-sensitive Na⁺-K⁺-2Cl⁻ cotransporter mBSC1 have been identified. A total of six isoforms with different COOH termini are expressed in the mouse kidney: three C9 forms (mBSC1-A9, -F9, and -B9) of ~150 kDa and three C4 forms (mBSC1-4A, -4B, and -4F) of ~120 kDa due to truncation of COOH termini (570). When expressed in *Xenopus* oocytes, the three C9 isoforms induced a furosemide-sensitive Na⁺-K⁺-2Cl⁻ cotransport activity that was not sensitive to PKA (640). In contrast, expression of the C4 isoforms induced no sodium transport activity unless the oocytes were preexposed to hypotonic medium for 1 h; under such conditions, furosemide-sensitive and potassium-independent Na⁺-Cl⁻ cotransport activity appeared and was inhibited by PKA stimulation (639). Moreover, coexpression of C4 isoforms in normal *Xenopus* oocytes exerted a dominant negative effect on C9-mediated Na⁺-K⁺-2Cl⁻ cotransport activity, and this inhibitory effect was reversed by activation of PKA (640). If confirmed in mouse MTAL, this process would account for the cAMP-induced shift from Na-Cl to Na⁺-K⁺-2Cl⁻ cotransport. The sensitivity of the C4 isoforms to tonicity may also account for the inhibitory effect of hypertonicity on both basal and vasopressin-stimulated sodium chloride reabsorption (380).

In cultured cells derived from mouse MTAL, acute stimulation of Na⁺-K⁺-2Cl⁻ cotransport by forskolin or vasopressin was associated with F-actin redistribution and was impaired by stabilization of actin filaments by phalloidin (901), suggesting that vasopressin acts at least in part through actin depolymerization (739).

In addition to the short-term control of Na⁺-K⁺-2Cl⁻ cotransport activity, cAMP generation might be an important regulator of Na⁺-K⁺-2Cl⁻ cotransporter expression in TAL. Indeed, 1-wk vasopressin infusion to Brattleboro rats (which exhibit a spontaneous knockout of the vasopressin gene) or dehydration of normal rats (which increases endogenous vasopressin secretion) increased the expression of the Na⁺-K⁺-2Cl⁻ cotransporter BSC1 (461). Furthermore, expression of adenylyl cyclase type

VI and of BSC1 decreased in mice with heterozygous disruption of the $G\alpha_s$ gene (232).

3. Potassium and chloride channels

Stimulation of apical sodium entry ($\text{Na}^+/\text{K}^+/\text{2Cl}^-$ co-transporter) and basolateral extrusion ($\text{Na}^+/\text{K}^+/\text{ATPase}$) is not sufficient to account for increased solute reabsorption in the TAL. Because of the tight coupling between the different transporters, it also requires stimulation of apical potassium recycling and basolateral chloride exit. Early experiments by *in vitro* microperfusion indicated that activation of PKA hyperpolarized the basolateral membrane (377, 714). However, this observation was interpreted differently. According to Andreoli's group (377), this was accounted for by primary stimulation of apical ion entry, involving stimulation of $\text{Na}^+/\text{K}^+/\text{2Cl}^-$ cotransport and potassium recycling through apical potassium channels, leading to increased intracellular chloride concentration and higher diffusion potential for chloride across basolateral membrane. According to Greger's group (714), it resulted from primary stimulation of basolateral chloride channels, that decreased intracellular chloride concentration which in turn activated apical ion entry and potassium recycling.

Although intracellular chloride concentration has not been measured, it seems likely that both apical ion entry, potassium recycling, and basolateral chloride exit steps are primarily activated through PKA stimulation. In any case, apical potassium channels (663, 851) and basolateral chloride channels (352, 664) may be activated through PKA stimulation.

To sum up, basal multihormonal stimulation of cAMP/PKA pathway maintains a high sodium chloride reabsorption in TAL. This tonic effect involves the stimulation of apical $\text{Na}^+/\text{K}^+/\text{2Cl}^-$ cotransporter and of potassium recycling through potassium channels associated with a coordinated increase in basolateral sodium and chloride exit through the stimulation of $\text{Na}^+/\text{K}^+/\text{ATPase}$ and chloride channels (Fig. 18). The simultaneous regulation of apical and basolateral transporters by cAMP allows the regulation of transcellular sodium flux without altering intracellular ionic strength. When oxygen availability is restricted, this stimulatory pathway is overridden by the activation of a PLA_2 -mediated pathway that inhibits $\text{Na}^+/\text{K}^+/\text{ATPase}$ and $\text{Na}^+/\text{K}^+/\text{2Cl}^-$ cotransporter activities leading to a decrease in sodium reabsorption (253). This latter mechanism might be important to ensure cell survival under pathological conditions. Finally, this basal stimulation is downregulated by numerous factors and through various pathways, as summarized below.

C. Inhibition of Sodium Transport in TALs

As already mentioned, the physiological regulation of the transport properties of TALs is accounted for mainly

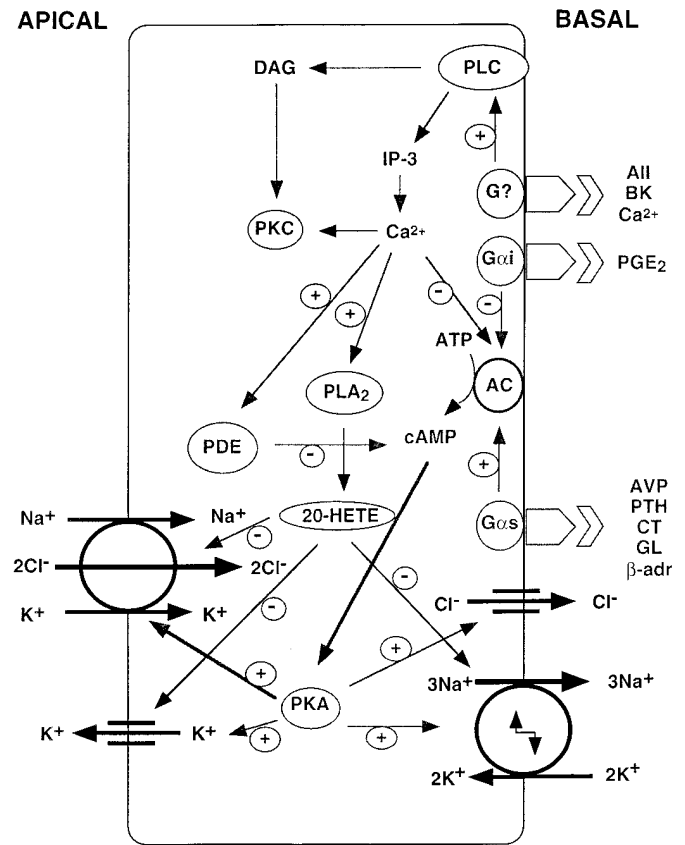


FIG. 18. Overview of the principal signaling pathways controlling the active sodium transport in cells of the thick ascending limb of Henle's loop. Arrows indicate the direction of the signaling cascade and the resulting stimulatory (+) or inhibitory (-) effect on their targets. PDE, phosphodiesterase; BK, bradykinin; CT, calcitonin; GL, glucagon.

by the negative modulation of the stimulatory effect of cAMP/PKA signaling pathway rather than by the stimulation itself. In fact, numerous agents and signaling pathways may inhibit sodium transport in TALs. In the following paragraphs, these are discussed according to the mechanism of inhibition rather than specific hormones. Part of the inhibition of sodium transport in TAL results from the unique properties of the adenylyl cyclase expressed in TAL. Indeed, TALs exclusively express type 6 adenylyl cyclase (141) which, along with type 5, displays the unique properties of being inhibited both by intracellular calcium ($[\text{Ca}^{2+}]_i$) and by coupling to $G\alpha_i$ (144). However, other mediators may inhibit TAL function independently of intracellular cAMP level.

1. Inhibition through $G\alpha_i$

Prostaglandins, particularly PGE_2 , inhibit vasopressin-induced solute transport in TAL (192, 772). The role of $G\alpha_i$ activation in this inhibition was suggested by the following: 1) PGE_2 suppressed the effect of vasopressin on mouse TAL sodium transport, but not that of forskolin

or cAMP (192); 2) PGE₂ reduced hormone-induced accumulation of cAMP in TAL from various species (291, 814); 3) PGE₂ effect was curtailed by pertussis toxin treatment (291, 789); and 4) EP₃ prostaglandin receptors (coupled to G_{α_i}) are expressed in TAL (112), whereas there is no functional evidence for EP₁ (coupled to PLC activation) and EP₂ (coupled to adenylyl cyclase activation) receptors in rat TAL (2, 202) (Fig. 18).

2. Inhibition through increased intracellular calcium concentration

ANG II, bradykinin, and extracellular calcium increase [Ca²⁺]_i through G protein-coupled receptors and inhibit solute reabsorption in the rat TAL (15, 202, 346–348). However, [Ca²⁺]_i may exert inhibitory action through different mechanisms, namely, a direct effect of calcium on transport systems, reduction of hormone-induced accumulation of intracellular cAMP, activation of PLA₂ and arachidonate metabolism, or activation of calcium-sensitive PKCs. These differences may be related to their cortical or medullary origin in the TAL.

A direct effect of [Ca²⁺]_i was proposed in view of the inhibitory effect of cytosolic calcium on the activity of apical potassium channels in excised patches from rat TAL (94).

In MTAL, increased [Ca²⁺]_i also activates calcium-sensitive PLA₂ and thereby the production of 20-hydroxy-eicosatetraenoic acid (20-HETE) through the cytochrome P-450 monooxygenase. 20-HETE was found to mediate the inhibition of apical potassium channel and/or Na⁺-K⁺-2Cl⁻ cotransporter in response to bradykinin (347), ANG II (15, 523), and extracellular calcium (853). As already discussed above, this pathway also inhibits Na⁺-K⁺-ATPase activity (Fig. 18).

Finally, in the CTAL, ANG II, extracellular calcium, and bradykinin decrease G_{α_s}-mediated intracellular accumulation of cAMP (144, 202). This inhibition resulted from two mechanisms: 1) stimulation of cAMP degradation by calcium-activated phosphodiesterases, and 2) pertussis toxin-insensitive inhibition of type 6 adenylyl cyclase (202). Interestingly, the first pathway was shared by the three mediators, whereas strong inhibition of adenylyl cyclase was elicited only through activation of the Ca²⁺-sensing receptor (202). This clearly indicates that in a same cell, increased [Ca²⁺]_i can elicit different effects according to the inducing agonist. This observation supposes an intracellular compartmentalization of [Ca²⁺]_i increases (Fig. 18).

3. Inhibition through cGMP

Cell-permeant analogs of cGMP also inhibit solute reabsorption in the TAL (592, 598). Inhibition through cGMP can be physiologically triggered by receptor guanylate cyclase in response to atrial natriuretic peptide and

urodilatin (592, 598), but also through activation of soluble guanylate cyclase (for example, by cytokines), since a nitric oxide donor such as nitroprusside reduced sodium chloride reabsorption (593). Finally, sodium reabsorption was also inhibited by platelet-activating factor (PAF) through increased production of cGMP (593). However, the coupling between PAF receptor and cGMP production is not understood as yet.

4. Calcium-insensitive PKC

Calcium-insensitive PKCs (new and atypical PKCs) have been involved in the effect of endothelin and insulin in the TAL.

Endothelin inhibited solute reabsorption in mouse TAL without increasing [Ca²⁺]_i, but its effect was blocked by PKC inhibitors and was mimicked by DAG analogs (201), suggesting the involvement of PKC of the new family in this process.

Insulin stimulates sodium chloride reabsorption in the rabbit and mouse MTAL (424, 534). This stimulation was blocked by genistein, by wortmannin, and by staurosporine and calphostin C, indicating the involvement of tyrosine kinase, PIK, and PKC (423). Interestingly, insulin effect on sodium transport did not require extracellular calcium, and insulin did not change [Ca²⁺]_i, indicating that relevant PKC should belong to the new or atypical family (425).

Thus stimulation of these new and/or atypical PKCs in TAL can either inhibit (endothelin) or stimulate (insulin) sodium reabsorption. These opposite effects might be mediated by different subtypes of PKCs, e.g., a new PKC for the inhibitory effect of endothelin and an atypical one for insulin stimulatory action. It is worth noting that besides classical PKCs (α and βII), both new (δ and ε) and atypical PKCs (ζ) have been detected in TAL (24).

D. Dopamine

In contrast to the other receptors coupled to the activation of adenylyl cyclase, activation of D₁-like receptors inhibited sodium reabsorption by the *in vitro* microperfused rat MTAL (348). Dopamine and D₁-like agonists were active from the basolateral but not the luminal side, conversely to the proximal tubule where they were active from both sides.

Consistently with the cAMP/PKA signaling mechanism (see above), but in contrast to its reported effect on sodium reabsorption (348), dopamine stimulated the apical Na⁺-K⁺-2Cl⁻ cotransport (19). Thus, according to these observations, the stimulation of apical sodium entry must be overwhelmed by an inhibition of the basolateral exit. The paradoxical dopamine-induced PKA-mediated inhibition of Na⁺-K⁺-ATPase V_{max} described in rat MTAL has been proposed to account for the inhibitory effect of

dopamine on sodium transport (551, 703). This inhibition would result from PKA-mediated phosphorylation of DARPP-32, which in turn would inhibit protein phosphatase-1. Activation of PKA and inhibition of protein phosphatase-1 would increase the phosphorylation level of the $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunit on Ser-943, i.e., the PKA phosphorylation site, and inhibit its activity (at the opposite to the demonstrated stimulatory effect). This mechanism was proposed on the basis of the following: 1) DARPP-32, a dopamine- and cAMP-regulated protein phosphatase-1 regulator (342), is expressed in thick ascending limb from various mammalian species (310, 551); 2) a phosphopeptide corresponding to amino acid residues 8–38 of DARPP-32 inhibited $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity in permeabilized rat MTAL cells (21); and 3) calyculin A, a protein phosphatase-1 inhibitor, inhibited $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity in rat MTAL (495). Unfortunately, the effect of dopamine on the phosphorylation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ α -subunit has not been evaluated in these studies. Because it is now established that PKA phosphorylation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ does not inhibit its activity in MTAL (467), alternative mechanisms of inhibition of the enzyme should be considered. Also, one might consider the involvement of PKC in dopamine-induced inhibition of $\text{Na}^+\text{-K}^+\text{-ATPase}$ since 1) PKC activation is a pathway for inhibiting sodium transport in MTAL (see above), and 2) D_1 -like receptors are also coupled to PKC stimulation through $\text{G}\alpha_q$ (408, 922).

E. Glucocorticoids

The first piece of evidence for corticosteroid action in TAL was provided as early as 1957 by Guinneau and Morel (353) who reported that adrenalectomy reduced the corticomedullary gradient of osmotic pressure. Decreased sodium chloride reabsorption along the TAL of ADX rats was further supported by *in vivo* micropuncture (387) and micropfusion experiments (578, 767) studies and was fully demonstrated by *in vitro* micropfusion of MTAL (900). Adrenalectomy also reduced bicarbonate reabsorption along the loop of Henle, and this effect was reversed by physiological doses of dexamethasone (832).

Adrenalectomy reduced $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity in rat and rabbit TAL (246, 247). In rabbit TAL, this decrease in $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity was accompanied by a parallel decrease in the numbers of $\text{Na}^+\text{-K}^+\text{-ATPase}$ at the plasma membrane, as determined by specific [^3H]ouabain binding (249). Conversely, chronic deoxycorticosterone acetate (DOCA) treatment of adrenal-intact rats and rabbits did not alter $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity along the TAL (245, 323). Within 3 h, *in vivo* administration of dexamethasone to ADX rabbits increased $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity in TAL back to the level observed in normal animals, whereas aldosterone administration had no effect during the same

time frame (247). However, no change in $\text{Na}^+\text{-K}^+\text{-ATPase}$ abundance was observed during this short-term stimulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ (245), suggesting that dexamethasone activated preexisting ATPase units. Short-term (<3 h) stimulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ was reproduced by *in vitro* addition of dexamethasone, but not aldosterone, to MTAL from ADX rats (221, 662). This effect was blocked by actinomycin D and cycloheximide (221), suggesting that dexamethasone induces the expression of a protein, which in turn modulates the activity of $\text{Na}^+\text{-K}^+\text{-ATPase}$. It has been proposed that dexamethasone would inhibit PLA_2 activity through induction of an inhibitor, and thereby relieve $\text{Na}^+\text{-K}^+\text{-ATPase}$ from the tonic inhibitory influence of arachidonate metabolites (219).

Curiously, no attempt was made to evaluate the role of corticosteroids on either apical $\text{Na}^+\text{-K}^+\text{-2Cl}^-$ cotransporter and potassium channel, or basolateral $\text{K}^+\text{-Cl}^-$ cotransporter and chloride channel in TAL. Only a recent study demonstrated that the Na^+/H^+ exchanger NHE-3 was upregulated by chronic (>3 days) dexamethasone treatment in TAL of both adrenal-intact and ADX rats, although adrenalectomy had no effect (514).

VI. HORMONAL CONTROL OF SODIUM AND POTASSIUM TRANSPORT IN THE COLLECTING DUCT

A. General Transport Properties of Collecting Ducts

In mammals, the collecting duct is the final site of regulation of sodium, potassium, acid/base, and water excretion. Accordingly, the collecting duct may reabsorb between 0 and 5% of the filtered sodium, reabsorb or not water, and either reabsorb or secrete bicarbonate. Regulation of acid/base balance originates in intercalated cells and is not related to $\text{Na}^+\text{-K}^+\text{-ATPase}$ -generated ion gradients but to $\text{H}^+\text{-ATPase}$ - and $\text{H}^+\text{-K}^+\text{-ATPase}$ -generated proton gradients. Therefore, the cellular and molecular mechanisms underlying acid/base transport and regulation are not discussed here. In contrast, because $\text{Na}^+\text{-K}^+\text{-ATPase}$ drives both sodium reabsorption and potassium secretion in the principal cells, transport and regulation of these two cations is discussed.

The collecting duct constitutes a tight epithelium displaying high transepithelial resistance and very low paracellular water permeability. Active electrogenic sodium reabsorption generates a large lumen-negative transepithelial voltage (–10 to –60 mV) in the CCD. In deeper portions of the collecting duct, this transepithelial voltage decreases and turns slightly lumen positive as a result of decreased sodium reabsorption by principal cells combined with increased electrogenic proton secretion by intercalated cells.

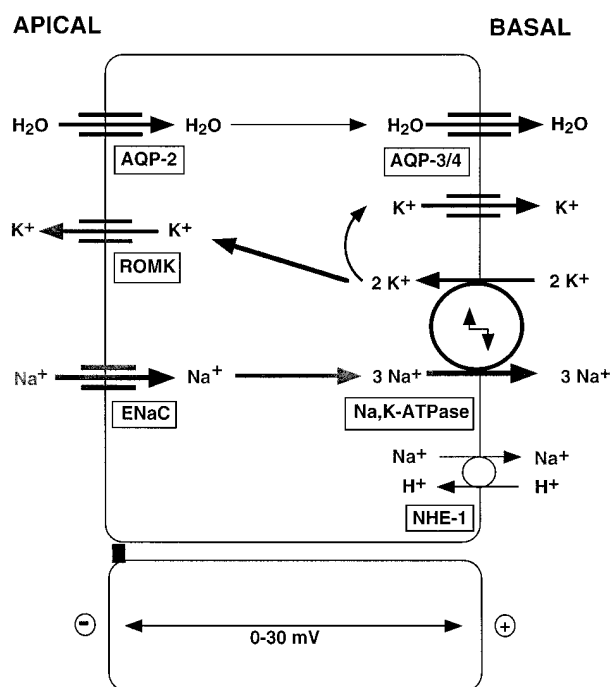


FIG. 19. Cellular mechanism of sodium, potassium, and water transport in principal cells of the collecting duct. Arrows indicate net fluxes of water and ions. The names of the currently cloned transporters are mentioned into rectangular boxes.

As summarized in Figure 19, sodium reabsorption in principal cells is linked to potassium secretion through a two-step mechanism: pumping of potassium within and sodium out of the cell by the basolateral Na⁺-K⁺-ATPase generates driving forces for apical sodium entry and potassium exit. Through this mechanism, potassium secretion is primarily coupled to sodium reabsorption with the 2K⁺:3Na⁺ stoichiometry of Na⁺-K⁺-ATPase.

The major fraction of apical sodium entry is mediated by amiloride-sensitive ENaC, although thiazide-sensitive Na⁺-Cl⁻ cotransporter (TSC) may contribute somewhat in the rat CCD (800). The epithelial sodium channel belongs to a new family of sodium channels displaying homologies with *Caenorhabditis elegans* degenerins (125, 506). Like all the members of the degenerin/ENaC gene superfamily, ENaC displays two hydrophobic membrane-spanning regions with intracellular NH₂ and COOH termini and a large extracellular loop with highly conserved cysteine residues (670, 755). ENaC is a multimeric channel made of homologous α -, β -, and γ -subunits (126), associated in a 2:1:1 stoichiometry (292), surrounding the channel pore (126). ENaC is potently and specifically inhibited by submicromolar concentrations of the diuretic amiloride and its derivative benzamilamide. For more information on the structure and function of ENaC, readers are referred to recent reviews (44, 317, 325).

Apical membrane of principal cells contains two distinct types of potassium channels, maxi potassium chan-

nels (619) that are activated by membrane depolarization and calcium and low-conductance (10–30 pS) inwardly rectifying potassium channels (304) that likely correspond to the cloned ROMK channel (389), in particular the ROMK-1 and ROMK-2 isoforms (101). Maxi potassium channels are probably not involved in potassium secretion because they are sensitive to tetraethylammonium, whereas collecting duct secretion of potassium is not (303). Basolateral membranes of the principal cells also display several types of potassium channels of various conductance (30, 85, and 140 pS) that are inhibited by intracellular acidification and activated by hyperpolarization (849). Their respective role in potassium transport is not clearly understood. However, secretion of potassium through the apical membrane is favored over recycling across the basolateral membrane because diffusive sodium entry depolarizes the apical membrane and thereby increases the driving force for potassium secretion.

In addition, collecting duct principal cells are also the site of water reabsorption through apical vasopressin-induced water channels (AQP-2) and constitutive basolateral water channels (AQP-3 and AQP-4). Although the driving force for water absorption is mainly provided by the countercurrent concentrating mechanism in the loop of Henle (see above), sodium reabsorption along the collecting duct, especially in CCD, dilutes the luminal fluid and contributes to the generation of an osmotic gradient favorable to water reabsorption. Finally, the basolateral membrane of collecting duct principal cells contains a Na⁺/H⁺ exchanger (NHE-1) involved in the regulation of intracellular pH, and which might be involved in the mediation of mineralocorticoid action (47).

The two major hormonal factors that positively control sodium reabsorption by the collecting duct are aldosterone and vasopressin. Insulin may play a significant role in the postprandial period. The stimulatory effects of these factors might be balanced by the negative influence of several mediators such as dopamine, α_2 -adrenergic agonist, and prostaglandins.

B. Aldosterone

Concomitantly to the purification of aldosterone from adrenal cortex, clinicians isolated from the urine of patients with abnormal sodium retention a substance that later proved to be aldosterone (524), a first indication that aldosterone might be involved in the regulation of sodium handling. Later, injection of aldosterone in dog renal artery was reported to alter the electrolytic composition of their urine, identifying the kidney as a target for aldosterone (45). Aldosterone decreases urinary sodium excretion (antinatriuretic effect) and increases that of potassium (kaliuretic effect) and of protons (31, 45, 188, 731). Stop-flow experiments revealed quite early that the distal

parts of the nephron were the sites of action of aldosterone (834). Later, aldosterone was also shown to facilitate the hydrosmotic action of vasopressin (341, 659). In this review we consider only the effects of aldosterone on sodium and potassium excretion. Before analyzing these effects of aldosterone on ion transport, it is important to briefly describe the experimental models that allowed their study.

1. Experimental models to study aldosterone action

The effects of aldosterone on renal sodium and potassium handling were assessed first by clearance studies in which were recorded the changes in urine composition induced by administration of aldosterone to normal or ADX animals. Due to the restricted site of aldosterone action along the nephron, further study of the cell and molecular targets was performed on isolated collecting ducts.

Two types of *in vitro* experiments were attempted to elucidate the action of aldosterone on isolated collecting ducts. In most studies, the plasma level of aldosterone was manipulated *in vivo* (by adrenalectomy, acute or chronic administration of aldosterone, or change of the cation content of the diet), and the transport function of the tubules was determined *in vitro* after their isolation by microdissection. This approach supposes that the cells keep the “memory” of their *in vivo* steroidal environment, which is likely for hormones acting through induction of protein synthesis. In a few studies, the effects of aldosterone were evaluated after *in vitro* addition on nephron segments dissected from either normal or mineralocorticoid-deficient animals. This approach is limited by the short duration of *in vitro* survival of isolated nephron compared with the delay of steroid response.

Experimental models of tight epithelia, such as the frog skin or the urinary bladder of amphibians, palliated this limitation and were very useful to study the action of aldosterone *in vitro*. In addition, these are planar epithelia that can be mounted easily in Ussing's chambers for flux and electrophysiological measurements. According to Ussing-Koeffoed-Johnson model (475), sodium flux across these epithelia can be estimated by the short-circuit current measured when the two faces of the epithelia are bathed with symmetrical solutions. A main limitation of these epithelia is their much lower capacity to reabsorb sodium, compared with renal collecting duct. This has been circumvented in part by developing cell lines such as A6 cells derived from amphibian kidney (630), which can be mounted in Ussing's chambers, when grown on filters. It should be noted, however, that all the conclusions derived from these models may not be directly transposable to the mammalian nephron. Thus efforts were made recently to develop cell lines derived

from mammalian collecting duct principal cells that keep their sensitivity to corticosteroids (75, 230).

2. Effects on sodium transport

Despite the early recognition of impaired renal capacity to reabsorb sodium in patients with Addison's disease, a direct stimulatory effect of aldosterone on sodium transport was demonstrated only in 1961 by Crabbé (188) in amphibian epithelia. This report indicated that aldosterone increased the short-circuit current across the toad bladder. Further characterization of this stimulatory effect (765) indicated that it appears after a 45- to 90-min lag period, followed by an early response, lasting for ~3 h, during which sodium transport nearly doubles and the transepithelial electrical resistance decreases by about one-half. Then, sodium transport keeps on increasing for 12–24 h, whereas the electrical resistance remains low.

In mammals, aldosterone effect on renal handling of sodium has been more difficult to characterize, probably because it depends critically on the experimental conditions. Due to the presence of both GR and MR in the collecting duct, aldosterone concentrations within the physiological range (10^{-10} to 10^{-8} M) must be tested to avoid activation of GRs. Furthermore, effects of acute administration of aldosterone must be distinguished from the chronic effects that may result from secondary associated changes such as extracellular volume expansion, alteration of tubular sodium delivery, or morphological adaptations of tubular cells.

Renal action of aldosterone was evaluated in the light of these considerations in only two studies. Horisberger et al. (394) evaluated aldosterone action on anesthetized ADX and glucocorticoid-supplemented rats, whereas Campen et al. (124) studied conscious ADX rats. A reduction of urinary sodium excretion occurred 30–60 min after aldosterone injection and persisted for several hours. The maximum antinatriuretic effect was observed with $<0.3 \mu\text{g}/100 \text{ g body wt}$ of aldosterone, corresponding to 5 nM plasma aldosterone concentration (a concentration allowing near saturation of MRs). Aldosterone induced antinatriuresis in the presence as well as in the absence of glucocorticoids, but the magnitude of the effect was directly related to the rate of sodium excretion before aldosterone administration. Antinatriuresis was inhibited by the MR antagonist spironolactone and by inhibitors of transcription such as actinomycin D (395), confirming that aldosterone induces the synthesis of proteins that account for its antinatriuretic effect.

Most studies by *in vitro* microperfusion of CCD evaluated the effect of long-term corticosteroid administration on transport functions. The first report (350) indicated that the transepithelial potential difference (PD) was higher in CCDs microdissected from rabbit treated with DOCA than in CCDs from mineralocorticoid-defi-

cient animals. It was subsequently shown that DOCA treatment also increased sodium reabsorption in rat and rabbit CCD (609, 668, 722, 775). Unexpectedly, changes in transepithelial PD and sodium reabsorption were observed only after several days of treatment with DOCA, peaking after 4–18 days (415, 609). When the plasma concentration of aldosterone was varied within physiological range by modifying the cation content of the diet, both the transepithelial PD and the sodium reabsorption flux measured *in vitro* were correlated with the *in vivo* aldosterone concentration; half-maximal increases in voltage and sodium transport were observed at 0.2–0.5 nM plasma aldosterone, a concentration corresponding to the affinity of MR for aldosterone. However, here again, these changes reflect the chronic action of aldosterone, correlated with morphological changes of the principal cells of the CCD (844), and do not correspond to the early (<3 h) effect of aldosterone.

Reports of short-term effects triggered by adding aldosterone to *in vitro* micropperfused CCDs remain few and controversial. Gross and Kokko (351) first reported that, after a 10- to 20-min latency following the addition of aldosterone to CCD from ADX rabbits, the transepithelial PD increased from near-zero control values to values in the –20 mV range after 1.5–2 h (351). Using a similar protocol for CCDs from rabbits with normal plasma aldosterone level, Schwartz and Burg (722) failed to observe any effect of aldosterone added *in vitro* on either transepithelial PD or sodium transport. This apparent discrepancy suggests that the latency before observing a stimulation of sodium transport by aldosterone depends on the aldosterone status of the animals from which CCD were obtained (ADX vs. normal rabbits) and/or on the basal transport capacity of the CCD before *in vitro* addition of hormone. Finally, Wingo et al. (886) reported that *in vitro* addition of aldosterone to CCD from ADX rabbits enhanced sodium reabsorption without altering the transepithelial PD (886), an observation hard to reconcile with the mechanism of sodium reabsorption usually admitted.

Only a few studies investigated the effect of aldosterone on the tubular transport of sodium by other parts of the collecting duct: aldosterone was ineffective in rabbit OMCD (350, 775), and it increased sodium reabsorption in rat IMCD (410). Thus the following discussion is restricted to the CCD.

Short-term effect of aldosterone was recently evaluated in an immortalized mouse collecting duct principal cell line (75). When grown at confluence on permeable filters, these mpkCCD_{c14} cells displayed the typical electrophysiological features of a tight epithelium with a high transepithelial electrical resistance (R_T), a negative transepithelial voltage, and a positive short-circuit current (I_{sc}). I_{sc} was fully inhibited by ENaC blockers such as amiloride and benzamilamide. Addition of aldosterone (10^{-7} M) increased I_{sc} and reduced R_T after a 30- to

60-min lag period, and the maximal effects on these two parameters were observed after 4–6 h. Increased I_{sc} was abolished by cycloheximide and actinomycin D. The threshold of aldosterone action was observed with 10^{-10} M aldosterone, and the effect of low concentrations of aldosterone (10^{-9} M) was not altered by RU486, a specific antagonist of GR. These last two findings strongly suggest that aldosterone is active through occupancy of MRs, the presence of which was verified in these cells by RT-PCR and binding experiments.

3. Effects on potassium transport

Addison's disease is often associated with hyperkalemia, whereas patients with hyperaldosteronism tend to display a negative potassium balance. However, whether the kaliuretic effect of aldosterone is a direct action of the hormone on tubular potassium handling or whether it is secondary to other changes is still a subject of debate. Indeed, early evaluations of the effect of mineralocorticoid administration on urinary potassium excretion led to controversial results (656). The issue to be discussed here focuses on whether the kaliuretic action of aldosterone is entirely secondary to its antinatriuretic action or whether regulation of sodium and potassium transport may be uncoupled. Here again, results are different for the short-term and the long-term effects of aldosterone.

Long-term treatment with mineralocorticoid increases potassium secretion in isolated CCDs (609, 773). In rabbits fed diets with various cation contents, not only the rate of sodium reabsorption but also that of potassium secretion measured *in vitro* in isolated CCDs were correlated with the *in vivo* aldosterone plasma levels (722). Stokes (773) carefully examined, by means of *in vitro* micropfusion, the relationship between sodium reabsorption and potassium secretion in CCDs from normal and DOCA-treated rabbits (773); the rate of sodium reabsorption varied in a wide range, and a linear relationship was observed between these rates and those of potassium secretion in the same tubules. The sodium over potassium flux ratio was 1.34, which is close to the 1.5 stoichiometry of Na⁺-K⁺-ATPase. These data suggest that long-term mineralocorticoid treatment alters sodium and potassium transport in parallel, probably through a common mechanism.

Conversely, dissociation between sodium and potassium transport was reported in some circumstances in response to short-term aldosterone treatment. For instance, despite consistent effects on sodium reabsorption, aldosterone increased potassium transport in some (309, 394) but not all studies (89, 246, 656). In addition, actinomycin D reduced aldosterone-induced changes in potassium transport in one (395) but not all studies (504, 884). In fact, several factors (including dietary potassium intake, glomerular filtration rate, acid/base status, trans-

epithelial PD, or the rate of sodium reabsorption in the distal nephron) may influence the overall potassium excretion and thereby modulate the action of aldosterone on the collecting duct. For example, stimulation of potassium excretion by aldosterone is better evidenced in potassium-depleted animals than in normal ones (290, 878), and adequate sodium supply to the distal nephron is required for observing mineralocorticoid-induced kaliuresis (399, 632).

In summary, the long-term effects of aldosterone on sodium and potassium transport in the collecting duct are tightly coupled, whereas in the short term, stimulation of potassium secretion by aldosterone may be counterbalanced by other phenomena and therefore may be dissociated from antinatriuresis.

4. Induction and activation of $\text{Na}^+\text{-K}^+\text{-ATPase}$

In the mammalian kidney, aldosterone induces three successive responses: an early response (0–2 h) that includes a lag period and the early onset of stimulation of sodium reabsorption, a late response (2–24 h) during which stimulation of sodium transport fully develops, and a delayed response (>2 days) that includes morphological remodeling of collecting duct. The two first responses are mainly observed either after a single administration of aldosterone to aldosterone-depleted animals or after *in vitro* addition of the hormone to aldosterone-deprived tissue preparations. The delayed response is observed following repeated injections of aldosterone to adrenal-intact animals. The following discussion is mainly focused on the early and late responses, and reference to long-term changes will be noted only when they highlight the short-term mechanisms.

As previously mentioned, Edelman et al. (233) have demonstrated in the early 1960s that the stimulation of sodium transport observed in response to aldosterone requires RNA and protein synthesis. Since then, most efforts focused on the characterization of the proteins specifically induced by aldosterone (aldosterone-induced proteins, AIP) and involved in sodium transport, using a candidate approach. The first candidates were $\text{Na}^+\text{-K}^+\text{-ATPase}$ and the apical sodium channel ENaC, the two main effectors of sodium reabsorption, and the mitochondrial enzymes involved in the synthesis of ATP, the fuel required by the pump. Only the first two are discussed here, and the reader is referred to reviews for metabolic aspects (540, 678).

Adrenalectomy reduced $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity by >70% in rat, rabbit, and mouse CCD (222, 246, 247); this effect occurred after a 1- to 1.5-day lag period during which a latent pool of $\text{Na}^+\text{-K}^+\text{-ATPase}$ was activated (50, 98), and reached its maximum after 4–5 days (222). A single injection of aldosterone (2–10 $\mu\text{g/kg}$ body wt) to ADX rats and rabbits restored within 3 h $\text{Na}^+\text{-K}^+\text{-ATPase}$

activity back to its level in CCD of adrenal-intact animals (246, 247). This effect was abolished by the MR antagonist spironolactone (247, 657). The time courses of aldosterone effect (single administration to ADX rats) on urinary sodium excretion and on $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity in CCD were similar (247). In adrenal-intact animals, mineralocorticoids also stimulated $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity in the collecting duct, but the response was delayed (onset and the maximal effects are observed within 2 days and 1 wk, respectively) (245), as was the effect on sodium transport. In fact, the latency before detecting aldosterone-induced stimulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ is directly related to the initial ATPase activity (the lower the initial activity, the shorter the latency period) (375), suggesting that additional parameters modulate aldosterone action on $\text{Na}^+\text{-K}^+\text{-ATPase}$. 3,3',5-Triiodothyronine (T_3) might be one of these parameters since *in vitro* incubation of CCD from normal rats with aldosterone alone failed to stimulate $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity whereas incubation with a combination of aldosterone and T_3 stimulated it within 3 h (49). This effect of T_3 is specific for mammals, since in amphibian epithelia, T_3 antagonizes the effect of aldosterone (329).

The question has long been debated whether aldosterone activates preexisting $\text{Na}^+\text{-K}^+\text{-ATPase}$ units or whether it induces *de novo* synthesis of $\text{Na}^+\text{-K}^+\text{-ATPase}$. The following findings support that $\text{Na}^+\text{-K}^+\text{-ATPase}$ is induced by aldosterone: 1) aldosterone increased both the activity and the number of $\text{Na}^+\text{-K}^+\text{-ATPase}$ units in CCD (49, 249), 2) aldosterone-induced stimulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity in CCD was blocked by actinomycin D and cycloheximide (49), 3) adrenalectomy reduced and aldosterone restored the amount of mRNAs encoding for the α_1 -subunit (but not the β_1 -subunit) of $\text{Na}^+\text{-K}^+\text{-ATPase}$ in CCD (255, 260, 818), and 4) the 5'-flanking region of $\text{Na}^+\text{-K}^+\text{-ATPase}$ α_1 -subunit gene contains GREs (909). However, this does not mean that the early increase in activity and number of $\text{Na}^+\text{-K}^+\text{-ATPase}$ units corresponds to membrane expression of *de novo* synthesized units. Indeed, *in vivo* administration of aldosterone to ADX rats restored a control level of α_1 -subunit mRNAs after 6 h (818), whereas $\text{Na}^+\text{-K}^+\text{-ATPase}$ activity was already restored after 2–3 h (246). Thus aldosterone rapidly triggers the transcription of $\text{Na}^+\text{-K}^+\text{-ATPase}$ α_1 -subunit (early induced mRNA), but the early stimulation in the enzyme activity is likely accounted for by the activation of preexisting pump units through induction of an unknown regulatory protein. Because the latent pool of $\text{Na}^+\text{-K}^+\text{-ATPase}$ present in CCD from normal rats disappears after adrenalectomy (50), its activation cannot account for the early stimulation. On the other hand, the early increase in sodium affinity of $\text{Na}^+\text{-K}^+\text{-ATPase}$ in response to aldosterone in A6 cells (78) may participate in the early stimulation but remains to be confirmed in mammalian principal cells. Interestingly, aldosterone was

shown to increase calcineurin activity within 30 min in rat CCD (822). Because inhibition of calcineurin by either cyclosporine or FK506 inhibited Na⁺-K⁺-ATPase activity in the rat CCD (486, 823), the early stimulation of calcineurin activity might be involved in the early stimulation of Na⁺-K⁺-ATPase by aldosterone. It should be noted, however, that conversely to early activation of Na⁺-K⁺-ATPase which was blocked by actinomycin D and cycloheximide (49), aldosterone-induced early stimulation of calcineurin was not blocked by actinomycin D (822); rather, it seems to be triggered by the heat shock protein released by MRs in response to aldosterone binding (822).

The question of whether Na⁺-K⁺-ATPase is an early aldosterone-induced protein has received further elements of response from studies in amphibian cell cultures. In A6 cells, aldosterone increased very early the transcription rate of the Na⁺-K⁺-ATPase α - and β -subunit mRNAs: stimulation occurred as early as 15–30 min after addition of aldosterone (842), and within 6 h, the amount of the mRNAs of α_1 - and the β_1 -subunits increased four- and twofold, respectively (843). Although aldosterone induced rapidly the transcription of Na⁺-K⁺-ATPase genes, the expression of the newly synthesized pump units in the basolateral membrane was only observed after 6–18 h of latency (329, 436, 487). This delayed membrane expression of the pump is accounted for by the time required for accumulation of mRNAs, translation, and assembly of the α - and β -subunits, and insertion into the membrane (252, 679). That this process takes longer in amphibian than in mammalian cells may be related to the difference in metabolic rates between poikilotherms and homeotherms.

Another long-debated question is whether induction of Na⁺-K⁺-ATPase is a primary effect of aldosterone or whether it is secondary to increased apical sodium entry. In addition to its actions on the recruitment of an endogenous latent pool of Na⁺-K⁺-ATPase (which corresponds to a nongenomic increase in pump density) and on the activation of already active pumps (by a substrate effect), increased sodium entry was thought to induce the genomic expression of Na⁺-K⁺-ATPase through increasing intracellular sodium concentration. In the collecting duct, this hypothesis was based on the fact that in vivo treatment of ADX rabbits with the ENaC blocker amiloride before aldosterone injection abolished Na⁺-K⁺-ATPase stimulation (633). However, when reevaluated in vitro, it was shown that at a concentration sufficient to block totally and specifically sodium channels (622), amiloride did not alter the induction of Na⁺-K⁺-ATPase by aldosterone in the CCD (49). This demonstrated that early Na⁺-K⁺-ATPase stimulation was independent of an increment of intracellular concentration of sodium brought about by increased apical sodium conductance. In fact, the inhibitory effect of amiloride observed in vivo might be due to inhibition of the basolateral Na⁺/H⁺ exchanger (NHE-1) rather than inhibition of the sodium

channels. Indeed, Oberleithner et al. (601) reported that aldosterone increased intracellular pH through activation of the Na⁺/H⁺ exchanger in frog distal nephron cells (601). Furthermore, specific inhibition of the Na⁺/H⁺ exchanger by EIPA abolishes the in vitro induction of Na⁺-K⁺-ATPase in the rat collecting duct, and the action of EIPA was antagonized by alkalinizing the cells by incubation at higher pH (47).

In summary, although transcription of Na⁺-K⁺-ATPase α - and β -subunit mRNAs is triggered very early in response to aldosterone, the early increase in its activity that parallels the stimulation of sodium transport is likely accounted for by activation of preexisting units (Fig. 20). The mechanisms underlying this stimulation are not known yet, but they are not related to changes occurring at the apical cell border. Finally, the time course of the early stimulation of Na⁺-K⁺-ATPase varies with the initial status of the animals, in particular with their basal aldosterone and T₃ status, but other factors are likely involved.

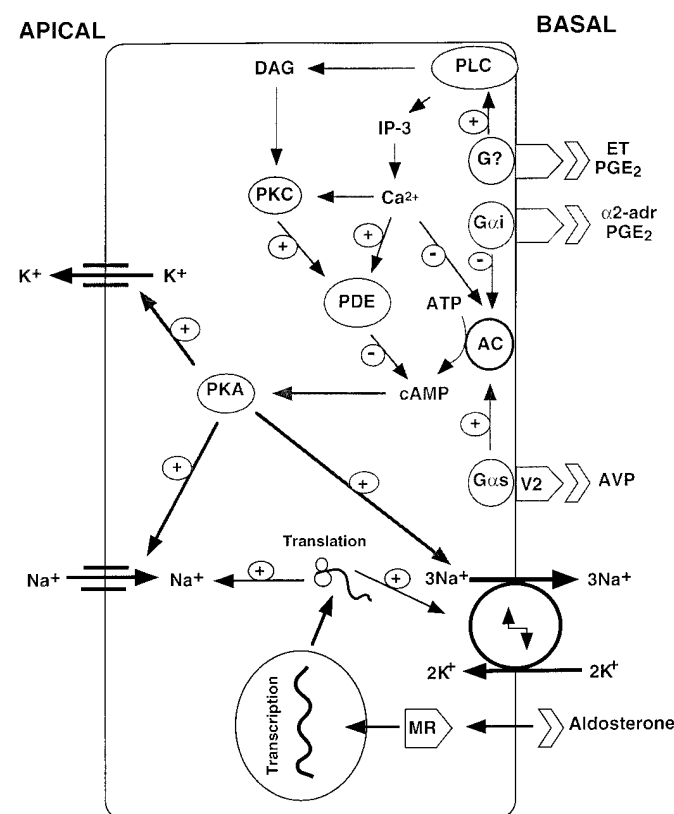


FIG. 20. Overview of the principal signaling pathways controlling the active sodium transport in principal cells of the collecting duct. Arrows indicate the direction of the signaling cascade and the resulting stimulatory (+) or inhibitory (-) effect on their targets. V₂, vasopressin V₂ receptor; MR, mineralocorticoid receptor.

5. Induction and activation of epithelial sodium channels

The early response of amphibian tight epithelia to aldosterone was mimicked by addition of the sodium ionophore amphotericin B at the apical pole of the cells (503). In addition, the effect of amphotericin B was not additive with that of aldosterone (189), suggesting that the early response involves an increased rate of apical sodium entry (which accounts for both increased sodium transport and decreased transepithelial resistance). Direct demonstration of aldosterone effect on apical sodium conductance in toad skin was first provided by Nagel and Crabbé (583), who showed that aldosterone increased threefold the sodium conductance of the apical membrane while sodium transport rate increased 2.7-fold. By electrophysiological analysis of the toad urinary bladder, Palmer et al. (623) reported that *in vitro* addition of aldosterone increased the density of active sodium channels without altering single-channel current, demonstrating the recruitment and/or the activation of preexisting but electrically silent sodium channels.

In the mammalian kidney, chronic changes in plasma aldosterone concentration also increased the apical amiloride-sensitive sodium conductance measured *in vitro* in rat and rabbit CCD (306, 694, 709). Cell-attached patch-clamp analysis of the apical membrane of CCD principal cells indicated that feeding rats with a low-sodium diet for 2 days markedly enhanced the density of active channels at the apical pole of principal cells (618). However, no data are available concerning the short-term effect (either *in vivo* or *in vitro*) of aldosterone on apical sodium conductance.

The mechanism underlying the increased number of active sodium channels (ENaC) at the apical membrane is not elucidated yet. It could be accounted for by either an increase in the number of channels in the membrane, as a result of *de novo* synthesis or of recruitment of an intracellular reservoir of channels, or by activation of silent channels already present in the membrane by aldosterone-induced regulatory factors.

Although corticosteroids stimulate the transcription of ENaC through transactivation of GREs in the 5'-flanking region of ENaC α -subunit gene (704), this transcriptional effect is likely not responsible for the early increase in channel density. Indeed, in A6 cells, the abundance of mRNAs for α -, β -, and γ -subunits of ENaC remained unchanged during the first 3 h of stimulation by aldosterone, and a marked increase was observed only after 24 h (546). In addition, the rate of synthesis of the α -subunit of ENaC increased significantly after 3 h of aldosterone treatment, whereas the amiloride-sensitive electrogenic sodium transport was stimulated about threefold after 1 h (546). Similarly, in rat collecting duct, adrenalectomy decreased the abundance of the mRNAs encoding the α -subunit (but

not the β - and γ -subunits) of ENaC, but administration of aldosterone restored the expression of ENaC α -subunit mRNAs only after >2 days of treatment (30, 255). Within 2 days, aldosterone did not increase the immunodetected amount of all three subunits of ENaC (670), whereas after 10 days of dietary NaCl restriction or aldosterone administration, the abundance of ENaC α -subunit was markedly increased in rat CCD (542). These results demonstrate that aldosterone-induced early and late (up to 2 days) increases of apical sodium conductance in the mammalian CCD are not accounted for by *de novo* synthesis of ENaC, but rather by membrane insertion and/or activation of preexisting channels. Conversely to amphibian epithelia and rat CCD, in the mouse collecting duct principal cell line mpkCCD_{c14}, the time course of induction of ENaC synthesis is compatible with the early changes in I_{sc} and R_T . Indeed, the abundance of α -ENaC transcripts and the rate of synthesis of the cognate protein increased over twofold as early as 2 h after addition of aldosterone. The increased rate of synthesis of the ENaC α -subunit was blocked by actinomycin D (75). Here again, aldosterone effect was restricted to the α -subunit, since neither ENaC β - nor the γ -subunit transcripts were induced even after 24 h (75).

In fact, several results support that channels rapidly activated by aldosterone are already present in the apical membrane. For example, trypsinization of the apical sodium channels of toad bladders before aldosterone addition markedly reduced aldosterone effect on sodium transport (324), suggesting that the channels that were stimulated by aldosterone preexisted in the membrane. Also, Kleyman et al. (471) reported that aldosterone altered neither the binding of the ENaC blocker [³H]benzamil (471) nor the rate of synthesis and expression of sodium channels at the apical cell surface in A6 cells.

What are the mechanisms responsible for the early activation of preexisting ENaC by aldosterone? Several factors have been proposed and investigated. Because the early response to aldosterone depends on mRNA and protein synthesis, a prerequisite is that such factors must be transcriptionally activated (Fig. 20). Several mechanisms, including changes in intracellular pH, methylation, and phosphorylation, have been postulated and are described below. These are neither exclusive nor exhaustive possibilities.

In rat CCD, intracellular alkalinization within physiological range markedly increases the open probability of apical sodium channels (622), in a manner that could account for early aldosterone effect. In addition, aldosterone was reported to rapidly (20 min) induce an intracellular alkalinization, sufficient to activate sodium channels, in both the amphibian early distal tubule (601) and the frog skin (369). This alkalinization was mediated through the activation of the Na⁺/H⁺ exchanger (369, 864). Whether this early stimulation of Na⁺/H⁺ exchange

by aldosterone is a genomic effect has not been established. However, it was mediated by MR occupancy since it was blocked by spironolactone (864). Activation of preexisting channels by cytosolic alkalization would account for the fact that early activation of sodium channels by aldosterone was not retained in membrane vesicle preparation (29).

Incubation of apical membrane vesicles from A6 cells with the methyl donor *S*-adenosylmethionine increased the membrane methylation (both proteins and lipid) and doubled the rate of amiloride-sensitive sodium transport. When A6 cells were pretreated with aldosterone, treatment of the vesicles with *S*-adenosylmethionine increased neither the membrane methylation nor sodium transport, which were already high, indicating that the effects of aldosterone and methylation were not additive (696). Thus aldosterone might stimulate a transmethylation reaction that participates to the activation of the apical sodium channel. The nature of the transmethylated proteins and/or lipids of importance for activation of the sodium channels is not known yet, although several proteins have been identified (reviewed in Ref. 697). In contrast, the transmethylation pathway involved in aldosterone action has been identified in part. First, isoprenylcysteine-*O*-carboxyl methyltransferase (pcMTase) appears to be responsible for aldosterone-induced transmethylation (771). Indeed, in A6 cells, 1) aldosterone increased pcMTase activity, without inducing its expression; 2) inhibition of pcMTase reduced aldosterone-induced sodium transport; and 3) overexpression of pcMTase potentiated the effect of aldosterone on sodium transport. Second, *S*-adenosyl-*L*-homocysteine hydrolase (SAHHase) regulates aldosterone-induced sodium transport (770). SAHHase is the only enzyme in vertebrates that is able to catabolize *S*-adenosyl-*L*-homocysteine, an end product and an inhibitor of transmethylation processes. In A6 cells, 1) aldosterone stimulated SAHHase activity without inducing its expression, 2) inhibition of SAHHase reduced sodium transport, and 3) overexpression of SAHHase increased methylation processes and potentiated aldosterone effect on sodium transport. Thus, although the transmethylase pcMTase and the transmethylation regulator SAHHase are not induced by aldosterone, their activity is stimulated by aldosterone, and this stimulation is essential for membrane methylation and stimulation of sodium transport.

A serum- and glucocorticoid-regulated serine/threonine kinase (sgk) was identified by differential screens for glucocorticoid-inducible transcripts in a rat mammary tumor cell line (859, 860). sgk mRNAs are expressed in most rat tissues. However, in situ hybridization on kidney indicated that it was expressed at low level, and mainly in the glomeruli of ADX rats, whereas in ADX rats treated with aldosterone for 4 h, a strong expression was seen in the distal nephron (157). More recently, sgk mRNAs were

shown to be induced as soon as 30 min after addition of aldosterone on rat collecting ducts, an effect which was mediated by mineralocorticoid receptors and did not require protein synthesis (586). Coexpression in *Xenopus* oocytes or rat sgk or of its amphibian ortholog with ENaC strongly stimulated ENaC-mediated sodium current (13, 157). This stimulation resulted from increased number of active ENaCs at the oocyte membrane with no change in single-channel properties (13). Although aldosterone increased the phosphorylation of the β - and γ -subunits of ENaC Madin-Darby canine kidney (MDCK) cells (733), the effect of sgk is not mediated through direct phosphorylation of ENaC subunits because deletion of the COOH termini of the three subunits did not prevent sgk action (13).

Analysis of cDNAs generated by differential display PCR from aldosterone-treated or untreated A6 cells allowed the characterization of several adrenal steroid up-regulated RNAs (ASURs) (764). Among them was the *Xenopus* ortholog of the mammalian monomeric G protein K-Ras2. When coexpressed with ENaC in *Xenopus* oocytes, a constitutively active mutant of K-Ras2 was found to decrease, through activation of endocytosis, the number of ENaCs present at the membrane, but also to increase markedly the intrinsic activity of the remaining surface-expressed channels (543). The pathway underlying physiological activation of K-Ras during aldosterone stimulation is not yet known.

In summary, aldosterone-induced late increase in apical sodium conductance is likely mediated through membrane insertion of newly synthesized ENaCs, whereas the early stimulation is mediated by activation of preexisting channels. This early activation is controlled by multiple factors, including intracellular pH, methylation, and phosphorylation cascades as well as small G proteins.

6. Regulation of potassium channels

Increased activity of apical ENaC and basolateral Na⁺-K⁺-ATPase is theoretically sufficient to account for both aldosterone-induced sodium reabsorption and potassium secretion. Indeed, stimulation of Na⁺-K⁺-ATPase increases intracellular potassium concentration and hyperpolarizes the basolateral membrane, and activation of ENaC depolarizes the apical membrane, thereby favoring apical potassium extrusion. Nonetheless, aldosterone may also control apical and basolateral potassium channels, which would permit some dissociation between the effects of aldosterone on sodium and on potassium transport.

Within 4 days, DOCA treatment doubled the apical potassium conductance in rabbit CCD (694). In ADX rabbits, this stimulatory effect of mineralocorticoids occurred as early as 3 h (693). Thus aldosterone would not only increase the driving force for potassium secretion

across the apical membrane, but also the conductance of this membrane. However, no stimulation of apical potassium conductance was found in CCDs from rats either chronically treated with DOCA treatment (707, 708) or fed a low-salt diet (304). Nonetheless, expression in the kidney cortex of mRNAs encoding the apical potassium channel ROMK was downregulated in ADX rats and up-regulated in response to aldosterone (65, 845).

Because amiloride abolished the aldosterone-induced early increase in apical potassium conductance in rabbit CCD, it was proposed that this increase was secondary to increased sodium reabsorption (693). However, as already discussed for $\text{Na}^+\text{-K}^+\text{-ATPase}$, the inhibitory effect of amiloride is likely to be secondary to inhibition of the basolateral Na^+/H^+ exchanger. In MDCK cells, a dog kidney-derived cell line exhibiting some properties of collecting duct cells, aldosterone stimulated the Na^+/H^+ exchanger and alkalinized the cells, and thereby increased potassium secretion via the setting of preexisting potassium channels in the apical membrane (600). In the frog distal renal tubule, aldosterone-enhanced density of apical potassium channels was mimicked by increasing intracellular pH and was reduced by amiloride, consistent with the involvement of a stimulation of the Na^+/H^+ exchanger (850). Thus early regulation of apical potassium channels by aldosterone results from intracellular alkalinization-mediated recruitment of inactive channels, whereas late regulation might be accounted for by de novo synthesis of new channels.

Adrenalectomy decreased (708) and chronic DOCA treatment increased (695) the basolateral potassium conductance of rabbit CCD. However, during chronic DOCA treatment, the marked induction of $\text{Na}^+\text{-K}^+\text{-ATPase}$ hyperpolarizes basolateral membrane so that the electrochemical gradient becomes favorable to potassium entry and not exit (774). Thus, coupled to the stimulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ and the enhanced apical potassium conductance, changes at the basolateral border contribute to increase potassium secretion.

According to the molecular events underlying aldosterone action on potassium transport, it appears that part of the kaliuretic effect (that accounted for by increased driving force across the apical membrane) is tightly coupled to the antinatriuretic effect, whereas the part resulting from increased potassium conductance of the two cell membranes is independent from increased sodium transport.

C. Vasopressin and Activation of the cAMP/PKA Signaling Pathway

In collecting ducts principal cells, the cAMP/PKA signaling pathway is mainly stimulated by vasopressin (through its V_2 receptors coupled to adenylyl cyclase) and

by glucagon. In collecting ducts, the main actions of vasopressin are to permeabilize the apical membrane to water through expression of apical AQP-2 and to increase urea permeability of IMCD. However, vasopressin also stimulates sodium reabsorption and potassium secretion along the CCD and OMCD. The following discussion focuses exclusively on the regulation of these two cation transports.

1. Effect on sodium transport

In rat and rabbit CCDs, in vitro microperfusion studies demonstrated that cell-permeant cAMP analogs stimulate sodium reabsorption (111, 371). In contrast, CCDs from rat and rabbits responded differently when triggered by vasopressin. In the in vitro microperfused rat CCD, vasopressin induced a sustained increase in the lumen-negative transepithelial voltage (588, 667), reflecting the stimulation of sodium reabsorption (668, 812). In contrast, in the rabbit in vitro microperfused CCD, vasopressin produced a transient increase in sodium reabsorption followed by a sustained inhibition (159, 302, 391). As discussed below, the inhibitory effect of vasopressin in the rabbit CCD most likely results from increased synthesis of prostaglandins E_2 (391). The lack of inhibitory effect of cAMP analogs in rabbit CCD suggests that the inhibitory effect of prostaglandins occurs through inhibition of cAMP production (see below). Finally, it should be mentioned that the stimulatory effect of vasopressin on sodium transport by the rat CCD and in A6 cells is potentiated by in vivo mineralocorticoid treatment (148, 372, 668, 839).

Vasopressin also increases renal potassium excretion (287, 762), secondarily to an increase in potassium secretion in late distal tubule (287) and CCD (706, 812) associated with an inhibition of potassium reabsorption by the OMCD (762). In the in vitro microperfused rat CCD, vasopressin induced a sustained stimulation of potassium secretion (812).

2. Stimulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$

Although stimulation of $\text{Na}^+\text{-K}^+\text{-ATPase}$ is a prerequisite for increasing sodium reabsorption in the CCD, initial studies by Satoh et al. (700) concluded to an inhibition of the maximal hydrolytic activity of $\text{Na}^+\text{-K}^+\text{-ATPase}$ in response to forskolin and to cell-permeant cAMP analogs in isolated rat CCD. This effect of cAMP was indirect and relied on the PLA_2 /arachidonate/cytochrome P-450-monooxygenase pathway (700, 701). However, recent unpublished results from our laboratories indicate that in CCD as in MTAL (see above), this inhibitory pathway is promoted by artefactual metabolic stress. Indeed, in well-oxygenated isolated rat CCDs, cell-permeant analog of cAMP induced a twofold stimulation of both the transport and the hydrolytic activity of $\text{Na}^+\text{-K}^+\text{-ATPase}$.

This effect was associated with a twofold increase in the cell surface expression of Na⁺-K⁺-ATPase, suggesting that cAMP induces the recruitment of active Na⁺-K⁺-ATPase units from intracellular stores to the plasma membrane, a mechanism previously evidenced in the rat proximal tubule (136). These findings indicate that increased Na⁺-K⁺-ATPase activity in response to the activation of PKA participates in the stimulation of sodium reabsorption (Fig. 20).

The stimulatory effect of the cAMP/PKA pathway on Na⁺-K⁺-ATPase is also promoted by vasopressin. In vivo infusion and in vitro addition of vasopressin increased the V_{\max} of Na⁺-K⁺-ATPase in rat (812) and in mouse (96, 187) CCD, respectively. In mouse CCDs, increased V_{\max} was paralleled by increased number of cell surface active Na⁺-K⁺-ATPase units, as measured by [³H]ouabain binding (187). This stimulatory effect of vasopressin is mediated through V₂ receptor (187) and requires protein phosphatase activity (96). In addition, as previously shown for the stimulation of sodium reabsorption, the effects of vasopressin and aldosterone on Na⁺-K⁺-ATPase were synergistic (187). This observation may indicate that aldosterone sensitizes the principal cells of the collecting duct to the action of vasopressin.

In addition to its short-term effect on Na⁺-K⁺-ATPase activity, vasopressin also increases the translational rate of the α -subunit in cultured cells derived from rat CCD (215). Altogether, these observations suggest that vasopressin controls both Na⁺-K⁺-ATPase activity and expression level in principal cells of the mammalian CCD.

3. ENaC

Vasopressin and/or cAMP stimulation of sodium transport in the CCD is associated with a depolarization of the apical membrane (588, 709) and an increase in apical membrane sodium conductance (708, 716). The stimulatory effect of cAMP on ENaC (Fig. 20) was confirmed by patch-clamping the apical membrane of principal cells from isolated rat CCDs (305, 308); cAMP treatment before formation of the patch increases the density of active channels (308).

The mechanism of activation/recruitment of ENaC by the vasopressin/cAMP/PKA pathway was further studied in A6 cells. Vasopressin, forskolin, and cAMP analogs increased the density of active ENaCs in A6 cells (250, 472, 538). This increase in ENaC density was prevented by pretreatment with brefeldin A (472), a drug that disrupts the Golgi apparatus and prevents delivery of newly synthesized or recycling proteins from this intracellular compartment. Taken together with the stimulatory effect of vasotocin, i.e., the amphibian analog of vasopressin, on apical membrane exocytosis (840) and with the requirement of PIK activity (234), these results suggest that vasopressin in-

duces a translocation of ENaC from an intracellular pool to the plasma membrane. This hypothesis is further supported by the inhibitory effect of microtubules and actin microfilaments disruption on the vasopressin-stimulated sodium transport and apical exocytosis (841). Indeed, in polarized renal epithelial cells, apical membrane trafficking events are facilitated by microtubules and actin microfilaments (115, 362).

In addition, cAMP may also activate preexisting sodium channels, since incubation of excised inside-out patches from A6 cells in the presence of ATP and the catalytic subunit of PKA increased ENaC activity (646). The activation of these preexisting channels by ATP and PKA required phosphorylation of actin filaments (647) and may also involve direct phosphorylation of the β - and γ -subunits of ENaC by PKA (733).

In addition to its short-term (minutes) effect on apical sodium conductance, long-term (hours) vasopressin treatment increased amiloride-sensitive sodium transport, cell surface expression of ENaC, and the translation rate of the β - and γ -subunits of ENaC in cultured cells derived from rat CCD (215).

These results suggest that vasopressin controls both the synthesis, the membrane recruitment, and the activity of ENaC in principal cells of the mammalian collecting duct.

4. Potassium transporters

Stimulation of apical sodium reabsorption by vasopressin (709) increases the driving force for potassium secretion through apical potassium channels (706). In addition, vasopressin and cAMP increased the density and/or activated apical low-conductance potassium channel (ROMK) in rat CCD (138, 364, 852) (Fig. 20). Whether vasopressin induces translocation of potassium channels from an intracellular pool or activates silent plasma membrane potassium channels remains to be determined.

D. Negative Modulation of Vasopressin Action

The stimulatory effects of vasopressin on the collecting duct are negatively modulated by several factors such as prostaglandins, adenosine, α_2 -adrenergic agonists, endothelin, or bradykinin. Most of these mediators modulate the intracellular concentration of cAMP at the level of its production and/or degradation. A general feature of these secondary modulations is their cellular and species specificity as they often differ between rat and rabbit as well as between CCD and OMCD.

1. Prostaglandins

In rat CCD, PGE₂ did not alter either vasopressin-dependent cAMP content (146) or vasopressin-stimulated

sodium transport and transepithelial voltage (158). In contrast, PGE₂ reduced vasopressin-dependent cAMP content in rat OMCD (1). This resulted mainly from an increased rate of cAMP degradation by calcium-activated phosphodiesterases (146) mediated by a pertussis toxin-insensitive increase in intracellular calcium concentration (1). Curiously, this effect was blocked by phorbol esters (2). However, the functional effect of PGE₂ on cation transport and water permeability has not been evaluated in rat OMCD.

In rabbit CCD, PGE₂ inhibited vasopressin-stimulated synthesis of cAMP (349) and vasopressin-induced water permeability (378) through pertussis toxin-sensitive inhibition of adenylyl cyclase (Gα_i). PGE₂ also inhibited vasopressin-stimulated sodium reabsorption and transepithelial voltage in the rabbit CCD (158, 413, 776), but apparently through another mechanism. Indeed, inhibition of sodium reabsorption was mimicked by phorbol esters (18), in agreement with its mediation by pertussis toxin-insensitive increase in intracellular calcium and PKC (378). The pertussis toxin-sensitive and -insensitive signaling pathways triggered by PGE₂ in the rabbit CCD are activated through different receptors (Fig. 20) with distinct affinities for PGE₂ and its analog sulprostone. The role of PKC in the inhibitory effect of PGE₂ on sodium transport is further supported by the sustained stimulatory effect of vasopressin on sodium transport observed after downregulation of the novel PKC-ε by antisense oligonucleotides in primary cultures of rabbit CCD cells (197).

In agreement with the stimulatory effect of vasopressin on Na⁺-K⁺-ATPase activity, chronic inhibition of PGE₂ synthesis by indomethacin treatment increased Na⁺-K⁺-ATPase activity in rabbit CCD (185). An in vitro inhibitory effect of PGE₂ on Na⁺-K⁺-ATPase was also reported in rabbit IMCD (427); however, the very high doses of PGE₂ used (micromolar range) preclude any physiological relevance of this effect.

Both rabbit and rat CCD (104, 419, 432, 468, 717) and interstitial cells (100, 485) synthesize PGE₂, and this process is stimulated by vasopressin (468, 717) likely through V₁ receptors (433). Thus vasopressin-induced synthesis of prostaglandins is part of a regulatory feedback mechanism that limits vasopressin action. This may be more important for limiting water transport rather than cation transport, as it may prevent excessive swelling and dilution of cell compartment. Nonetheless, we already mentioned that such feedback regulation also applies to sodium transport in the rabbit CCD. Indeed, inhibition of prostaglandin synthesis by meclofenamate suppressed the fall in sodium transport consecutive to its transient stimulation by vasopressin (391).

2. Bradykinin

Like prostaglandins, bradykinin had no effect alone but inhibited the vasopressin-induced water permeability in rabbit CCD (721). Bradykinin was also reported to inhibit sodium reabsorption in rat CCD by some (813) but not all authors (371). Curiously, in the study of Tomita et al. (813), bradykinin antagonized the vasopressin-induced sodium reabsorption but did not alter vasopressin-induced rise in transepithelial voltage and potassium secretion. In the rabbit CCD, the effects of bradykinin are likely mediated by a stimulation of prostaglandin synthesis by CCD and interstitial cells (934) and the subsequent inhibition of vasopressin response by PGE₂ (see above). The rat CCD principal cells, however, are insensitive to PGE₂, and therefore, another mechanism may account for the inhibitory effect of bradykinin. As mentioned before for PGE₂, bradykinin may also constitute the efferent limb of a negative-feedback mechanism, since vasopressin stimulates the renal kallikrein-kinin system (267).

3. α₂-Adrenergic agonists

The site of increased urinary sodium and water excretion observed in response to an α₂-adrenergic receptor agonist was localized to the collecting duct by micropuncture studies in normal rat (768). This result was confirmed by in vitro microperfusion studies performed in rat CCD, in which epinephrine and the α₂-agonist clonidine antagonized vasopressin-induced stimulation of sodium and water reabsorption (158, 371). Conversely, clonidine altered neither water permeability nor sodium reabsorption promoted by vasopressin in the rabbit CCD (158). This species difference is consistent with the pattern of inhibition of vasopressin-dependent cAMP accumulation in rat and rabbit CCD; clonidine inhibited cAMP production in rat but not in rabbit CCD (140).

Inhibition of cAMP production by α₂-adrenergic agonists in rat collecting duct largely results from Gα_i-mediated inhibition of adenylyl cyclase (1, 145) (Fig. 20). However, because epinephrine also antagonized the stimulatory effect of a cell-permeant cAMP analog on sodium transport (371), a post cAMP effect may also be involved in the functional inhibition.

4. Dopamine

Dopamine has no effect per se on sodium transport, but it inhibits vasopressin-induced sodium reabsorption in the in vitro microperfused rat CCD (781). This effect is mediated through D₄ receptors (D₂-like) and is likely secondary to a decrease in cAMP generation in response to vasopressin (497). It should be mentioned that in contrast to the D₁-like agonist fenoldopam (606), dopamine did not increase the intracellular cAMP content in the rat CCD (497). These observations can be accounted for by a

balanced activation of D₁-like and D₂-like receptors, which are positively and negatively coupled to adenylyl cyclase, respectively. An inhibition of Na⁺-K⁺-ATPase activity in response to dopamine and fenoldopam has been reported in isolated rat CCD (790).

5. Endothelin

The stimulatory effects of vasopressin on both water and cation reabsorption are also antagonized by endothelin (235, 481, 811) through its ET_B receptors (235). Endothelin reduces vasopressin-induced cAMP production (235, 810) through a calcium-dependent (481, 587) stimulation of PKC (810) (Fig. 20). This mechanism seems to be shared by rat (810, 811), rabbit (481), and mouse CCD (587).

In the rabbit CCD, the inhibitory effect of endothelin was accompanied by an inhibition of ENaC (481).

E. Insulin

In contrast to its inhibitory effect on potassium secretion and sodium reabsorption reported in the *in vitro* perfused rabbit CCD (316), insulin increases Na⁺-K⁺-ATPase-mediated cation transport in a time- and concentration-dependent manner in isolated rat CCDs (281). The reason for this discrepancy remains unexplained, since in every system studied so far, including the A6 cells (286), insulin stimulated Na⁺-K⁺-ATPase-coupled sodium transport (178, 196, 266, 355, 520, 671).

The mechanism of the stimulation of Na⁺-K⁺-ATPase transport activity by insulin has been studied in isolated rat CCD and OMCD (282). It is independent of apical sodium entry through amiloride-sensitive sodium channels. In contrast to PCT, the transport activity of Na⁺-K⁺-ATPase was stimulated both under rate-limiting and saturating sodium concentrations, revealing a *V*_{max} effect. Because insulin did not alter the number of active pump units, an increase in turnover of Na⁺-K⁺-ATPase activity has been proposed. In addition, the effect of insulin was abolished by permeabilization of cells, suggesting the requirement of soluble cofactors. These results point out the cellular specificity of the mechanisms of control of Na⁺-K⁺-ATPase activity by insulin. In A6 cells, insulin also stimulated the apical sodium entry through ENaC (251, 539).

VII. CONCLUSION AND PERSPECTIVES

Along this review, we summarized the current knowledge of the hormonal regulatory mechanisms that control Na⁺-K⁺-ATPase-dependent sodium transport along the kidney tubule. During the past decade, tremendous efforts were made to identify the molecular players that

account for the transport properties of individual nephron segments. Currently, the major sodium transporters expressed along the kidney tubule have been cloned, their expression pattern along the kidney tubule has been established, and their major intrinsic properties regarding ion transport kinetics have been determined. In parallel, numerous hormone receptors expressed along the kidney tubule as well as many signaling intermediates have been identified at the molecular level. New approaches, including SAGE, DNA microarrays, and sequencing the genome of entire organisms, will undoubtedly lead to the identification of the remaining molecular players.

The identification of hormones involved in the control of active sodium reabsorption by the kidney tubule and the delineation of their sites of action lead to the discovery of a highly complex regulatory network. Among the factors increasing the complexity of this hormonal control, one can underline the following: 1) a given hormone can bind to distinct molecular subtypes of receptors that couple to different signaling pathways with different effects on target transporters (e.g., vasopressin V_{1a} and V₂ receptor coupled to PKA and PKC, respectively); 2) a molecular receptor species generally couples to more than one signaling pathway (e.g., activation of PKA and PKCs by PTH-PTHrP receptor); 3) activation of basolateral and apical receptors can generate different effects (e.g., ANG II); 4) the final effect of a hormone on active sodium transport is dependent on the concentration of the hormone (e.g., ANG II), the cellular context (e.g., PTH in proximal tubule and TAL), and external factors (e.g., oxygen supply, metabolic substrate availability); and 5) the effect of a hormone can be modulated by the presence of other hormones or local factors (e.g., interactions between vasopressin and prostaglandins). Thus a "physiological effect" can be viewed as the result of a transient imbalance between numerous positive and negative influences exerted from the cell surface and from the interior of the cell. However, some general conclusions can be drawn. Several hormones (e.g., aldosterone) can exert long-term effects (within hours or days) that generally alter the expression level of sodium transporters and thereby reset the reabsorption capacity of the target nephron segment. Many hormones can also acutely (within seconds or minutes) modulate the activity of presynthesized sodium transporters to ensure homeostatic adjustments. This short-term control can be achieved either through an alteration in kinetics of transporters and/or changes in their cell surface expression. Another emerging picture illustrated in this review is the coordinated control of apical and basolateral sodium transport systems. This coordination (cross-talk) minimizes the changes in intracellular ion concentrations, intracellular pH, and cell volume that would otherwise alter many cellular functions.

Although the major hormonal and paracrine/auto-

crine factors influencing tubular sodium transport and the initial steps of intracellular signaling initiated by the activation of their cognate receptors are currently identified, many intermediate signaling molecules remain to be found. In addition, the identification of regulatory sites (e.g., phosphorylation sites, protein-protein interaction sites) in the currently cloned sodium transporters is an area of intensive research that will shed some light on the molecular mechanisms that modulate the function and govern the subcellular distribution of these transporters. The study of the interactions between ion transporters, signaling molecules, cytoskeleton, and vesicular transport machinery is another exciting area for future research in cell physiology. Finally, the generation of transgenic animals will allow the *in vivo* validation of the *in vitro* models. However, the most important challenge will be to put molecules together to get a coherent dynamic picture of the regulation of the system at the cellular, the organ, and the whole organism levels so as to understand how the dysfunction of one player may interfere with the function of the whole machinery.

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