K^+ Channels: Function-Structural Overview

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ABSTRACT

Potassium channels are particularly important in determining the shape and duration of the action potential, controlling the membrane potential, modulating hormone secretion, epithelial function and, in the case of those K^+ channels activated by Ca^{2+}, damping excitatory signals. The multiplicity of roles played by K^+ channels is only possible to their mammoth diversity that includes at present 70 K^+ channels encoding genes in mammals. Today, thanks to the use of cloning, mutagenesis, and the more recent structural studies using x-ray crystallography, we are in a unique position to understand the origins of the enormous diversity of this superfamily of ion channels, the roles they play in different cell types, and the relations that exist between structure and function. With the exception of two-pore K^+ channels that are dimers, voltage-dependent K^+ channels are tetrameric assemblies and share an extremely well conserved pore region, in which the ion-selectivity filter resides. In the present overview, we discuss in the function, localization, and the relations between function and structure of the five different subfamilies of K^+ channels: (a) inward rectifiers, Kir; (b) four transmembrane segments-2 pores, K_{2P}; (c) voltage-gated, Kv; (d) the Slo family; and (e) Ca^{2+}-activated SK family, SKCa. © 2012 American Physiological Society. *Compr Physiol* 2:2087-2149, 2012.

Introduction

It is most probable that K^+ channels started to evolve from the moment that life appeared on earth, as the presence of more than 200 potassium channel-related proteins in archea and bacteria attest. Once K^+ channels were identified in bacteria (485), the dream of many biophysicists, to have large quantities of channel protein to produce crystals amenable to x-ray analysis, became a reality. This feat was performed by MacKinnon's group (115) when they crystallized the K^+ channel (KcsA) from the bacterium *Streptomyces lividans*. This primitive K^+ channel is a tetramer composed of four identical subunits consisting in two transmembrane (TM) domains connected by a pore region, in which the ion-selectivity filter resides. The exquisite K^+ selectivity of this class of ion channels is conferred by amino acids located in the pore region, the signature sequence T/SXGXGX (193).

This structure of the pore present in KcsA channels is retained in all the K^+ channels known to date, including those present in fungi, protozoans, and metazoans but although the pore structure did not evolved considerably, other parts of the channel sequence show considerable structural diversity. Thus, we have organized the present overview by dividing K^+ channels in three structural classes (157, 181, 280, 377, 467, 569) (Fig. 1): (i) the inward rectifier (Kir) family that follows the same structural pattern of the KcsA channel, their subunits contain two TM segments flanking the pore-forming domain and they assemble as tetramers. In mammals, Kir channels are encoded by 15 different genes grouped into 7 subfamilies, Kir1.x to Kir7.x and this diversity has been greatly increased by the identification of 6 alternative splicing isoforms in the case of Kir1.1 and the ability of the proteins inside the subfamilies to form heteromultimers (203, 436); (ii) the two-pore four TM segments K^+ channels (K_{2P}) family, which in contrast to the other families we discuss in the present article, their subunits assemble as dimers. Fifteen different genes of this family has been found in mammals and surprisingly this class of channels has 46 genes in the worm *Caenorhabditis elegans*; (iii) the six TM (S1-S6) segments K^+ channels with one pore domain (S5-P-S6) that include the subfamily of voltage-gated channels, Kv1.x to Kv4.x (corresponding to Shaker, Shab, Shaw, and Shal channels, respectively, in *Drosophila*). Consisting of eight different genes the Kv1.x (*Shaker*) subfamily is the largest in this structural class of K^+ channels. Voltage-dependent K^+ channels are characterized by containing a voltage-sensor domain (VSD; S1-S4) in which the S4 contains positively charged amino acids that constitute the voltage-sensing elements. The six TM domains class also includes the KCNQ (Kv7.x), ether-a-go-go (Kv10.x; gated by voltage and cyclic nucleotides), erg (Kv11.x), and elk (Kv12.2) subfamilies.

Despite the fact that Kv5, Kv6, Kv8, and Kv9 share the same general structure with other members of the Kv

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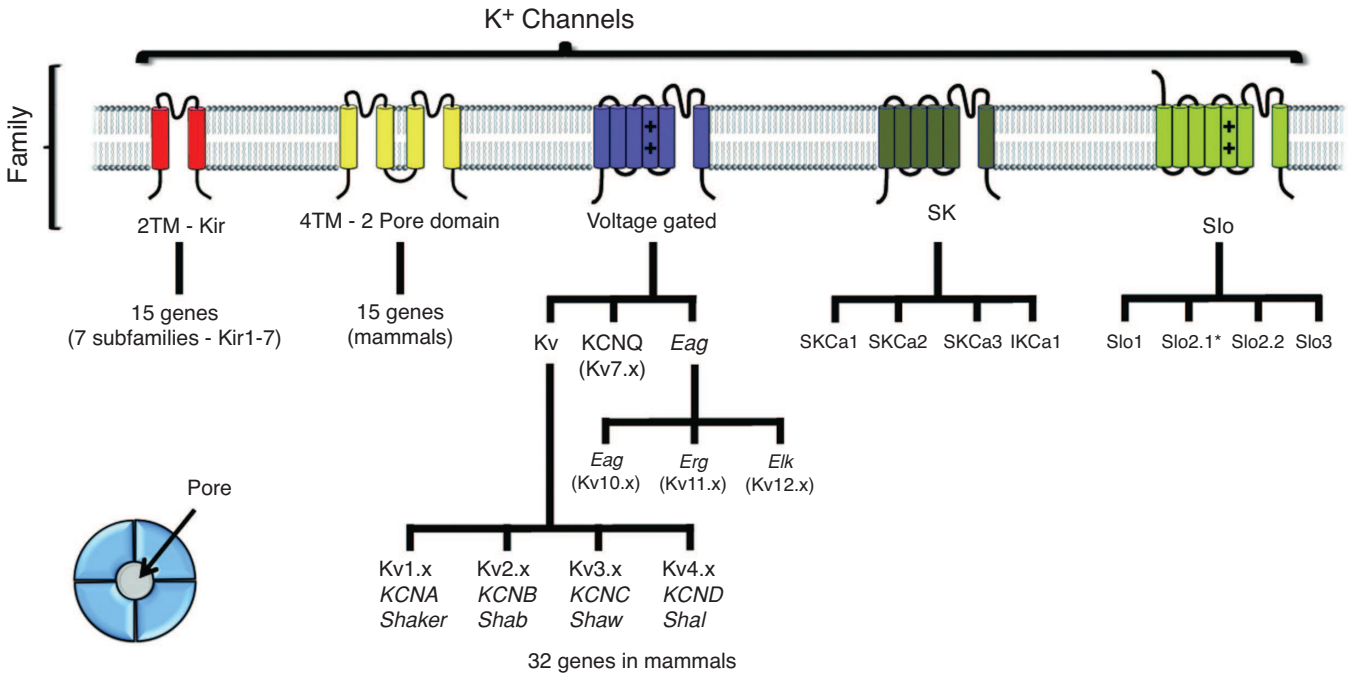


Figure 1 Potassium channel families arranged according to their subunit structure. Potassium channel families can be grouped in those having two transmembrane segments (2TM; Kir), 4TM (2-pore domain), 6TM (voltage gated and SK), and 7TM (Slo). Note that for the sake of simplicity the large-conductance Slo channel family includes the Slo2.x channels, which have only six transmembrane domains. The 6TM domain class can be divided into four families: Voltage-gated Kv, voltage-gated KCNQ-type (KCNQ); ether-a-go-go (Eag), and Ca^{2+}-activated channels (SK). Subdivisions of the voltage-gated Kv channels into four subfamilies and Eag into three subfamilies are also named according to the *Drosophila melanogaster* genes. In the SK family IKCa1 stands for intermediate conductance Ca^{2+}-activated K^+ channel.

family, they do not form functional channels. These proteins have been denominated silent (KvS) subunits. However, by forming heterotetrameric channels with Kv2 and Kv3 α-subunits they modulate the biophysical properties and inhibit the expression of these outward rectifier channels (181, 224, 408, 472).

To this extended six TM domains family, we must add the small conductance (SKCa) Ca^{2+}-activated K^+ channels (271, 569) and the Slo channel subfamily. SKCa channels, although containing two arginines in the S4 segment, are voltage insensitive and gated by submicromolar levels of intracellular Ca^{2+}. On the other hand, the Slo channel subfamily α-subunits (466,569) consist of four members; Slo1 and Slo3, unlike the other K^+ channels, contain seven TM segments α-subunits and hence their N-terminus faces the extracellular medium. The other two members of this subfamily, Slo2.1 and Slo2.2 (Slick and Slack, respectively) have; however, α-subunits containing six TM domains.

After this bird's-eye look on K^+ channel diversity, several questions arise: why is there such a large diversity of K^+ channels? What role does each of them play? How their activity is regulated? What are the relations between structure and function? Precisely, because of this huge channel diversity, it would be impossible to give a detailed response to all these questions, either because the answer to each of them will require a treatise or simply because the answer is unknown. Given this complex scenario, our choice has been to give an overview of what (arbitrarily), we think is important to know about this superfamily of ion channels that may be considered the guardians of the cellular electrical homeostasis.

Kir Channels Family

The seven Kir channel subfamilies (Fig. 2A) can be classified into four functional groups [Hibino et al. (203)]: (i) classical Kir; (ii) G-protein-gated channels (Kir3.x); (iii) ATP-sensitive K^+ channels (Kir6.x); and (iv) K^+-transport channels.

Function and localization

In 1949, Bernard Katz (255) reported in muscle the presence of a potassium current that behave "anomalously" when compared with the outwardly rectifying K^+ like the one present in the squid axon. Depending of the electrochemical gradient, K^+ current was flowing inwardly (Fig. 2B). This was the first Kir channel characterized and since this K^+ conductance only develops at voltages negative to the equilibrium potential for K^+ (E_K), it will become important in setting the resting potential near E_K (185). In Kir channels, the inward arises from a voltage-dependent block induced by Mg^{2+} or polyamines (319, 320, 358, 557). Not all Kir channels show the same degree of inward rectification. There are "weak" (Fig. 2C) and "strong" Kir (Fig. 2D) channels and the molecular nature of the differences between these two types of

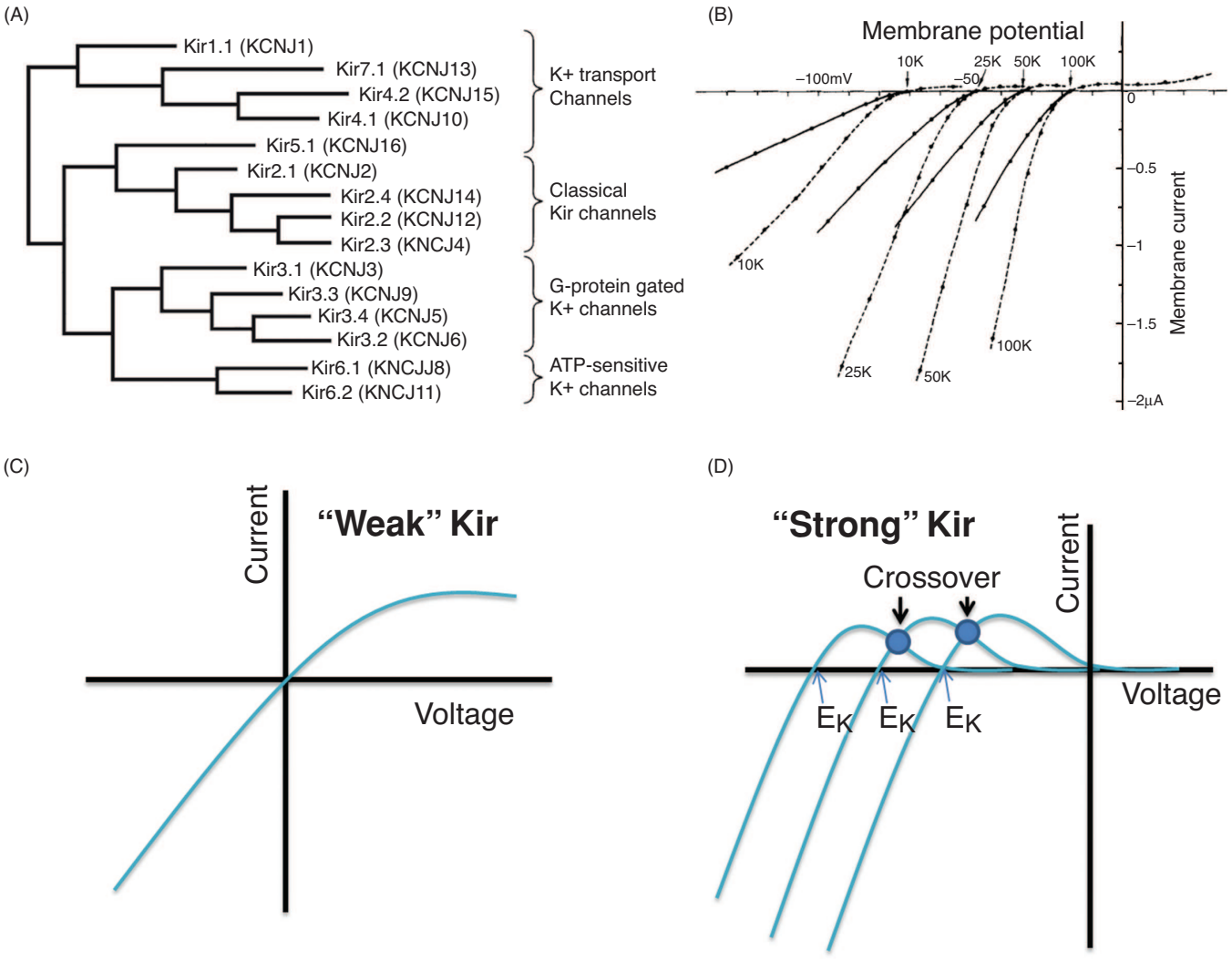


Figure 2 Phylogenetic tree of Kir channels and their current-voltage curves. (A) Amino acid sequence alignments and phylogenetic analysis for the 15 known members of the human Kir family. International Union of Pharmacology and Hugo Gene Nomenclature Committee names of the genes are shown. The subunits were classified into four functional groups following Hibino et al. (203). (B) Inward rectification and conductance are strongly external K^+ concentration-dependent. I-V relationships are of the starfish egg cell membrane at four different K_{ext} concentrations in Na^+-free media. Continuous and broken line indicates instantaneous and steady-state current, respectively (adapted. with permission, from reference 185). Notice that K^+ conductance develops at voltages negative to the equilibrium potential for K^+ (E_K). (C) I-V relationship characteristic of a "weak" inward rectifier. (D) In "strong" inward rectifiers K^+ conductance tends to zero as the membrane potential is depolarized and contrary to expectations the crossover phenomena produces an increase in K^+ conductance at voltages larger than the crossover voltage despite the decrease in the K^+ driving force.

channels will be discussed later when we look at the Kir channel structure. Gating in Kir channels is also modulated by nucleotides such as adenosine-tri-phosphate (ATP) and adenosine-di-phosphate (ADP), phosphorylation, G-proteins, and phosphatidyl-inositol-4,5-bisphosphate (PIP_2). It is important to note here that in the absence of PIP_2 a large number of different Kir channels [e.g., Kir2.1, Kir6.2/SUR2A, and Kir3.x; (530)] suffer a pronounced rundown suggesting that this lipid is essential for normal channel functioning. In the absence of PIP2, current rundown is complete in the whole Kir3.x subfamily (GIRK).

Kir channels are blocked by Ba^{2+} and Cs^+ but some of the classical K^+ channels inhibitors like tetraethyammonium (TEA) or 4-aminopyridine (4-AP) have little effect on Kir channels [e.g., Hibino et al. (205)]. However, the sensitivity to external Ba^{2+} depends, on the type of Kir channels. We can find large differences in Ba^{2+} sensitivity within a subfamily and in between different Kir subfamilies. Kir2.2 is about 65-fold more sensitive to Ba^{2+} than Kir2.4 (545), and Kir3.x channels are approximately 100-fold less sensitive than Kir2.1 when tested under similar experimental conditions (303, 496). Tertiapin, a toxin present in the honeybee venom, is able to block Kir3.x and Kir1.1 channels at nanomolar concentrations) and the oxidation-resistant product known as tertiapinQ is able to specifically block Kir3.x channels (241, 242).

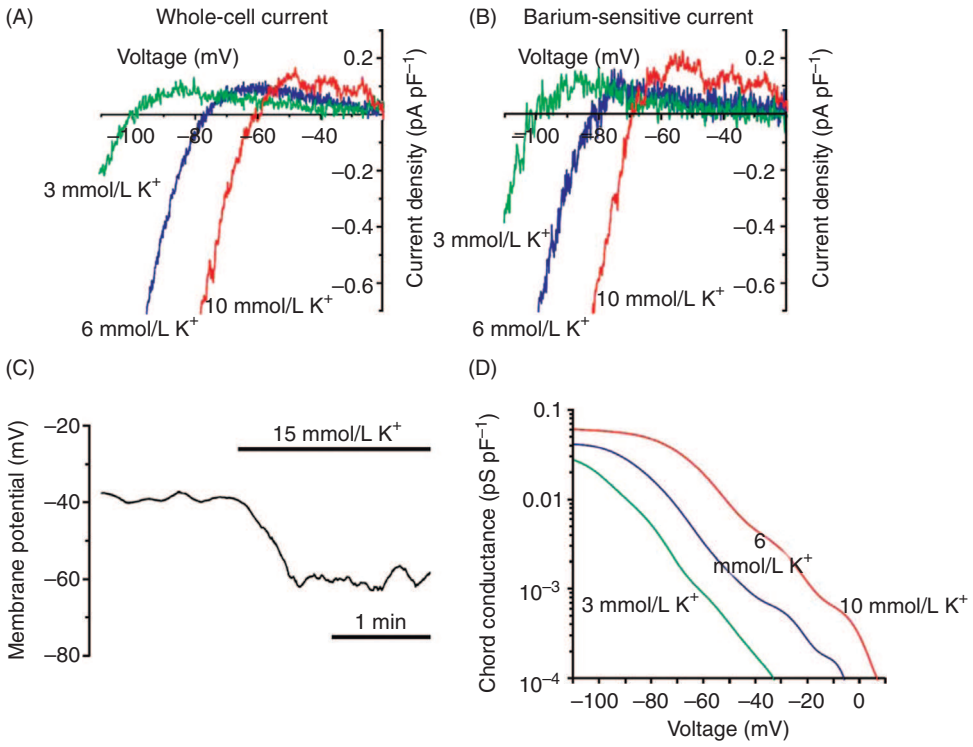


Figure 3 Kir2.1 induces a smooth muscle cell hyperpolarization when K_{ext} increases. (A) The average current densities at three different [K_{ext}] were obtained in response to a voltage ramp from −130 to 0 mV lasting for 140 ms. (B) Ba^{2+}-sensitive currents densities recorded in the same condition as in A. (C) Elevation of K_{ext} from 3 mmol/L to 15 mmol/L caused a membrane potential hyperpolarization of smooth muscle cells [adapted, with permission, from Filosa et al. (139)]. (D) Chord conductance-voltage curve at the same experimental conditions as in B. Notice that there is an appreciable increase in smooth muscle cells Kir conductance as the [K_{ext}] is raised at physiological membrane potentials (−50 to −40 mV).

The seven Kir channel subfamilies (Fig. 2A) can be classified into four functional groups [Hibino et al. (203)].

Classical Kir (Kir2.x)

These channels exhibit a strong inward rectification, are constitutively active, and are most prominent in ventricular tissue. In cardiac myocytes, they give origin to the background current, I_{K1}, and stabilize the resting potential (≈ -90 mV) near the K^+ equilibrium potential [E_K (8)]. This background current becomes negligible at $V > E_K$ and the absence of I_{K1} at depolarizing potentials results in a maintained depolarization that shapes the plateau of the cardiac action potential. I_{K1} is induced by Kir2.1/Kir2.2 heteromeric channels (633). It is important to note here that about 50% of the background current is lost in the Kir2.2 knockout mice whereas removal of the Kir2.1 channel promotes the complete disappearance of I_{K1} (617). Unlike wild-type ventricular myocytes that are quiescent, ventricular myocytes isolated from the heart of Kir2.1 knockout mice show spontaneous activity and broader action potentials. These observations strongly suggest that Kir2.1 commands the I_{K1} currents in the heart.

Classical Kirs, mainly Kir 2.2 (133), are also present in endothelial cells and smooth muscle cells where they play an important role in setting the vascular tone. In endothelial cell, by setting a negative resting potential, they provide the driving force for Ca^{2+} to enter the cell and activate the metabolic machinery that produces the vasorelaxant, NO (288,571). In vascular smooth muscle cells (VSMCs), contrary to expectations and as a consequence of the crossover effect (Figs. 2D and 3A and B), Kir2.1 (617) hyperpolarize the cells in response to an increase in the external K^+ concentration (Fig. 3C; e.g., reference 268) promoting *dilation* of rat coronary and cerebral arteries. This is the result of an increase in Kir-dependent conductance (Fig. 3D). In the brain, the perivascular space K^+ concentration can be elevated due to K^+ secretion mediated by Slo1 channels (see the Slo family channel section) present in the astrocytic bouton, a secretion promoted by neuronal activity. Therefore, the presence of a strong Kir in the VSMC, allows that the increase in K^+ couples neuronal activity to vasodilation in the brain (139).

All classical Kir channels are expressed in the brain and their expression is restricted to neurons, soma, and dendrites where they are important in determining the resting potential

and in the control neuronal excitability (106). Interestingly, Kir2.1 and Kir2.3 are located in the microvilli of Schwann cells where they can play the role of "keepers" of the external potassium concentration by absorbing the excess of K^+ secreted by the neurons during excitation (366).

In the kidney, we found classical Kir (Kir2.3) channels localized in the basolateral membrane of the cortical collecting duct where they maintain the membrane potential at a value that suffices to drive the K^+ flux from the basolateral to the apical side (192).

G-protein-gated channels (Kir3.x)

These channels (K_G also known as GIRK), which are gated by membrane-bound G proteins as first reported by Kurachi et al. (286), are formed by a variety of combinations of the four subunits, Kir3.1-Kir3.4, that give origin to this functional group of Kir channels (234, 270, 276, 303, 332). Actually, Kir3.1 and Kir3.3 subunits are unable to form independently functional channels but can coassemble forming Kir3.1/Kir3.3 and Kir3.2/Kir3.3 heterotetrameric channels.

K_G channels are activated by the $\beta\gamma$-subunits ($G_{\beta\gamma}$) of pertussin toxin-sensitive guanosine triphosphate (GTP)-activated proteins (G_i or G_o-type G protein. (285, 315, 574). The dissociation of the $\beta\gamma$-subunits from the α-subunit of the G protein is induced by binding of agonists [acetylcholine, adenosine, γ-aminobutyric acid type B ($GABA_B$), dopamine] to G protein-coupled receptors (GPCRs) in the presence of GTP.The $\beta\gamma$-subunits bind to both N- and C-terminus of K_G channel subunits (191, 231, 504). $G_{\beta\gamma}$ is unable to activate K_G channels in the absence of PIP2 since if Kir3.1/Kir41 channels are allowed to rundown completely, they are not activated by addition of $G_{\beta\gamma}$, but addition of PIP2 rapidly restores K_G channel-induced currents (223, 521). Several other modulators are able to activate K_G channels, including internal Na^+ and phosphorylation mediated by protein kinase A [PKA; (207, 363, 380, 520)]. The channels GIRK2 (Kir3.2) and GIRK4 (Kir3.4) are sensitive to intracellular Na^+, where the aspartate in the sequence DXRXXH is coordinating the sodium ion.

K_G channels show a basal activity even in the absence of receptor activation by agonists, activity due to the direct binding of the G_α a result supporting the hypothesis that GPCRs, G-proteins, regulatory proteins [G protein signaling (RGS) protein] and sorting nexin (SNX27) and K_G channels reside together in a signaling microdomain [Fig. 4A (145, 426)].

K_G channels are inhibited by a number of excitatory transmitters or hormones (e.g., acetylcholine, substance P, thyroid-stimulating hormone (TSH)-releasing hormones] (269, 301, 529). These transmitters or hormones by interacting with a GPCR coupled to a *pertussis toxin-insensitive* G protein (Gq) induce the activation of phospholipase C (PLC) (301, 494, 529). The depletion of PIP2 induced by the activation of PLC mediates the inhibitory/desensitization effect of some neurotranmitters on K_G channels [(102, 269, 301); see Fig. 4A]. The activation of PLC also promotes the activation of protein kinase C (PKC) and the PKC-dependent phosphorylation of K_G channels (Kir3.1/Kir3.4) underlies the inhibition of K_G channels by substance P (347).

In the heart, Kir3.1 and Kir3.4 subunits (276) form the K_{ACh}, channel that, activated by the ACh released from the vagal nerve, decelerates the heartbeat (reviewed in reference 8). However, we should point out here that the data of reference 34 may suggest that the subunit stoichiometry of this type of channels may vary since homotetrameric Kir3.4 can be expressed in rat atrial myocytes. I_{KACh} is most prominent in atrial tissue and in sino atrial node (SAN) and current rectification is "weak" compared to that shown by the I_{K1}.

Atrial fibrillation (AF) is the most common cardiac arrhythmia in clinical practice. AF can become persistent due to remodeling of atrial electrophysiology. Electrical remodeling in AF patients causes an increase in constitutively active component of I_{KACh} and a decrease of its ACh-induced component (112). This switch from a ligand-gated current to constitutively active behavior would lead K_G/Kir3.x channels to shorten atrial action potential duration and refractory period in cAF patients.

In the pancreas, catecholamines and somatostatin suppress insulin secretion from β-cells (232, 451, 501, 604) by activating K_G-mediated currents. In pancreatic islets, Kir3.2 and Kir3.4 DNAs were identified and homo and heterotetramers of these two types of K_G channel subunit are probably originating the G protein-gated currents than regulate hormone secretion from islet cells (53, 136).

Present in a number of brain regions, K_G channels localized in dendritic spines, in the postsynaptic density as well as extra synaptic sites are involved in the generation of slow inhibitory postsynaptic potential [sIPSP; (331,503); reviewed in references 203, 330, and 332]. Different types of K_G channels are, however, found in synaptic and extrasynaptic regions of neurons. Kir3.2 is present in the postsynaptic density of neurons of the *substantia nigra pars compacta*, while Kir3.1 and Kir3.2 can be detected in the extrasynaptic membrane of CA1 hippocampal pyramidal neurons (275). At extrasynaptic sites of Purkinje cells K_G channels are formed by Kir3.1/Kir3.2/Kir3.3, postsynaptic densities contain Kir3.2/Kir3.3 heterotetrameric channels, and dendritic shafts contain Kir3.1/Kir3.3 (134).

Receptor activation of K_G channels mediate at least three different changes in electrical signaling in the nervous system (332). We consider first the case of the low-threshold spiking (LTS) in neocortical neurons that possess a form of long-lasting self-inhibition mediated by endocannabinoids (22). Endocannabinoids release from dendrites activates cannabinoid receptor 1 which is coupled to K_G of the same dendrite resulting in a long-lasting hyperpolarization. Second, in CA1 hippocampal pyramidal neurons K_G channels colocalize with and are functionally coupled to γ-aminobutyric acid type B (GABAB) receptors (275). This proximity allows

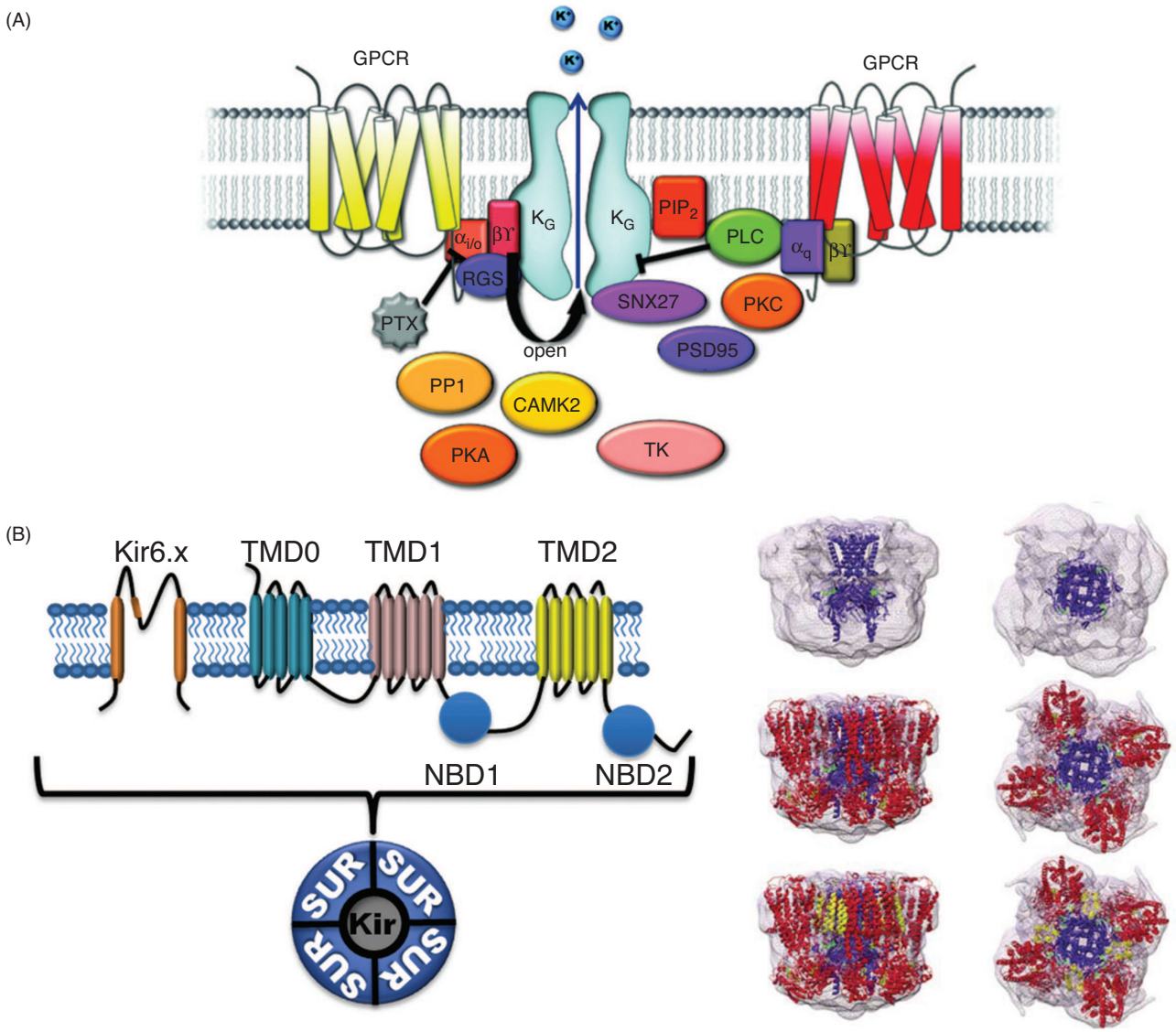


Figure 4 Dual modulation of K_G channels by G protein-coupled receptor (GPCR) and the topology and structure of Kir6.x. (A) Agonist activation of GPCR coupled to pertussis (PTX)-sensitive $\alpha_{i/o}$-type of G protein promotes activation of K_G channels. Activation of K_G channels is induced by binding to the channel-forming protein of the $\beta\gamma$ complex of the G protein. Agonist binding to α_q-type of G protein results in channel inhibition that is a consequence of the activation of phospholipase C (PLC), which in turn hydrolyses phosphatidyl-inositol-4,5-bisphosphate (PIP_2). Other modulators include tyrosine kinase (TK), Ca^{2+}-calmodulin-dependent kinase 2 (CAMK2), and protein phosphatase (PP1). Modified, with permission, from reference 332. For more details, see text. (B) SUR subunits contain 17 transmembrane segments assembled in three domains, TMD0-2, and containing two nucleotide-binding domains (NBD) contained between TMD1 and TMD2 (NBD1) and in the C-terminus (NBD2). The structures show top and side views of the entire K_{ATP} channel complex analyzed at 18 Å resolution. Blue represents Kir6.x. Red represents the rest of SUR and yellow represents TMD0 of SUR [adapted, with permission, from Mikhailov et al. (367)].

the activation of K_G induced by GABAB diffusion from nearby inhibitory synaptic contacts, which end result is the sIPSP crucial in the control of rhythmic hippocampal activity (479). Third, K_G channels are also involved in large-scale neuronal network modulation through a process known as volume transmission whereby the neurotransmitter release from many neurons diffuses to activate K_G channels on target neurons. The net result of the elevation of the ambient concentration of neurotransmitters is to reduce network activity of neurons (reviewed in reference 332).

ATP-sensitive K^+ channels (Kir6.x)

K_{ATP} channels were discovered in cardiac tissue where they are present in the sarcolemmal membranes in high density (399). These channels show a weak inward rectification and, as the classical Kir2.x channels, they have constitutive activities--in excised patches, K_{ATP} channels open spontaneously, openings that are inhibited by internal ATP. Composed of four Kir6.x and four sulfonylurea receptor (SUR1, SUR2A, and SUR2B) subunits, these channels have an

octameric stoichiometry (Fig. 4B) (81, 500). The Kir subunits form the ion channel pore and are responsible for the internal ATP channel inhibition whereas the SUR subunits, containing two nucleotide-binding domains, bind nucleotide diphosphates (NDPs; e.g., ADP) and activate K_{ATP} channels.

An array of inhibitory and stimulatory substances binds to SUR. The sulfonylureas (e.g., chlorpropamide) act as K_{ATP} channel inhibitors whereas agents such as pinacidil work as K^+ channel openers (KCOs) (see references 18 and 116). In pancreatic β-cells, K_{ATP} channels, made up of Kir6.2 and SUR1 subunits (226, 227), play a crucial role not only in setting the resting potential but also in modulating insulin secretion (19). The small cytoplasmic ATP concentration kept by low levels of blood glucose allows the opening of K_{ATP} channels which, under those conditions are able to maintain the resting potential. As the blood glucose concentration increases, the influx of glucose produces an increase in the internal β-cell ATP concentration and K_{ATP} channels closed. The closing of K_{ATP} channels depolarizes the β-cell causing the opening of L-type voltage-dependent Ca^{2+} (VDCC) channels. The influx of Ca^{2+} through VDCC induces the fusion of insulin-containing vesicles to the plasma membrane with the consequent hormone release. Thus, K_{ATP} channels play the important role of coupling blood glucose concentration to insulin secretion.

K_{ATP} channels in the heart, due to the high internal ATP concentration in this tissue, are quiescent but they open in response to metabolic insult such as ischemia. Opening of K_{ATP} channels will shorten the cardiac action potential, reducing the Ca^{2+} influx through VDCC (252, 390, 399). Thus, in the heart, K_{ATP} channels provide protection against the insult of ischemia. These channels are directly involved in the protective role that brief periods of ischemia (preconditioning) have on a subsequent severe ischemic insult (172). The importance of Kir6.2 in determining the protection against severe ischemic insult has become clear since preconditioning disappears in the Kir6.2 knockout mice (178). K_{ATP} channels also play a protective role during acute exercise stress avoiding the cytosolic Ca^{2+} overload induced by hyperadrenergic conditions. Supporting the protective role that K_{ATP} channels play in stress adaptation, the Kir6.2 knockout mice is unable to shorten the cardiac action potential upon adrenergic stress (632).

It is of importance to mention here that K_{ATP} channel are present in the SAN and that metabolic inhibition antagonizes pacemaker activity by activating this type of channels. Activation of K_{ATP} channels in SAN may have dramatic effects on the rate of diastolic depolarization (188).

In hypothalamic glucose-sensitive neurons extracellular glucose removal causes a cell hyperpolarization and an inhibition of action potential firing. Kir6.2 channels are involved in the generation of the glucose-sensitive K^+ current in neurons indicating that the increase in neuronal excitation observed when the concentration of external glucose raises is due to closure of K_{ATP} channels (368, 618). However, some glucose-sensitive neurons (e.g., neurons in the rat ventromedial hypothalamus) express K_{ATP} channels formed by Kir6.1 and SUR1 (298).

K^+-transport channels (Kir1.1, Kir4.x, Kir5.x, and Kir7.1)

Kir1.1 Previously known as ROMK1, Kir1.1 is a weak Kir having six alternative splicing isoforms (reviewed in reference 203). Kir1.1 channels are found in numerous different types of cells and, in particular, in polarized cells (e.g., kidney cells) they play an important physiological role not only in setting the resting membrane potential, but located in the apical or in basolateral membranes, they are involved in the regulation of the K^+ concentration as well as in the Na^+ and Cl^- concentration (e.g., references 192 and 566). For example, the efflux of K^+ mediated by Kir1.1, located in the apical membrane of thick ascending limb cells, promotes the necessary K^+ recycling for the activation of the Na^+-K^+-$2Cl^-$ cotransporter needed for about 25% of the reabsorbed Na^+ (51).

Kir4.x and Kir5.1 Most expressed in glial cells, Kir4.1 controls neuronal function by exerting a K^+-buffering capacity (389). Kir4.1 can form homotetramers or heterotetramers with Kir5.1 (55, 202, 429, 536). However, Kir5.1 is unable to form functional homotetramers and only play physiological roles in combination with Kir 4.1 or Kir4.2 albeit with different biophysical properties. Kir 4.1 shows an intermediate inward rectification that turns into a strong inward rectification when forming heteromers with Kir5.1. Kir4.1/Kir5.1 channels are activated by internal Na^+ a property conferred to the channel by aspartate205 in the Kir5.1 subunit, a residue not conserved in Kir4.1 (454).

Situated in the basolateral side of distal convoluted tubule cells, Kir4.1/Kir5.1 plays an important role in Na^+ reabsorption (192). Kir4.1/Kir5.1 channels supply the necessary external K^+ to the Na^+-K^+-ATPase pump that, coupled with epithelial Na^+ channels in the apical membrane, allows the Na^+ movement from the apical to the basolateral side of the epithelium. Since the pump internalizes the K^+ supplied by the K^+ efflux mediated by the Kir4.1/Kir5.1 channel, this process is called "K^+ recycling."

Kir 4.1 plays several others important physiological roles. Expressed in the apical membrane of intermediate cells in the cochlear *stria vascularis* (7) is the molecular component in charge of the K^+ secretion that maintains the high K^+ concentration in the endolymph and sets the endocochlear positive potential (~80 mV) with reference to the perylymph (204, 393, 531). Kir4.1 knockout mice are deaf, the endocochlear potential is near 0 mV and the K^+ concentration in the endolymph is reduced by approximately 50% (350). In glial cells, on the other hand, Kir4.1 is fundamental in the clearance of the excess of external K^+ produced by neuronal activity (e.g., reference 388 and 538). However, it is important to point out here, that in cortical astrocytes of the brain Kir4.1 and Kir4.1/Kir5.1channels are expressed in perisynaptic

processes whereas Kir4.1/Kir5.1are only expressed at the end feet (310). It is possible to interpret these results by assuming that in astrocytes external K^+ is taken up by Kir4.1 and Kir4.1/Kir5 channels and secreted only by Kir4.1.

Kir7.1 Only one isoform of Kir7.1 has been isolated and although its physiological role is largely unknown, colocalize with the Na^+-K^+-ATPase pump in epithelial cells suggesting that, like Kir1.1 and Kir 4.1, may play a role in K^+ recycling (see reference 203).

Kir channels structure-function relationships

Molecular determinants of inward rectification

As discussed before, inward rectification in Kir channels is a consequence of a voltage-dependent block by Mg^{2+} or polyamines and is not due to the movement of gating charges intrinsic to the channel-forming protein. The displacement of a blocking ion within the electric field produces a voltage-dependent block that according to Woodhull (581) depends of the location of the blocker-binding site inside the electric field. For example, if a polyamine having a valence of 2 "sees" the whole voltage drop across the pore (defined as an electrical distance, δ, of 1), the valence, $z\delta$, of the voltage-dependent reaction should reach a *maximum* value of 2. How is possible then that alkyl bis-and mono-amines carrying 1 or 2 positives charges are able to generate a voltage dependence with a $z\delta$ as large as 4 with increasing chain length? The most economical explanation to this anomalous large voltage dependence is to assume a strong coupling between polyamines or Mg^{2+} block and K^+ movements through a long pore (179, 320, 325, 421). In this case, the voltage dependence of the block arises, not as a consequence of the blocking ion moving within the electric field but rather the blocker, entering the long pore from the cytoplasmic side, forces multiple K^+ ions to move in a queue in front of the blocker (Fig. 5A). Thus a channel containing m K^+ ions will become one containing $m - n$ K^+ ions after the blocking particle (BP that can be Mg^{2+} or a polyamine) is in its equilibrium position inside the pore according to the reaction

$$ChK_m + BP \overset{K_D}{\longleftrightarrow} ChK_{m-n}BP + nK_{ext} \qquad (1)$$

where K_D is the dissociation constant.

The proposed mechanism to explain the large voltage dependence of spermine block needs; therefore, a single file of at least 5 K^+ ions contained in a pore toward the cytoplasmic side of the selectivity filter (497). The elucidation at 1.8 Å resolution of the crystal structure of the protein originated from the intracellular N- and C-termini of a bacterial Kir Kir3.1 (GIRK1) by Nishida and MacKinnon (395) gave the first structural confirmation to the long-pore hypothesis. The structure of the N- and C-terminus of Kir3.1 consisting of 14 β-strands and 2 α-helices, contains a pore, dubbed the cytoplasmic pore that forced a K^+ ion to travel more than 60 Å from the extracellular side to the end of the C-terminus (284, 395) (Fig. 5B). In this journey, the K^+ ion would have to diffuse about 30 Å in the membrane and another 30 Å in the cytoplasmic pore before reaching the internal solution, a distance nearly twice that found in other K^+ channels. The long-pore characteristic of Kir channels was soon confirmed by Kuo et al. (284) who elucidated the crystal structure of a prokaryotic Kir channel, KirBac1.1. The KirBac1.1 structure was crystallized in the closed configuration characterized by an ion conduction pathway blocked by the side chains of phenylalanine 146 localized near the C-terminus of TM2 (see Fig. 5B). This residue is highly conserved in the Kir channel family and defines a closed helix bundle gate since replacement of the bulky Phe (F181 in Kir3.1 and F187 in Kir3.4) with Ala or Ser converted channels from agonist activation to constitutive active (80).

The entire Kir channel assembly showed a conduction machinery possessing a well-conserved selectivity filter with the characteristic T-X-G-Y-G signature sequence, and a central cavity, not different from other K^+ channels (for more structural details about the selectivity filter, see section on Kv channels). However, it should be mentioned here that in the canonical selectivity filters the last glycine of the GYG motif is followed by an aspartate whereas in most Kir channels there is a phenylalanine in that position. The crystal structure of Kir2.2 shows that this phenylalanine projects directly into the external solution. This together with the fact that the Kir2.2 turrets are larger and come closer together makes the pore external entryway much narrower when compared to that of Kv1.2 (539). Since other K^+ channels present a flat surface surrounding the external aspect of the selectivity filter opening, the protrusion created by the phenylalanines and the large turret hinder toxin docking and are important factors in determining the insensitivity of Kir channels to toxins (539).

With the exception of Kir 7.1, the conductance of Kir channels increases with the square root of the external K^+ concentration (207, 277) a result in agreement with the multi-ion pore nature of this type of channels. Moreover, Lopatin and Nichols (321) showed that even in the absence of Mg^{2+} and polyamines, Kir2.1 also exhibits the square root dependence of the external K^+ suggesting that this is a property of the open pore. Nishida et al. (394) using a Kir3.1-prokaryotic Kir channel chimera showed that, as in KcsA, four K^+ ion positions were observed in the selectivity filter and one in the channel cavity. However, in contrast to KcsA channels, two ions were localized in the cytoplasmic pore (Fig. 5B). Although confirming the existence of K^+ ions localized in the cytoplasmic pore, their number is insufficient to explain the voltage dependence of Kir channels found experimentally. More recently, Xu et al. (594) solved the crystal structure of the isolated cytoplasmic pore of the Kir3.1 channels at 2 Å resolution. Using Na^+ as a K^+ surrogated, they were able to show the presence of five ions in sites denominated S7-S11 (Fig. 5C), most of them coordinated by the side chains of polar or negatively charged amino acids with the exception of S10, a site consisting of a ring of four phenylalanines (Phe255) implying that in this case the central ion is stabilized by

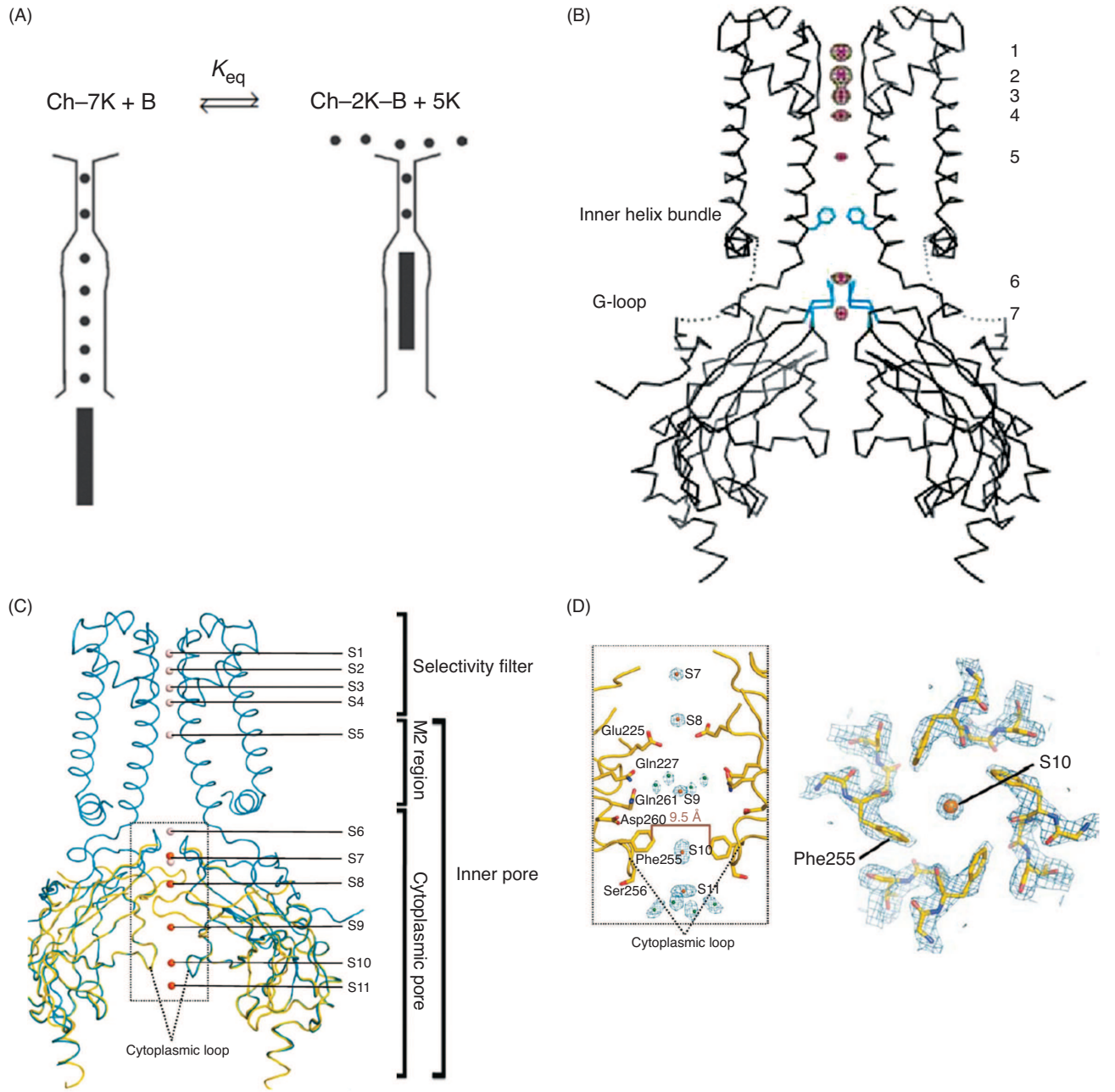


Figure 5 Kir channel crystal structure and cation-binding sites. (A) Voltage dependence in Kir channels arises as a consequence of the movement of K^+ ions contained in the cytoplasmic pore. (B) Crystal structure of a Kir3.1-prokaryotic Kir channel chimera determined at 2.2 Å. Seven Rb^+ ions were located in the conduction pore. Two constriction sites, F181 side chain and residues 302-309 Cα atoms in the G-loop are colored in blue. For the sake of clarity only two subunits are shown [adapted, with permission, from Nishida et al. (394)]. (C) Crystal structure of the cytoplasmic pore of S225E mutant of Kir3.1 (yellow) and the Kir chimera (308) (cyan). Na^+ ions are represented by orange spheres and Rb^+ ions by pink spheres. (D) Crystal structure model of the cytoplasmic pore of S225E mutant Kir3.1 corresponding to the boxed region in A. The residues, Q225, G227, G261, D260, F255, and S256, interact directly or through water molecules with the Na^+ ions located at S8-S11. The positions of the phenylalanines coordinating the Na^+ through π-cation interactions at site S10 are shown [adapted, with permission, from Xu et al. (594)].

π-cations interactions (Fig. 5D). These findings demonstrates that there are enough ions in the cytolasmic pore as to account for the strong voltage dependence of Kir channels and the presence of a constriction near the intracellular end of the cytoplasmic pore ensures an obligatory outward movement of the K^+ ions file induced by the entrance of the polyamine.

Acidic residues in M2 and the cytoplasmic pore determine inward rectification

The cloning, expression and mutagenesis of Kir channels gave the first clues about the possible location of the residues important in determining blocker affinity. Three different groups

found in the same year that an aspartate (D172 in Kir2.1) in TM2 is critical in conferring strong inward rectification (328,510,573). Moreover, a Kir channel like Kir1.1 that shows a weak inward rectification can be converted into a strong Kir if N171 (corresponding to D172 in Kir2.1) is replaced by an acidic residue (328). Blockade is electrostatically tuned since replacement of neutral residues by acidic residues in a number of positions of M2 confers high affinity for blocking ions and that a histidine replacement of D172 makes inward rectification pH dependent (179, 328, 329).

Taglialatela et al. (528) found that replacement of the C-terminus of the weak Kir Kir1.1 for the C-terminus of Kir2.1 transformed the former channel into a channel showing strong inward rectification. This result was a clear indication that the C-terminus is also a structural determinant of the affinity of Kir channels for intracellular blocking ions, and soon it was demonstrated that acidic amino acids in the cytoplasmic pore are also crucial for the underlying affinity of Kir channels for blocking ions. In Kir2.1 residue E224 is important in determining the degree of inward rectification (Fig. 6A and B) (281, 598). On the basis of the crystal structure of the cytoplasmic domain of Kir2.1 and electrophysiological studies a diaspartate cluster on the distal end of the cytoplasmic pore (D255/D259) and a glutamate 299 important in the

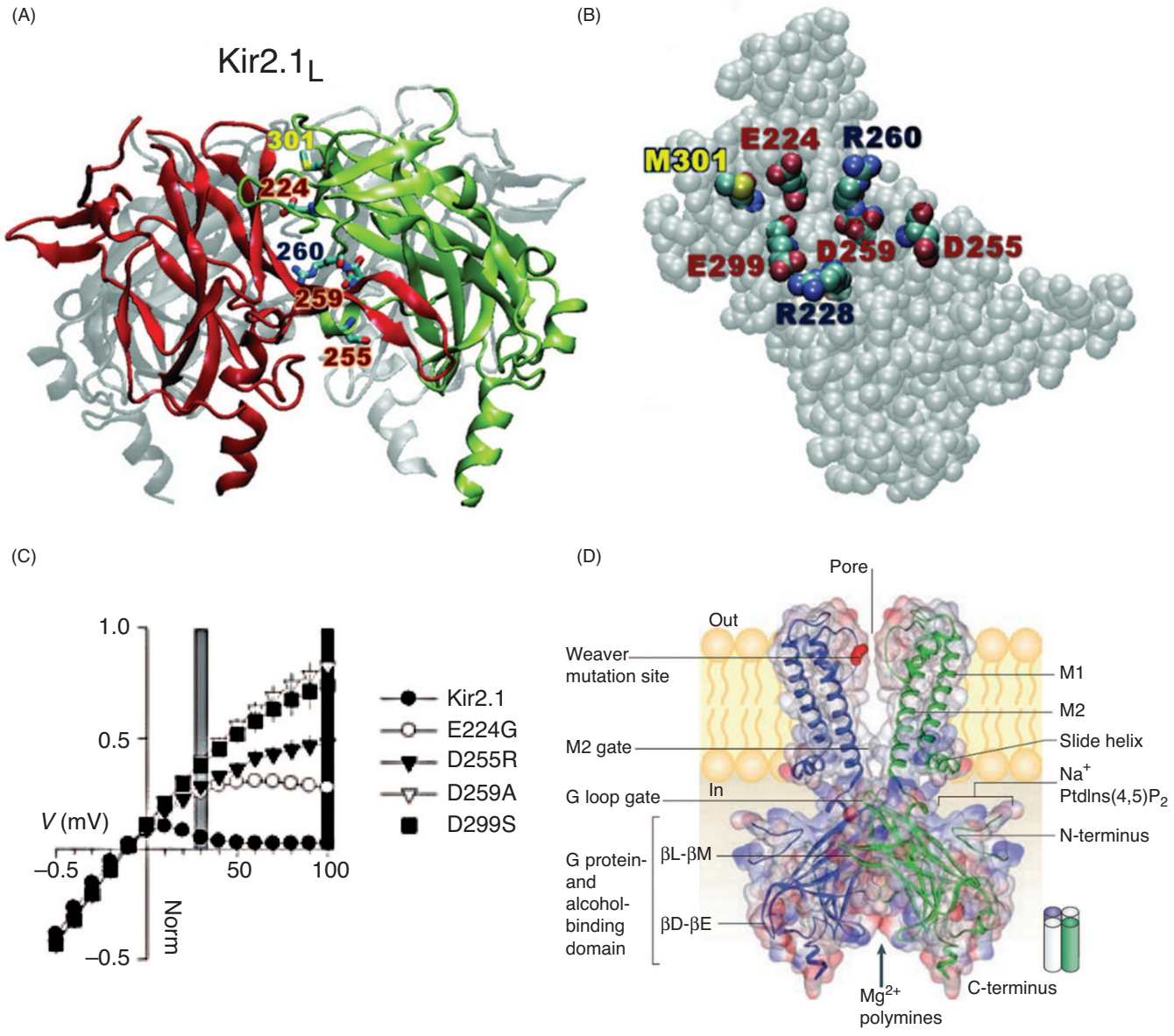


Figure 6 Molecular determinants of inward rectification and location of modulators binding sites in the cytoplasmic domain of K_G channels. (A, B) Amino acid residues in the cytoplasmic pore determining inward rectification in Kir2.1 channels. (C) Current-voltage relationships for different Kir2.1 point mutants [adapted, with permission, from Pegan et al. (425)]. (D) The structure shown contains the cytoplasmic domains of Kir3.1 a G protein-gated channel and the transmembrane domains and pore region of the chimeric Kir channel. The regions implicated in Na^+, PIP2, G protein, and alcohol binding are shown [adapted, with permission from Luscher and Slensinger (332)].

modulation of inward rectification were identified (Fig. 6A-C) (425). The crystal structure of Kir2.2, on the other hand, revealed several cation-binding sites in the conduction machinery of this channel; One in the TM pore (formed by D173) and two in the cytoplasmic pore constituted by a double ring of charges (upper ring, E225/E300) and a lower ring of charges (D256) (539). Interestingly, all three sites show a preference for Sr^{2+} over Rb^{+}, selectivity that due to the large diameter of the sites is likely to be electrostatic in origin. This brings the total number of acidic amino acids determining the Kir2.1 channel high affinity for Mg^{2+} and polyamines to 4-5. However, number *and* position of the negatively charged amino acids are important in determining the degree of inward rectification. For example, although Kir4.1 has only three negatively charged residues in the long pore, it shows strong inward rectification but Kir 1.1 containing the same number of acidic amino acids at sites implicated in rectification, shows a weak rectification (132, 328).

Some structural inferences about gating induced by agonists

The crystal structures of the cytoplasmic domains of Kir2.1 and the G-protein-gated Kir3.1 revealed that the cytoplasmic pore has four loops (the G-loop) that form a structure that in the case of Kir2.1 completely occludes the path of ions (425). The girdle formed by the G-loops is located near the junction between the cytoplasmic and TM pore domains (Figs. 5B and 6D). This a flexible structure and its conformational changes, induced for example by PIP_2 or other agonists, may modulate gating. In fact, mutations in the G-loop disrupt gating and inward rectification. The crystal structure of a chimeric Kir channel in which most of the pore domain belongs to the prokaryotic KirBac1.3 channel and the remainder including the slide helix and cytoplasmic pore are from the mouse Kir3.1 gave a strong support to the hypothesis that the G-loop behaves as a gate in the cytoplasmic pore (394). Two different structures for the chimeric channel were found in which the cytoplasmic pore adopted different conformations. In one the girdle formed by the G-loops is constricted (equivalent to a closed state of the channel) whereas in the other is dilated (open state). The dilated conformation leaves a pore sufficiently wide to permit the passage of mostly hydrated K^{+} ions. The constricted conformation of the G-loop, on the other hand, is so narrow that even a dehydrated K^{+} ion is unable to pass through this region.

As discussed previously, the activity of Kir channels depends critically on the interaction of the channel with PIP_2. Positively charged amino acid residues located in the C- and N-terminus of Kir channels were identified as essential for PIP2 channel activation (e.g., references 323 and 551). It is possible then that the chemical energy of binding of PIP2 to these residues, all located in the external surface of the cytoplasmic pore, may be allosterically coupled to conformational changes of the G-loop gate (Fig. 6D) (394). In agreement with this hypothesis, Ma et al. (334) found that a mutation of one of the amino acid located in the G-loop (V302M) profoundly alters the PIP2 sensitivity of Kir2.1 channels.

Amino acid residues located in the external aspect of the cytoplasmic domains are involved in both agonist-independent and receptor-induced $G\beta\gamma$ activation of Kir3.x channels (283, 332, 504). A leucine (L333) residue located in the C-terminal domain of Kir3.1 (βL-βM sheet; corresponding to L344 and L339 in Kir3.2 and Kir3.4, respectively) plays a vital role in the $G\beta\gamma$-dependent activation (Fig. 6D) (191). Importantly, direct binding of $G\beta\gamma$ to fragments of Kir3.x subunits shows that mutations of this important leucine do not reduce the binding of $G\beta\gamma$ suggesting that this residue is part of the coupling system involved in the transduction of the energy of binding to the mechanical energy necessary to open the channel (231). Riven et al. (447) using fluorescence resonance energy transfer (FRET) showed that the conformational rearrangement of the channel induced by $G\beta\gamma$ is consistent with a rotation and a widening of the cytoplasmic domains, movements that may be coupled to the G-loop or bundle crossing gates.

Two-Pore Domain Potassium Channels (K_{2P}) Family

Leak conductances also called background conductances, like inward rectifying K^{+} channels, mediate resting membrane potentials, and alter action potential height and duration (225, 430). Goldstein et al. (158) searched the DNA database for sequences homologous to the P-domain of previously cloned K^{+} channels and found a gene in the budding yeast *Saccharomyces cerevisae*, named TOK1. The discovery of TOK1 started a search for other two-pore domain K^{+} channel (K_{2P}) genes. In comparison with previously described K^{+} channels this type of channels were novel in two aspects: (1) the TOK1 channel-forming protein contains two pore-forming regions; and (2) TOK1 was the first cloned example of a new functional type of outward rectifier K^{+} channel. In 1996, another K_{2P} human K^{+} channel gene (*TWIK-1*) with four-TM segments was identified (304) and soon after, the cloning of nerves and muscles genes of *Drosophila melanogaster* resulted in the isolation of *Ork1*, the product of which was denominated $K_{2P\emptyset}$ (158, 225, 257, 430). From further electrophysiological studies, it became evident that these channels formed a single pore by making a *dimer* of two subunits, leaving both N- and C-termini facing the cytosol. The four-TM channels cloned and expressed are all selective to K^{+} presenting some small rectification. Given these characteristics these channels prove to be important in setting the resting potential, regulating cellular excitability, and in increasing K^{+} permeability of cells that need to transport K^{+} ions (354, 534).

$K_{2P\emptyset}$ has a linear current-voltage relationship under symmetrical K^{+} conditions; however, significant outward currents are seen only under physiological conditions with high internal K^{+} and low external K^{+}. After this first functional

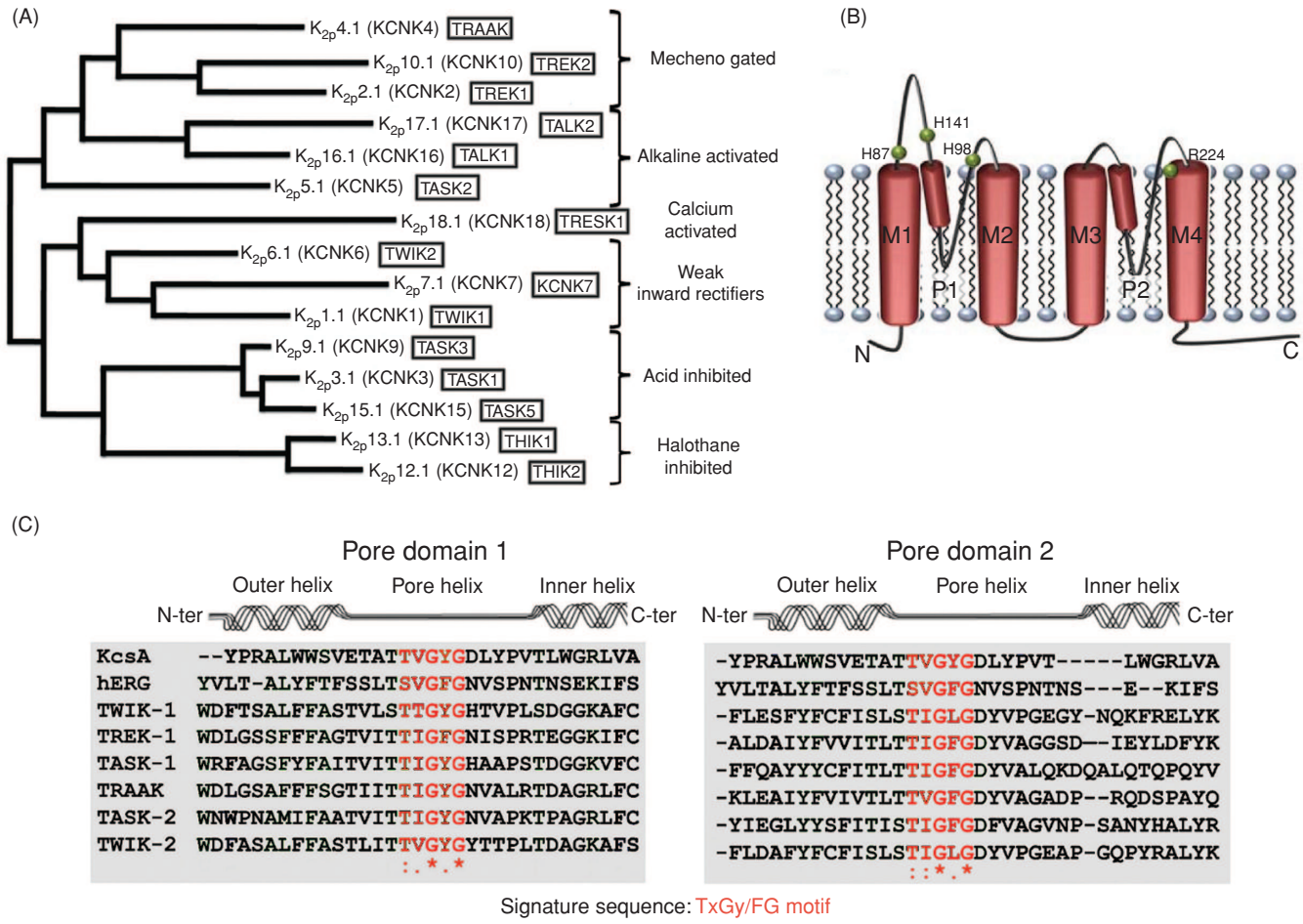


Figure 7 Diversity of 2-pore (2P)-domain K+ channel (K2P) subunits and membrane topology. (A) The alignment was made using the web tool: Phylogeny.fr (109), with different sequences of human two pore K+ channels obtained from gene bank accession numbers from *KCNK1* to *KCNK18*: NP_002236, NP_055032, NP_002237.1, NP_201567.1, NP_003731.1., NP_004814.1., NP_005705.1., NP_057685.1., NP_066984.1., NP_071338.1., NP_071337.2., NP_071753.1., NP_115491.1., NP_113648.2., and NP_862823.1. (B) Putative membrane topology of the two-pore domain K^+ channels. Green spheres indicate pH sensing residues and their predicted location in the first turret loop and M4 transmembrane domain. (C) Multiple sequence alignment of the outer and inner helix region of KcsA, hERG, and several K_{2P} K^+ channels. Amino acid residues colored in red show the K^+ channel signature sequence, corresponding to the selectivity filter.

characterization, the K_{2P} mammalian channels were formally named $K_{2P}1$, $K_{2P}2$, etc., and the encoding genes named accordingly, *KCNK1, KCNK2*, etc. (128, 203). Since their discovery, 15 human K_{2P} members have been identified, and most of them behave as pure leak or background K^+ channels (Fig. 7A), whose main function is to maintain the resting level of membrane potential (94, 354). Although, the K_{2P} channel subunits display the same structural motif (Fig. 7B), they share only moderate sequence homology outside their pore regions (Fig. 7C). In addition, to the four putative TM segments and the two P-domains, the more relevant structural features are: the short N-terminal, the long C-terminal, and a long extracellular loop between TM1 and P1 (305, 417) (Fig. 7B).

K_{2P} channel subfamilies

The K_{2P} channels are regulated by an extensive variety of stimuli: for example, pH, temperature, and membrane stretch. For example, an increase in the low basal activity of K_{2P} channels in response to sumoylation, and dephosphorylation, or to changes in physicochemical parameters including temperature, intracellular/extracellular pH, oxygen tension, and changes in osmolarity and/or membrane stretch enable rapid and significant changes in ion fluxes (430, 534). Evidence is accumulating for the potential importance of targeting and altering the activity of K2P channels in a number of therapeutic situations in the nervous system, including neuroprotection, neuropathic pain, depression, anaesthesia, and epilepsy (27, 29, 213, 314, 459). Due to the diversity of responses when confronted to different stimuli, members of the K_{2P} family were divided into six subfamilies (Fig. 7A): (i) mechanogated; (ii) alkaline-activated; (iii) Ca^{2+}-activated; (iv) weak Kirs; (v) acid-inhibited; and (vi) halothane-inhibited channels (213).

Other genes such as *KCNK6* and *KCNK7* code for silent subunits that probably require a partner to form functional

channels (29,95,305). Although the members of the different subfamilies show relatively low sequence similarity, (TWIK-1 and TREK-1 show only a 28% of identity at the protein level) all members of the background potassium channel family are characterized by the same general molecular architecture (Fig. 7B).

K_{2P} channels topology and stoichiometry

Lesage et al. showed that TWIK-1 self associates to form disulfide-bridged homodimers (306) and that this assembly involves a 44-amino acid region sufficient to promote the self-dimerization and located in the TM1-P1 interdomain. Therefore, unlike the assembly of Kv or Kir subunits that form noncovalently associated tetramers, K_{2P} channel subunits require the formation of a stabilizing interchain disulfide bridge (305, 306). It has been suggested that the domain that is essential for the dimerization in K2P channels might function as a regulatory region possibly by binding extracellular ligands (305). All mammalian K_{2P} channel subunits possess four TM segments; the 4TM/2P structure defines the membership in the K_{2P} channel family. Based on the pioneer characterization of the oligomeric state of TWIK-1, a dimeric structure has been assumed for all the other K_{2P} channels. Furthermore, all the cloned subunits, except TASK-1, contain a cysteine residue at a position equivalent to cysteine 69 of TWIK-1, and all these subunits (except TASK-1) are able to form covalent homodimers when heterologously expressed in insect or CV-1 (simian) cells, and carrying the SV40 genetic material (COS) cells. In addition, the covalent dimerization of TREK-1 and TRAAK was also observed in synaptic membranes (305). In this family, the K^+ channel signature sequence GYG is replaced by GFG in TREK-1, in both P motifs of the subunit, and in one P motif in Task-1, TASK-2, and TASK-3 (Fig. 7C). In TWIK1, and TWIK2 one of the P motifs the signature sequence GYG is replaced by GLG. Furthermore, in KCNK6 and KCNK7 (silent subunits) a glutamic residue GLE is found instead of the strictly conserved glycine residue (273, 305).

TREK and TRAAK channels

The first cloned K_{2P} mammalian mechanogated K^+ channels were named TREK and TRAAK. They are considered mechanosensitive ion channels since at atmospheric pressure their open probability is low, and channel activity is elicited by increasing the mechanical pressure applied to the cell membrane (Figs. 8A and 9A) (95,417). The TREK/TRAAK is a subfamily of polymodal K^+ channels since is regulated by several stimuli such as: stretch, osmolarity, pH, temperature, polyunsaturated FAs, lysophospholipids, neuroprotective agents, cationic amphipaths, volatile anaesthetics, and phosphorylation triggered by G-coupled receptors and other intracellular cascades (see Fig. 8B) (95, 147, 214, 282, 305, 417).

TASK-1: The perfect background K^+ channel

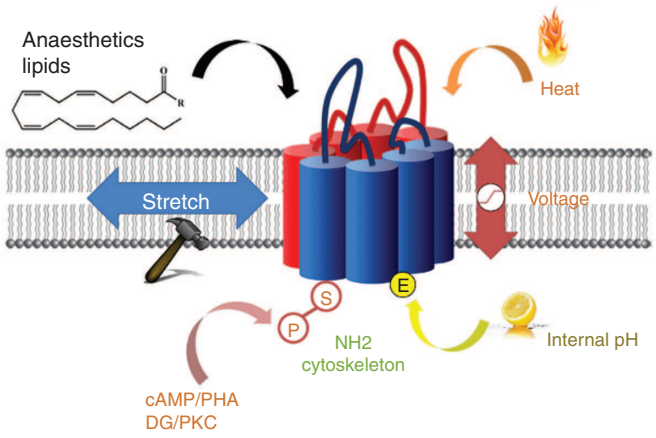
TASK-1 was the first cloned mammalian K^+ channel to produce time-independent currents with all the characteristics of a background or baseline conductance. This channel found in myelinated nerve, is insensitive to the classical K^+ channel blockers TEA, 4-AP, and Cs^+. TASK-1 current-voltage relationship curves are well fitted by the constant field theory (Goldman-Hodgkin-Katz rectification or open rectification) for simple electrodifussion through an open K^+ selective pore (305). Since both, TASK-1 and TASK-2 are constitutively active, they are predicted to contribute to the maintenance of the resting membrane potential, and/or to K^+ transport associated with recycling or secretion. Moreover, these channels are present in nonexcitable cells, with the exception of TASK-1 that is present in brain and heart (122, 262, 302). TASK channels respond to variety of extracellular calcium-mobilizing receptor agonists and are inhibited by antagonists such as extracellular acidosis, anandamide, volatile anaesthetics, and other stress processes such as hypoxia (Fig. 8C).

Compared with TASK channels, TREK-1 and TRAAK currents have a low basal activity when expressed in heterologous expression systems. This family is relatively insensitive to TEA and other K^+ channel blockers, and sensitive to the known blockers of stretch-sensitive ion channels, such as amiloride and Gd^{3+}. At the single channel level, TREK and TRAAK channels are highly flickering (see Fig. 9B and C), and their cord conductances in symmetric 150 mmol/L KCl are 100 and 45pS, respectively. Single-channel recordings from TRAAK show spike-like openings due to an extremely short mean open time (see Fig. 9B and C) and can be easily distinguished from TREK-1 and TREK-2, in symmetric K^+, by their linear current-voltage relationship (147, 187, 260, 305). In spite of the fact that TREK and TRAAK are both activated by membrane stretch, changes in pH have a differential effect. Particularly, TREK channels are activated by intracellular acidosis (Fig. 9D, top), converting TREK mechanogated into constitutively active channels. Lowering the intracellular pH shifts the pressure-activation relationship of TREK-1 toward positive values and ultimately leads to channel opening at atmospheric pressure. TRAAK, on the other hand, opens upon intracellular alkalosis (95, 147, 417). The channel sensor for stretch, acidosis, and temperature (at least in TREK-1) is on the C-terminus and the extracellular TM1-P1 loop (214, 345).

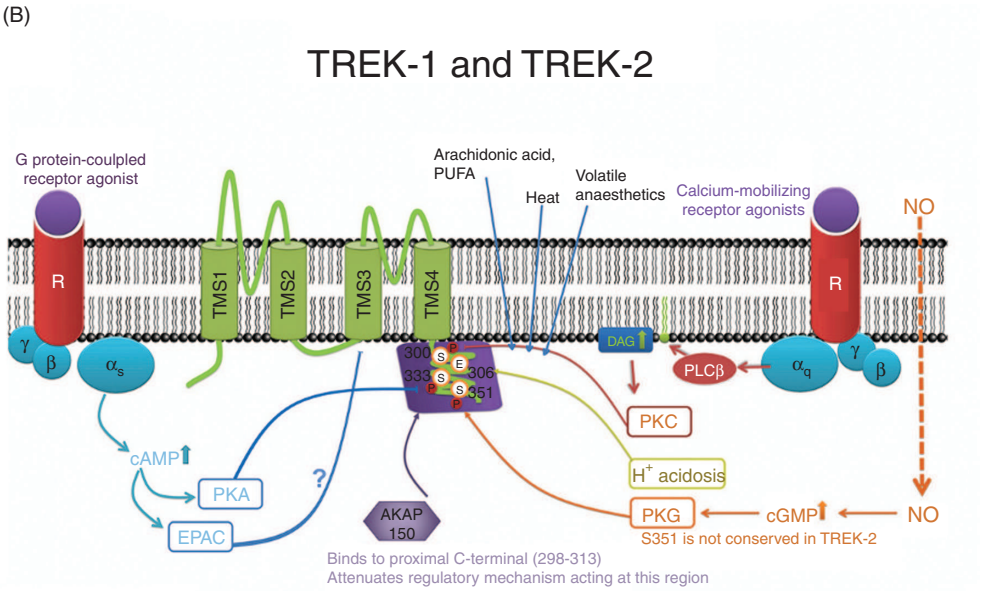
General TREK/TRAAK channels tissue distribution

TREK and TRAAK have been shown to be located in human peripheral organs and tissues of the central nervous system (CNS). However, they have different subcellular locations; for instance, TRAAK is mainly present in soma and, to a lesser degree, in axons and dendrites, whereas TREK-1 is concentrated in dendrites in almost all neuronal types expressing this channel [(197, 305, 362, 534); for review, see Talley et al. (533)]. The widespread distribution of TREK-1 in CNS might suggest that this channel participates in a number of potential physiological roles. For instance, TREK-1 is located throughout the brain and spinal cord but with specific areas appearing to be particularly enriched in TREK-1 protein, such as the

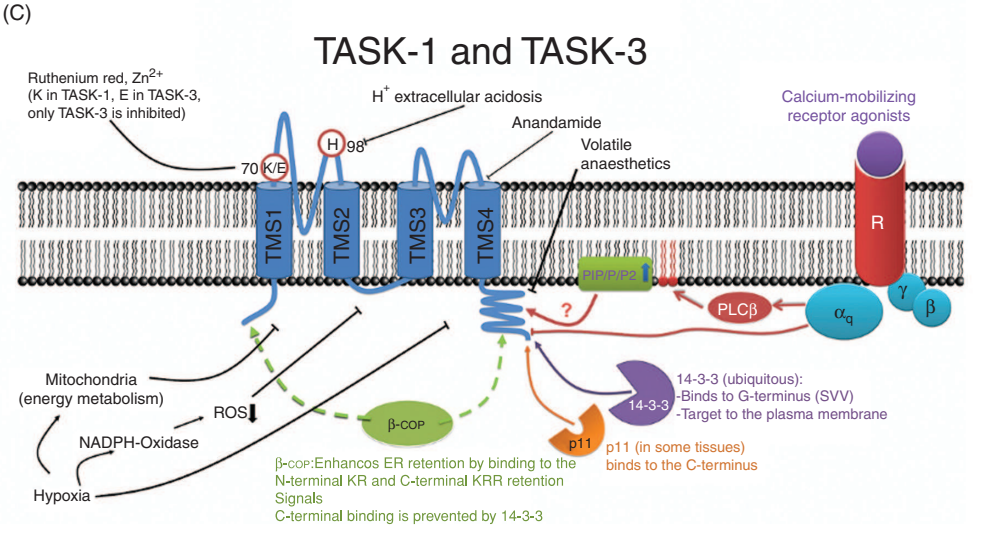
(A)


Anaesthetics
lipids
Heat
Stretch
Voltage
S
P
E
NH2
cytoskeleton
Internal pH
cAMP/PHA
DG/PKC

(B)


TREK-1 and TREK-2
G protein-coulpled
receptor agonist
Arachidonic acid,
PUFA
Heat
Volatile
anaesthetics
Calcium-mobilizing
receptor agonists
NO
R
TMS1
TMS2
TMS3
TMS4
γ
β
αs
αq
DAG
PLCβ
300
333
306
351
PKC
cAMP
PKA
EPAC
?
AKAP
150
H+ acidosis
PKG
cGMP
NO
S351 is not conserved in TREK-2
Binds to proximal C-terminal (298-313)
Attenuates regulatory mechanism acting at this region

(C)


TASK-1 and TASK-3
Ruthenium red, Zn2+
(K in TASK-1, E in TASK-3,
only TASK-3 is inhibited)
H+ extracellular acidosis
Anandamide
Volatile
anaesthetics
Calcium-mobilizing
receptor agonists
70 K/E
H 98
TMS1
TMS2
TMS3
TMS4
R
PIP/P/P2
PLCβ
αq
γ
β
?
Mitochondria
(energy metabolism)
ROS
NADPH-Oxidase
Hypoxia
β-COP
14-3-3
14-3-3 (ubiquitous):
-Binds to G-terminus (SVV)
-Target to the plasma membrane
p11
p11 (in some tissues)
binds to the C-terminus
β-COP:Enhancos ER retention by binding to the
N-terminal KR and C-terminal KRR retention
Signals
C-terminal binding is prevented by 14-3-3

cortex, hippocampal formation, thalamus, geniculate nuclei, hypothalamus, basal ganglia, periaqueductal gray, and the gray matter of the spinal cord. In addition, the fact that TREK-1 and TRAAK are expressed in cortex, hippocampus, and thalamic nuclei along with the presence of riluzole and polyunsaturated FAs (both known for their neuroprotective effects) is consistent with the idea that these channels may play a crucial role in the prevention of epileptic seizures (197). There are some inconsistencies in the literature regarding the location of some of the K_{2P} channel members. For instance, Talley et al. (534) found that the highest expression of TREK-1 is in the striatum, CA2 of the hippocampus, and layer IV of the neocortex. While Lazdunski laboratory (140) reported that TREK-1 levels in the striatum were unremarkable, and there was uniform labeling of hippocampal pyramidal neurons and in the various cortical laminas. TREK-2, was found to be primarily restricted to the cerebellum (534). In addition, the highest levels of TRAAK were localized in the cerebral cortex, and TWIK-1 is mainly present in the cerebellum and cortex.

Thermosensitivity

When expressed in heterologous systems, TREK-1 shows low activity at room temperature (253). Raising the temperature increases channel activity and a maximal response is observed in the 37 to 42°C range (Fig. 9C). This result suggests that TREK-1 is highly active at physiological temperature and contributes significantly to the background K^+ conductance in native conditions (95,253,343). Recently, Kang et al. (253) showed that not only TREK-1 is thermosensitive, but also TREK-2 and TRAAK (Fig. 9C), channels that, as TREK-1, have a high probability of opening at physiological temperatures. Therefore, TREK-1, TREK-2, and TRAAK contribute to the background K^+ conductance that helps to stabilize the resting membrane potential at physiological temperatures (253). Once it was established that the TREK/TRAAK subfamilies were tightly regulated by temperature, it became relevant to unveil the mechanism that promotes channel opening by temperature. Based on the observation that channel activity closely follows rapid changes in temperature, Kang et al. (253) ruled out the involvement of newly synthesized heat-inducible proteins. In addition, Maingret et al. (343) suggested that the temperature sensor could be a molecule closely associated with TREK-1, TREK-2, and TRAAK, but such a molecule has not been identified yet (253, 343). Deletion of 106 amino acids of the distal part of the C-terminus of TREK-1 generates a mutant that has a rather weak response to heat. Also, a chimeric channel in which the TREK-1 C-terminus was replaced with that of TASK-1 was found to be rather insensitive to heat (343). Thus, the C-terminus of TREK-1 plays an important role in providing the temperature sensitivity phenotype. It is noteworthy that, the mean open-time duration of TREK-1 was differentially affected by temperature in different cells. The reason of these differences is at present unknown but they can be due to the different membrane lipid composition of these cells (253). Since TREK-1 and TREK-2 are expressed along with several transient receptor potential (TRP) channels in the hypothalamus and dorsal root ganglion neurons, they might act in concert in the transduction of temperature and nociception. Kang et al. (253) have suggested that TREK channels could act as suppressors of the excitation elicited by the activation of TRP channels.

Anaesthetics

General anaesthetics are compounds that produce loss of consciousness and pain relief when breathed in through the lungs. Indeed, the first anaesthetics that were used in clinical practice were the inhalational agents diethyl ether and nitrous oxide. The most commonly used inhalational anaesthetics are halogenated ethers (isoflurane, sevoflurane, and desflurane) or halothene (147). Despite the over 150 years of use, there is little consensus on how general volatile anaesthetics act at the molecular level. Several targets have been proposed over the years but the relative nonselectivity and low potency of inhalational anaesthetics has made it difficult to identify which molecular targets are pharmacologically relevant. It has been suggested that anaesthetics might reduce neuronal excitability by opening K^+ channels, along with the already established role of certain ligand-gated ion channels (147). In 1999, Maingret et al. (345) established that TREK channels, unlike TRAAK, are reversibly opened by clinical concentrations of volatile anaesthetics such as chloroform, diethyl ether, halothane, and isoflurane (Fig. 9E) The opening of TREK

Figure 8 Polymodal nature of K_{2P} channels receptors. (A) TREK-1 channels are modulated by stretch, heat, intracellular acidosis, depolarization, lipids, general anaesthetics, and tonically inhibited by the actin cytoskeleton [adapted, with permission, from Patel and Honoré (417)]. (B) Polymodal regulation of TREK-1 and TREK-2. Activation of the Gs/cAMP/protein kinase A (PKA) and the Gq/phospholipase C (PLC)/Diacyl Glycerol (DAG)/protein kinase C (PKC) signaling pathway inhibit TREK channels by phosphorylating serine residues present on the C-terminal. TREK-1 is activated via the NO/cGMP/Protei kinase G (PKG) pathway, but the PKG phosphorylation consensus site is missing in TREK-2. (Arrows indicate stimulation; lines with T ending represent inhibition.) [Modified, with permission, from Enyedi and Czirják (128).] (C) Regulation of TASK-1 and TASK-3. The channels are inhibited by extracellular acidification (EC) acidification as a result of protonation of histidine98 in the second extracellular loop. Anandamide inhibits both TASK-1 and TASK-3. Hypoxia inhibits TASK current indirectly. TASK channels are activated by halothane and isoflurane but they are not influenced by chloroform or ether. The polycation ruthenium red and Zn^{2+} allow pharmacological distinction between the two closely related channel subunits. Dashed lines represent effects on targets; arrows indicate stimulation; lines with T ending represent inhibition. [Modified, with permission, from Enyedi and Czirják (128).]

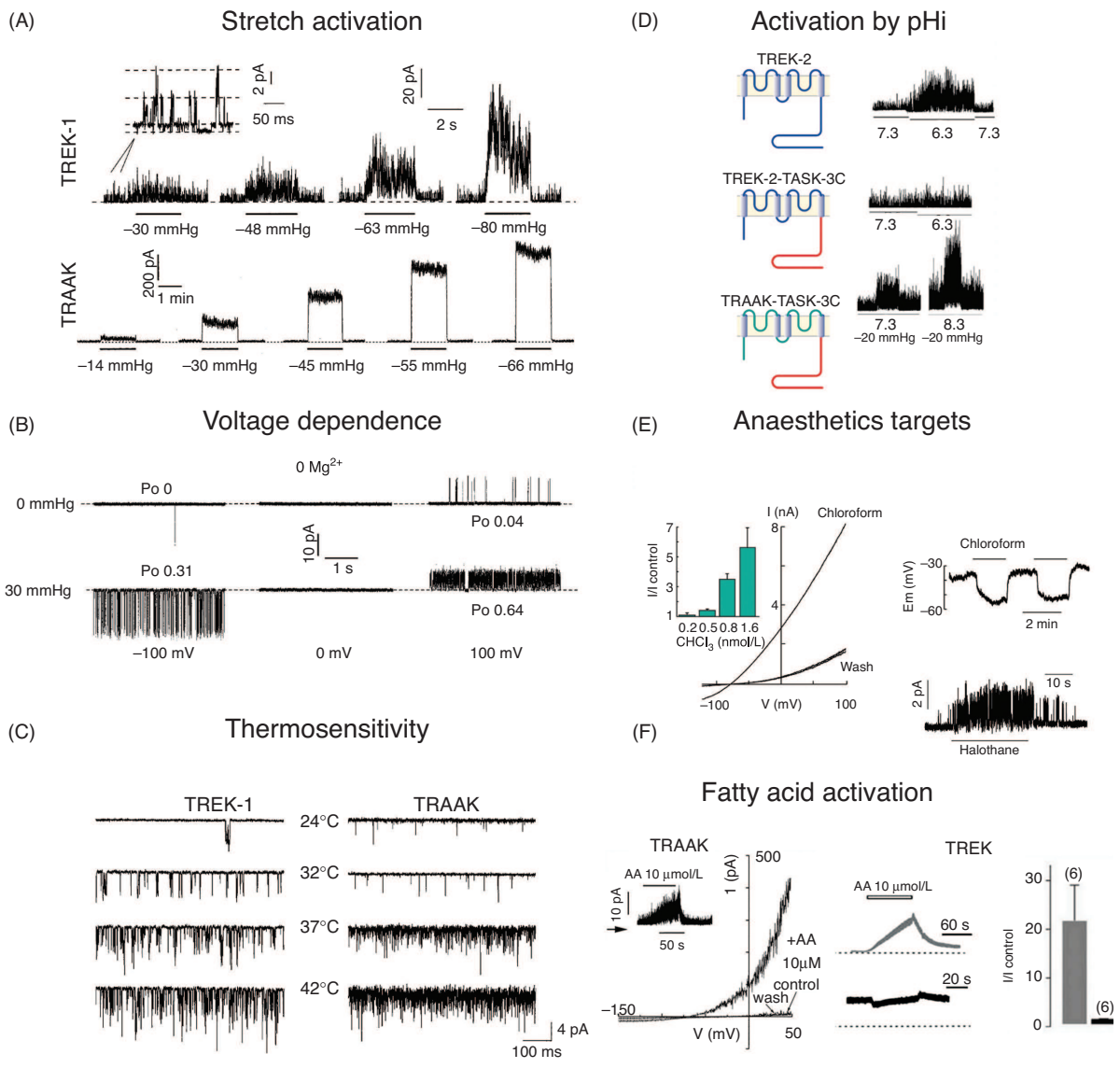


Figure 9 K2P channel activation by different stimuli. (A) Top: TREK-1 activation was graded with membrane stretch in a cell-attached patch from oocytes expressing TREK-1. The inset shows channel openings with an enlarged time scale. In this patch, a small conductance endogenous channel was also present. Bottom-graded reversible negative pressure activation of hTRAAK in physiological K^+ conditions. The patch was held at 0 mV and the zero current is indicated by a dashed line [from Patél et. al (418) and Lesage and Lazdunski (305)]. (B) TREK-1 channels show outward rectification. Single-channel currents recorded in absence of Mg^{2+} at −100 mV (left trace), 0 mV (middle trace), and 100 mV (right trace) at atmospheric pressure (top traces) and at a steady pressure of −30 mm Hg (bottom traces). Po denotes open probability [adapted, with permission, from Maingret et al. (342)]. (C) Thermosensitivity. Cell-attached patches from COS-7 cells incubated at different bath temperatures are shown for TREK-1 and TRAAK [adapted, with permission, from Kang et al. (253)]. (D) The C-terminus of TREK-2 is required for sensitivity to fatty acids and pH. (Top) Wild-type TREK-2 expressed in COS-7 cells is robustly activated by a decrease in intracellular pH. Middle. The pH sensitivity is abolished in a chimeric mutant that consists of the core transmembrane segments of TREK-2 and the C-terminus of TASK-3 (red) (chimera TREK-2–TASK-3C) indicating that C-terminus of TREK-2 is require to pH sensitivity. (Bottom) The sensitivity of a TRAAK–TASK-3C chimera to pH is similar to wild-type TRAAK, which indicates that the C-terminus of TRAAK is unlikely to mediate activation by pH [adapted, with permission, from Kim (260)]. (E) Left. TREK-1 is reversibly opened by chloroform (0.8 mmol/L). Voltage was linearly depolarized with a voltage ramp from −120 to 100 mV. Current becomes zero at a membrane potential equal to the equilibrium potential for K^+ (−80 mV). Inset: stimulation of the K^+ current by chloroform ($CHCl_3$) is concentration dependent and observed at pharmacologically relevant concentrations. Right top. Chloroform (0.8 mmol/L) induces reproducible membrane hyperpolarizations. Right bottom. Halothane (1 mmol/L; 0 mV) induces TREK-1 single-channel activity characterized by rapid flickering between closed and open states [modified, with permission, from Franks and Honore (147)]. (F) Fatty acid activation of TRAAK and TREK in COS cells. (Left side) Current-voltage relationships obtained in an inside-out patch with voltage ramps ranging from –150 to +50 mV, 500 ms in duration, before (control), after 3 min perfusion with 10 µmol/L AA and after the wash. Inset: effects of 10 µmol/L AA on TRAAK currents recorded in an inside-out patch clamped at +20 mV. The zero current level is indicated by an arrow. (Right side) Inside out patch currents were recorded at 0mV from transfected COS cells. The zero current levels are indicated by a dotted line. The histograms represent the ratio of the mean currents recorded before ($I_{control}$) or after 10 µmol/L of AA application (I), gray and black color denotes absence or coexpression of A-kinase anchoring protein (AKAP150), respectively [adapted, with permission, from Sandoz et al. (468) and Fink et al. (141)].

channels by these anaesthetics induces cell hyperpolarization (95, 147, 282, 417). The fact that the effect of volatile anaesthetics is independent of cell integrity in excised patches, and the lack of effect of volatile anaesthetics on TRAAK, indicates that an indirect membrane effect of volatile anaesthetics is unlikely (147). The use of TREK1 knockout mice has provided the most direct evidence for the role of TREK-1 in anesthesia. In these animals, the gene encoding TREK-1 was disrupted without interfering with brain mRNA expression of other members of the K_{2P} channel family or of the GABA receptor. These knockout mice did not display an abnormal phenotype; on the contrary both reflex and cognitive functions were not altered. However, under the presence of volatile agents such as chloroform, halothane, sevoflurane, and desflurane TREK-1 knockout mice showed a marked decrease in anesthetic sensitivity. In addition, to the longer time required to put TREK-$1^{-/-}$ mice under anesthesia, the concentrations required to reach loss of righting reflex and the failure to respond to a painful stimulus were significantly higher in knockout animals compared to wild type animals. It is also important to mention here that, there was no difference between knockout and wild-type animals following the administration of the barbiturate pentobarbital, which does not affect TREK-1, showing that the decrease in sensitivity to volatile anaesthetics of the knockout mice was unlikely to be due to a generalized increase in excitability (147).

Membrane stretch and lipid effect on the TREK-TRAAK subfamily

By inducing blebs without cytoskeletal elements, Zhang et al. (626), carefully established the role of membrane proteins as mechanotransducers studying mechanosensitive channels in the complex cell surface of *Xenopus* oocytes. Hyposmolarity promotes TREK/TRAAK channel opening and hyperosmolarity has the opposite effect, suggesting that these channels can be modulated by the cellular volume. These channels can be also activated by application of stretch or negative pressure to the cell membrane (Fig. 9A); the pressure to induce half-maximal activation is –36 mmHg for TREK-1 and –46mmHg for TRAAK (345). Similar to other eukaryotic mechanosensitive channels, disruption of the cytoskeleton by either biological (colchicine, cytochalasin) or mechanical agents (membrane excision) potentiates channel opening by membrane stretch. These results suggest that the mechanical force generated by osmotic changes and transmitted directly to the channel via the lipid bilayer is tonically repressed by the cytoskeleton. Moreover, agents that alter the cell shape by preferential insertion in one of the leaflets of the membrane modify the activity of these channels (147,253,305,417-419).

The TREK/TRAAK subfamilies are also stimulated by polyunsaturated fatty acids (PFAs; Fig. 9F), lysophospholipids containing large polar heads and by intracellular lysophosphatidic acid (LPA) either directly on the channel protein or via a membrane effect. The activation by arachidonic acid (AA) is reversible and concentration-dependent; moreover, channel activity does not decrease when the AA perfusion is supplemented with a mixture of inhibitors of the AA metabolism pathway. This supports the idea that the AA effect is direct and not due to another eicosanoid, either by interaction with the channel protein or as a consequence of partitioning into the lipid bilayer and indirectly affecting channel gating. This effect can be also induced by other unsaturated FAs, such as oleate, linoleate, arachidonate, eicosapentaenoate, and docosehexaenoate, but not by saturated FAs like palmitate, stearate, or arachidate. In the particular case of LPA, TRAAK channels can be reversibly activated by intracellular LPA at atmospheric pressure and shows the highest sensitivity to intracellular LPA, compared with TREK-1 and TREK-2. Intracellular LPA shifts the mechanosensitivity of TRAAK toward lower tension values, leading to channel opening at atmospheric pressure (95, 147, 260, 305, 417, 419).

Since PKA-mediated phosphorylation of Ser333 in the C-terminus promotes channel closing, this enzyme is able to reverse the effect of lipids on TREK-1. TREK-1 activity is also inhibited by the protein kinase C pathway, although the phosphorylation site remains to be identified (417).

Arachidonic acid

AA is a PFA with 20 carbons and four *cis* double bonds that make this molecule extremely flexible. This acid affects the behavior of biological systems in two ways: First, the liberation of this FA from the cell membrane, via receptor-mediated activation of phospholipases, leads to the generation of biologically active AA metabolites that could account for the activation of K^+ channels; and Second, AA and FAs themselves elicit a second class of direct responses and not through metabolic pathways (405). Even before K_{2P} channels were cloned and identified, Kim and Clapham (261) found two types of K^+ selective channels activated by intracellular AA in neonatal rat atrial cells. They reported that in inside-out patches AA along with other FAs opened outwardly rectifying K^+ selective channels. Also Ordway et al. (405) reported that both AA and certain other FAs, at concentrations similar to those required for both metabolic-mediated and direct effects of a FAs, directly activated specific K^+ channels in smooth muscle cells isolated from the *Bufo marinus* stomach. With these results they were able to suggest that channel activation may be mediated by a FA-induced alteration of the physical properties of the membrane. In spite of the fact that a clear link could not be established between leak K^+ channels and the ones that were reported in the previously mentioned studies, they had enough data to propose an explanation for the role of these K^+ selective channels in the increase of K^+ conductance observed in ischemic cells. Ischemia or hypoxia can reduce the duration of the action potential and thereby cause an early repolarization of cardiac cells. The opening of these channels would cause a rapid hyperpolarization of the cell and limit additional entry of Ca^{2+} via voltage-sensitive Ca^{2+} channels as wells as minimize energy consumption by conserving ATP. Furthermore, a decrease in intracellular pH together with

the opening of the K^+ channels by AA would contribute to the cell hyperpolarization, further protecting the cells from ischemic damage. Another possible role for FA-sensitive K^+ channels might be to monitor the level of free FA and protons in the cell, thus providing a protective mechanism by reducing cell excitability. When metabolic inhibition occurs due to pathological processes, such as ischemia and hypoxia, the intracellular pH decreases, the cytosolic concentrations of free FAs and Ca^{2+}increase, phospholipases are activated, and neurons swell. All these alterations will contribute to open TREK, at both presynaptic and postsynaptic sites and the resulting hyperpolarization will inhibit the activation of the presynaptic voltage-gated Ca^{2+} channels and limit glutamate release. At postsynaptic level, hyperpolarization will enhance the Mg^{2+} block of the N-methyl D-aspartate (NMDA) glutamate receptors at negative membrane potentials, reduce Ca^{2+} influx, and thus lower glutamate transmission and excitotoxicity. The opening of TREK-1 at the postsynaptic level will also tend to antagonize the depolarization induced by the activation of the ionotropic Alpha-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA)/kainate glutamate receptors. On the other hand, stimulation of the metabotropic glutamate receptors will close TREK-1 and reduce neuroprotection. Thus, it is possible to suggest that the opening of TREK-1 is consistent with the action of an antagonist of metabotropic glutamate receptors to produce maximal neuroprotection (147, 201, 260). On the other hand, the finding that TRAAK knockout mice do not have an increased sensitivity to either ischemia or epilepsy, in spite of the fact that polyunsaturated FAs and lysophospholipids open this channel, implies that TRAAK channels do not play a significant role in neuronal protection. In addition, this negative result further demonstrates that the increased vulnerability that was found in the TREK-1 knockout mice is specific, and not due to a general increase in excitability (147, 201).

A chimeric channel in which the entire C-terminus of TREK-2 was replaced with that of TASK-3 preserves mechanosensitivity, but is neither activated neither by free FAs nor by protons (Fig. 9D). This result not only indicates that activation of TREK-2 by free FAs is dependent on the C-terminus, but also that membrane stretch involves distinct molecular mechanisms, and rules out the idea that increased tension of the lipid membrane activates K^+ channels by releasing free FAs (264). In TREK-1, a glutamate residue in a region closed to the fourth TM segment acts as a proton sensor that also tunes mechano- and lipid sensitivity. Mutation of this glutamate to an alanine produces gain-of-function mutant channels, which are trapped in the active state (260).

Lysophosphatidic acid

LPA is a lipid-derived second messenger very abundant in cells and it exerts multiple biological effects. LPA elicits growth cone collapse, neurite retraction, cortical neurogenesis, and cell rounding in various neurons, thus mediating a role in axonal growth and path finding (71,148,602). Extracellular LPA evokes biological responses that are mediated through the activation of three G-protein-coupled receptors. Since TREK-1, TREK-2, and LPA are all present in the brain at high levels, it is hypothesized that these channels are involved in the response of the CNS to hemorrhagic brain injury given that under this type of brain damage the concentration of LPA in the cerebrospinal fluid is increased (94). Intracellular LPA is a potent regulator of the TREK/TRAAK K_{2P} channels, since it converts the voltage-sensitive K^+ channel TREK-1 into a leak conductance. Thus opening of these K_{2P} channels by intracellular LPA directly links the lipid status to cell electrogenesis. LPA preferentially activates TREK-1 only when applied intracellularly (344). LPA activation is dependent on the presence of the phosphate head group and the acyl chain; the lack of the phosphate at position 3 of the glycerol renders the lipid completely ineffective (94). Intracellular LPA activation neither involves the C-terminal domain of TREK-1 nor the N-terminus. Thus, AA, intracellular pH, and LPA open TREK-1 by different mechanisms. Interestingly, when the TM1-TM3 intracellular loop of TREK-1 is exchanged with the loop of TRESK1 (another K_{2P} channel that is not stimulated by intracellular LPA) the stimulatory effect of intracellular LPA is strongly reduced. However, it cannot be ruled out that this effect could be due to the effect that the substitution has *per se*, and the question about what region of TREK-1 senses intracellular LPA is still open. It is important to keep in mind that TREK-1, TREK-2, and TRAAK are mechanosensitive, so it is possible that LPA mechanism might involve a membrane effect. Such a mechanism was proposed for the control of synaptic vesicle formation by endophilin I in presynaptic neurons in (94). Endophilin is a membrane-associated protein required for endocytosis of synaptic vesicles, which is thought to induce a negative membrane curvature. This effect might be product of the conversion of the inverted cone-shape lipid LPA to the cone-shape lipid phosphatidic acid in the cytoplasmic leaflet of the bilayer, thus promoting vesicle formation. It seems that the shape of the lipids is important for TREK-1 activation, as intracellular phosphatidic acid weakly stimulates TREK-1 compared with LPA. Furthermore, intracellular phosphatidic acid reversibly inhibits TREK-1 channel activity after AA stimulation. Thus, it is possible that TREK-1 activation can rely on a membrane effect by intracellular LPA, but the existence of a possible LPA-binding site, and an interaction between the cytosolic domain and the TM segments cannot be entirely rule out at present (94).

Activation gate of K_{2P} channels

Kollewe et al. (273) developed a structural model of K_{2P} channel (KCNK0) based on the Kv 1.2 crystal structure and the identification of pairs of sites that display electrostatic compensation (Fig. 10A). The systematic addition of a charge in the pore loop 1 (P1) or P2 promoted the restoration of channel function. The model supports the hitherto widely held assumption that K_{2P} channels form functional dimers with each subunit contributing two P regions to the pore. Also, this

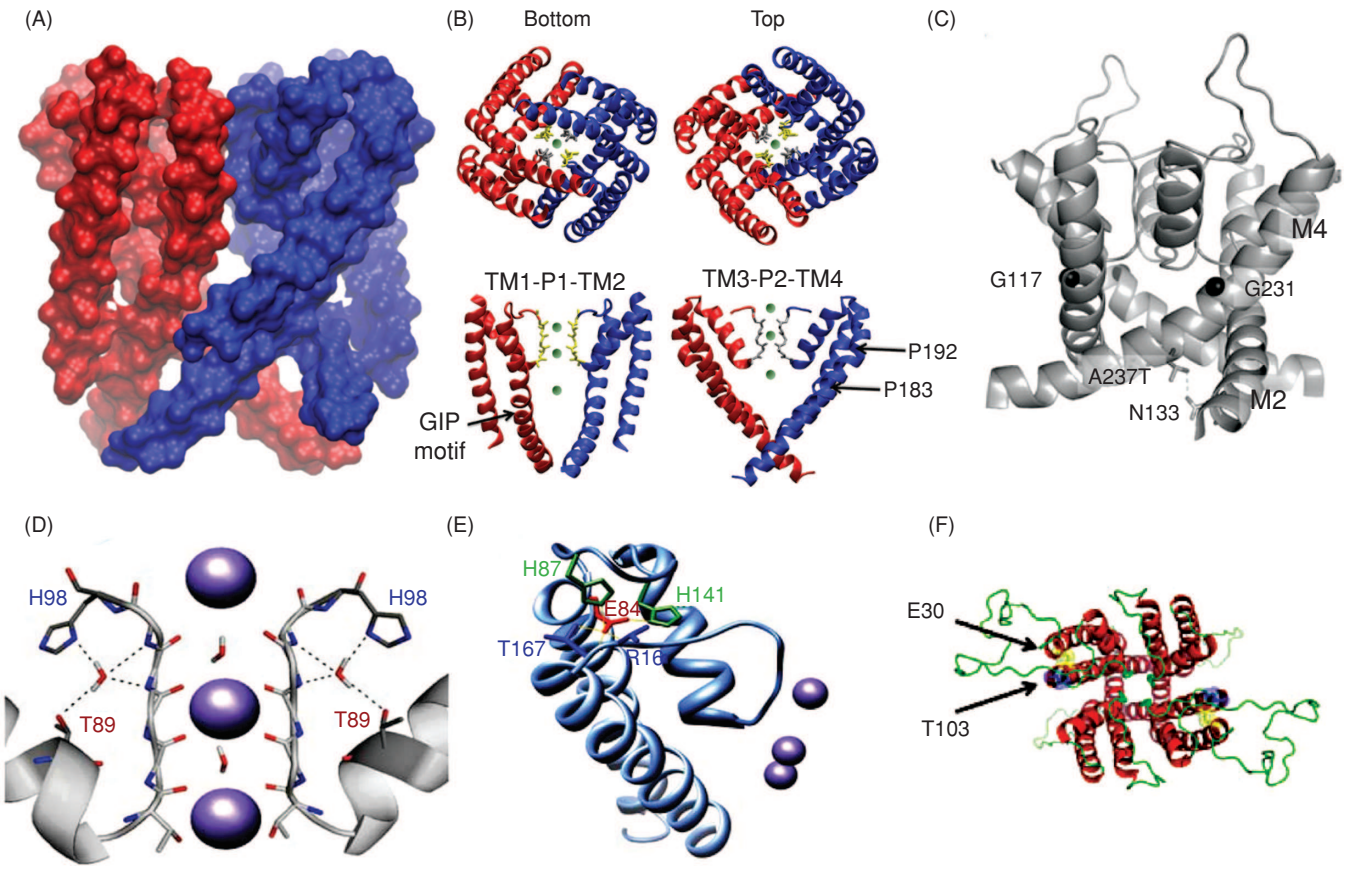


Figure 10 K_{2P} channel structure. (A) Homology model for ΔK2PØ (K2PØ channel variant lacking AA from 299 to 1000) channel shows bilateral symmetry with a 4-fold symmetric selectivity filter. Color red indicates monomer A (from residue 1 to 152) and color blue monomer B (from residue 174 to 276). (B) Extracellular (top) and cytoplasmic (bottom) sides reveals overall symmetry like a parallelogram. The model includes residues 1 to 276 without the TM1-P1 loop (residues 30-91), TM2-TM3 linker (residues 153-173), and TM2-P2 loop (residues 225-238). (Bottom) Side view of domain I of both subunits. The glutaminase interacting protein (GIP) motif (G129-I130-P131) in TM2 is indicated. Side view of domain II of both subunits. Proline residue 183 and 192 in TM3 are indicated. (C) Structure of a mutant TASK-3 channel modeled in an open state, using the structure of KvAP [adapted, with permission, from Jiang et al. (238)] as template. It is hypothesized that channels open through flexion of M2 and M4 around hinge glycines G117 and G231. The positions of these hinge glycines are indicated as spheres in the helices M2 and M4. Gain of function mutants stabilizes the open state through altered side chain-side chain interactions between residues. A possible H-bond between Thr in position 237 of M4 (in mutant A237T) and N133, which may contribute to stabilizing the open state, is indicated. The model gives a bond length of 3.2 Å. (D) K2P3.1 model, illustrating the interactions of a water molecule with the backbone of Tyr-96 and Gly-97 and the side chains of Thr-89 and His-98 in the unprotonated form of His-98, according to molecular dynamic simulations, based on Yuill et al. (608). (E) pH-sensing mechanism of human K2P2.1. Ribbon representation of one subunit of the bacterial KcsA potassium channel, based on the published structure [Doyle et al. (115)]. Predicted hydrogen bonds between KcsA residues are presented as orange lines. The side chain of Glu-51 is predicted to form hydrogen bonds with the backbone amide groups of Val-84 and Thr-85 and the side chain hydroxyl group of Thr-85. The homologous K2P2.1 residues are Glu-84 (red), Arg-166, and Thr-167 (blue), respectively. KcsA Ala-54 and Leu-59 were replaced in this presentation by histidines, as present at the homologous positions in K2P2.1 [i.e., His-87 and His-141 (green), respectively] based on Cohen et al. (82). (F) Homology model of the TASK-3 K2P channel. Illustrating the proximity of the two E30 (yellow) and two T103 (blue) residues (view looking from the top down). The model was created using Modeller 9v7 (465) based on the KcsA structure as template [originally solved by Doyle et al. (115)].

model showed the glycine hinge residues present in almost all K^+ and implicated in channel opening (237). This glycine residue is present in the M2 regions of K_{2P} channels within the glutaminase interacting protein (GIP) motif (glycine 129-isoleucine 130-proline 131) but not in the M4 regions (273). While K_{2P} channels are 4-fold symmetrical in the selectivity filter region, below this region they are only bilaterally symmetrical reflecting the low amino acid identity between M2 and M4 (Fig. 10B).

K_{2P} channels have a lower activation gate (glycine residues) and an upper slow inactivation gate (33,83). In contrast with Kv channels where these two gates are negatively coupled, lower and upper gates in K_{2P} channels are positively coupled, with the opening of the lower activation gate signaling the opening of the upper inactivation gate. However, for full-length mammalian K_{2P}s the resting Po is relatively low and mutations in residues close to the activation gate (A237T) can increase the open probability several folds. It has been suggested that the introduced threonine in M4 stabilizes the open state of the channel through altered side chain interaction between amino acid residues in M2. Channel activity may either increase or decrease through the action of regulators that influence this gate. Anesthetic activation, methanandamide inhibition and GPCR-mediated inhibition of TASK-1

and TASK-3 suggest that this introduced threonine residue in M4 stabilizes the open state of the channel through altered side-chain interactions between residues, possibly with N133 in M2 (see Fig. 10C). The results suggest that the alanine residue stabilizes the closed state of the channel through an interaction with residue L128 in M2 (20).

Voltage-dependent gating

TREK-1 is voltage-gated when S348 is phosphorylated by PKA or substituted with an aspartate to mimic phosphorylation. On the other hand, when TREK-1 is dephosphorylated by intracellular alkaline phosphatase or an alanine mutation (mimicking dephosphorylation), it behaves as a voltage-independent leak K^+ channel. It is possible that voltage- and mechanogating might be functionally linked because progressive deletion of the C-terminal region and chimera mutants that affect voltage-dependency, also dramatically impair mechanogating, and the pressure-response curve is affected (toward more negative pressure values) (52,342). It has been previously described that cell depolarization changes the membrane curvature and induces membrane tension, and this tension is enough to activate mechanosensitive ion channels (154,623). Thus, the existence of this phenomenon led Maingret et al. (342) to suggest that depolarization might be able to stimulate TREK-1 opening through an alteration in membrane curvature and tension. Since there are several clusters of charges in the C-terminal domain, it is possible that this domain may act as a voltage sensor, independently of the mechanogating mechanism, However, to be able to sense the TM voltage the C-terminus has to be deeply inserted into either the lipid bilayer or into the ionic pore (342).

Inactivation gate of K_{2P} channels

In KcsA channels hydrogen bonds between residues in the selectivity filter and its adjacent pore helix determine the degree of C-type inactivation process (84,85,92). This type of gating mechanism appears to be also present in K_{2P} channels. For example, in TASK-1 and TASK-3, primarily by binding to a histidine (H98) next to the selectivity filter, protons inhibit the K^+ currents (Fig. 10D) (263, 322, 439). In TASK-1, the residues in the outer pore mouth contribute to ion selectivity and the protonation of H98 initiates a C-type gating response that involves a conformational change in the selectivity filter of TASK-1 (see also reference 391).

Finally, a conserve glutamate residue (E28), located at the end of the first TM domain of the channel at the extracellular side of the membrane, has been shown to be important for gating in KCNK0 channel (631) and the equivalent residue (E418) in *Shaker* is a molecular determinant for C-type inactivation (294). The homologous residue in TASK-3 channels is E30 while in TREK-1 channels it is E84 (Fig. 10E). E28 stabilizes the open configuration of the channel by forming a hydrogen bond with amino acid residues in the pore region of the channel. For TASK-3 channels, mutation of the equivalent amino acid residue E30 to cysteine also reduces the current amplitude (see Fig. 10F).

The Structural Family of Voltage-Dependent (Kv) Channels

This family is composed by two structural and functional types of members: 36 genes of six TM K^+ channels (6TM) Kv: *KCNA* (Kv1 family), *KCNB* (Kv2), *KCNC* (Kv3), and *KCND* (Kv4), *KCNQ* (Kv7), *KCNH* (Kv10, Kv11, and Kv12, including ether-a-go-go-related gene (EAG) and human ether-a-go-go-related gene (ERG)], and the nonconducting group of gating modulator: *KCNF* (Kv5), *KCNG* (Kv6), *KCNV* (Kv8), and *KCNS* (Kv9). The phylogenetic tree for Kv channels depicted in Figure 11 shows the major classes of voltage-dependent K^+ channels.

To be fully functional, Kv channels require a minimal tetrameric organization, with the ion conduction pore lying in the axis of a 4-fold symmetric structure (115, 194, 337). The primary sequence of these hydrophobic segments shows similarities between all Kv α-subunits, including a voltage-sensing domain (VSD) formed by TM segments S1 to S4 (or S0-S4 in the Slo family) and the pore domain comprising S5 to S6 (Fig. 12).

Several crystal structures of two Kv channel α-subunits have been uncovered in Rod Mackinnon's lab: the structure of KvAP channel from *Aeropyrum pernix* (238), the Shaker relative Kv1.2 (316) and a more refined chimera of Kv1.2 with the "paddle" segment of Kv2.1 (318) (Fig. 12).

All they show a pore domain with structural features conserved with other channel of the 2TM design as the bacterial KcsA, or MthK channels or the Kir channels (115, 236, 394, 395).

Physiological function

The vertebrate α-subunit of voltage-gated K^+ delayed rectifier family (Kv channels) is composed of twelve members (K_v1–K_v12) according to amino acid sequence similarity (Fig. 11). $K_v1.1$ is the vertebrate homolog of the fruit fly *Drosophila Shaker*. In flies lacking the fast transient Shaker K^+ current in presynaptic terminals, the release of neurotransmitter is increased due to longer lasting action potential compared to the wild-type *Drosophila*.

To make a comprehensive description of Kv channel physiology based solely on their family diversity is impractical because the large variety of potassium channels type that arises from several factors (see later), makes a moderately complete description of Kv channels functional repertoire an encyclopedic task by itself. Thus, this revision must necessary be taken as a "primer" on the subject.

In general terms, potassium currents can be classified into showing A-type (inactivating) or delayed rectifier behavior (noninactivating). However, at the molecular level, functional diversity in different cells types stems from the expression

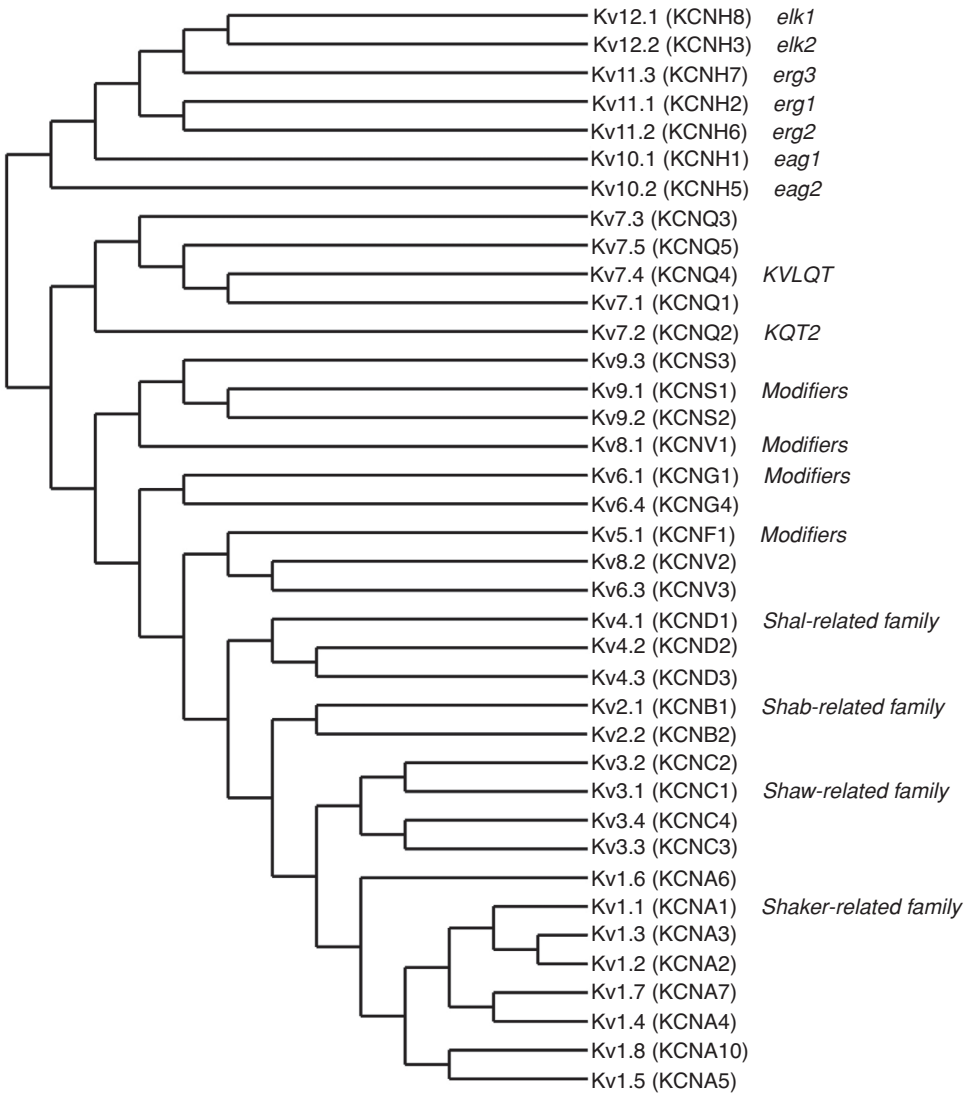


Figure 11 Organization of the voltage-dependent K^+ channel superfamily. Phylogenetic tree for the Kv1-12 families. Amino acid sequence alignments of the human channel Kv proteins were created using CLUSTALW. Only the hydrophobic cores (S1-S6) were used for analysis. The IUPHAR and HGNC names are shown together with the genes' chromosomal localization and other commonly used name. The alignment was made using the web tool: Phylogeny.fr (109), with different sequences of human two pore K^+ channels obtained from gene bank accession numbers: KCNH1: NM_002238.3, KCNH2: NP_000229.1., KCNH3:NP_036416.1., KCNH5: NP_647479.2., KCNH6: NP_110406.1., KCNH7: NP_150375.2., KCNH8: NP_653234.2., KCNQ1: NP_000209.2., KCNQ2: NP_004509.2., KCNQ3: NP_004510.1., KCNQ4: NP_004691.2., KCNQ5: NP_062816.2., KCNS1: NP_002242.2., KCNS2: NP_065748.1., KCNS3: NP_002243.3., KCNV1: NP_055194.1., KNCG1: NP_002228.2., KCNG4: NP_758857.1., KCNF1: NP_002227.2., KCNV2: NP_598004.1., KCNG3: NP_579875.1., KCND1: NP_004970.3., KCND2: NP_036413.1., KCND3: NP_004971.2., KCNB1: NP_004966.1., KCNB2: NP_004761.2., KCNC1: NP_004967.1., KCNC2: NP_631874.1., KCNC3: NP_004968.2., KCNC4: NP_004969.2., KCNA1: NP_000208.2., KCNA2: NP_004965.1., KCNA3: NP_002223.3., KCNA4: NP_002224.1., KCNA5: NP_002225.2., KCNA6: NP_002226.1., KCNA7: NP_114092.2., KCNA10: NP_005540.1.

of a subset of the approximately 35 genes of K_v channels. The multiplicity of Kv channels is further increased through: (i) heteromultimerization in which different gene products of the same family, as is the case of the Kv1, Kv7, and Kv10 families, form heterotetramers with novel functional properties not seen in the parental channels. (ii) Heteromultimerization with silent subunit families. For example, Kv2 family-form heterotetramers with novel properties with Kv5, Kv6, and Kv8, subunits that do no form functional channels as homotetramers (181). (iii) Multimerization of Kvα tetramers with accessory β-subunits. For example, Kv1.1, Kv1.2, Kv1.3, and Kv1.5 are delayed rectifiers but when expressed with Kvβ1.1, become rapidly inactivating as the Shaker channel in *Drosophila* (195, 446) (Fig. 13). Together with Kvβ1 and Kvβ2, other auxiliary subunits modify function of Kv channels: (a) KCHIP1 by interacting with the N-terminal

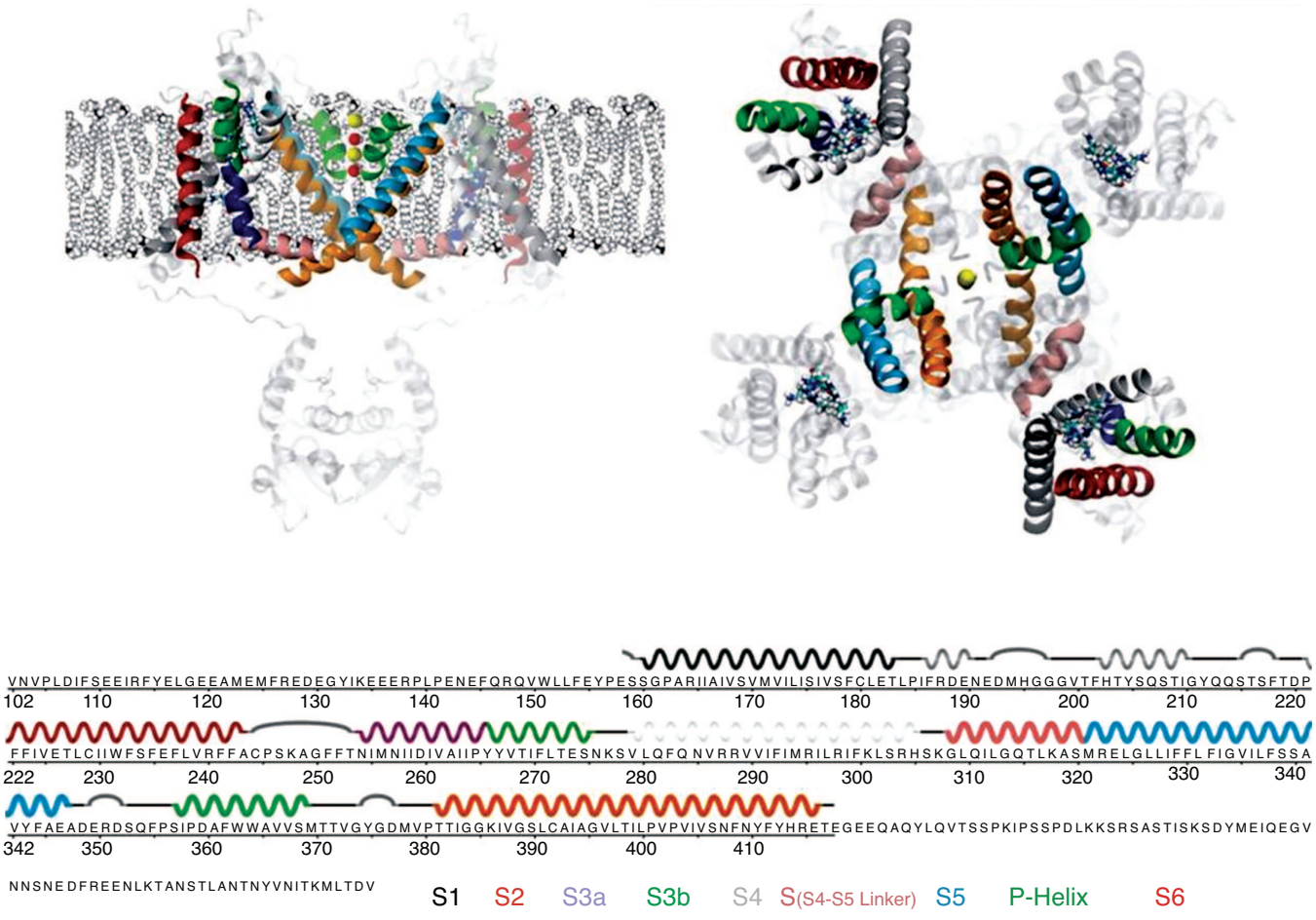


Figure 12 Organization and structure of the Kv1.2/Kv2.1 chimeric channel (PDB_ID: 2RAR). Lateral (left) and top (right) views of the protein embedded in the membrane. Arginine residues important for voltage dependence are shown in sticks. For clarity, two monomers are shown in light gray. The secondary structure of the amino acid sequence (below) is color coded to match the respective transmembrane and functional segments of the protein. Potassium ions are represented in green and the oxygen of water molecules in red. The cytosolic structure hanging from the main protein body is the tratramerization domain, T.

domain of Kv4.x channels modulates this class of ion channels surface expression and gating; (b) Ca^{2+}/calmodulin inhibits Kv10; and (c) minK greatly modifies the gating kinetics of Kv11 (181,567). (iv) Alternative splicing: Several families Kv3, Kv4, Kv6, Kv7, Kv9 Kv10, and Kv11 can be subject to alternative splicing (181). (v) mRNA editing by hydrolytic deamination of adenosine to inosine by adenosine to deaminase acting on RNA (609). mRNA editing of Kv1.1 channels changes the kinetics of Kvβ1-induced inactivation (45). (vi) Posttranslational modifications as phosphorylation, palmitoylation, ubiquitinylation, etc.

A-type currents

After a sustained positive going voltage pulse, A-type potassium channels activate and then inactivate, producing a

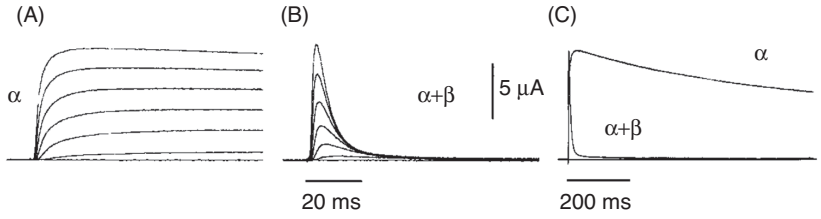


Figure 13 Kvβ1 inactivate currents of a Kv1 channel. (A) Delayed rectifier currents elicited by voltage steps in the absence of Kvβ-subunit. (B) Coexpression with Kvβ (α+β). (C) A single-voltage pulse shown in a large time scale. More details in reference 446.

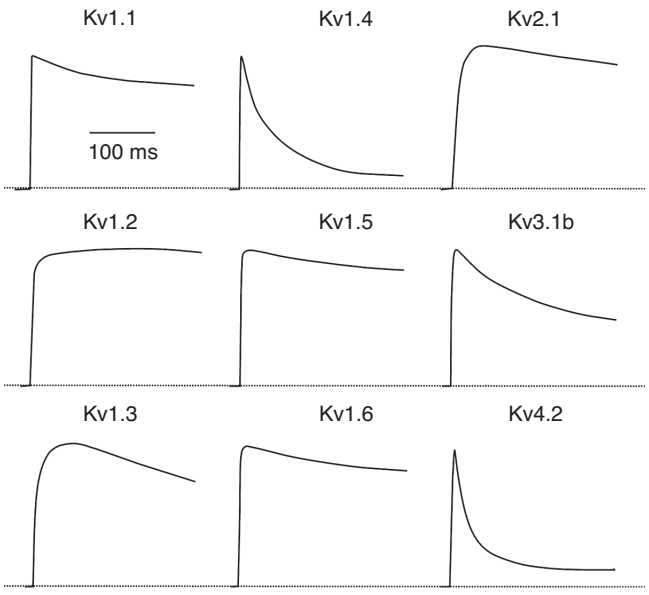


Figure 14 K^+ currents diversity in Kv channels family. The indicated rat Kv channels were transiently expressed in HEK 293 cells. For each channel, whole-cell K^+ currents at +40 mV were measured in similar physiological conditions. Modified, with permission, from reference 62.

transient response. Fast inactivation may play a role in setting the action potential interval because the Kv-dependent repolarization phase gets shorter if Kv channels inactivate and the neuron (or any excitable cell) is ready to fire a new action potential. Typical inactivating channels are Kv1.4, Kv3.3, and Kv3.4 and Kv4.1, Kv4.2, and Kv4.3 (Fig. 14). A complex formed by Kv4.2, Kv4.3, and KChIP2 may underlie the fast transient outward current (Ito fast) in cardiac muscle, while Kv1.4 may underlie a slower transient outward current (Ito slow) (180, 420). Kv 4.2 also encodes A-type K^+ currents in dendrites of CA1 pyramidal neurons where they antagonize the back propagation of centrally generated action potentials, impeding the development of Long Term Potentiation (LTP) (100). On the other hand, Kv3.3 appears to block either excitability or Ca^{2+} signal propagation in cerebellum Purkinje cells (611) and mutations in Kv3.3 cause spinocerebellar ataxia in humans (SCA13) (138).

Kv1 channels are the *Shaker* counterparts of *Drosophila,* of which Kv1.4 α-subunit is the only member containing a N-type inactivation domain as *Shaker*. Kv1.4 can coassemble with other Kv1.x subunits to form Kv1-only heterotetramers. Kv1.4/Kv1.2 heteromultimers may underlie the presynaptic A-type K-current. Kv1.4 associate with accessory subunits such as Kvβ-subunits, and with PSD96, SAP97, KChaP among others. CaMKII/calcineurin regulation through phosphorylation/dephosphorylation induces a $Ca^{2+'}$-dependent inactivation. Kv1.4 homotetramers are sensitive to micromolar 4-AP, riluzole, quinidine, and nanomolar UK78282 and nicardipine. Kv1.4 expresses in brain (mainly olfactory bulb, corpus striatum), lung-carcinoid, skeletal muscle, heart, and pancreatic islet. Kv1.4 expression increases in ventricular myocytes after myocardial infarction and induction of diabetes (181).

Kv4 channels are *Shal* counterparts of *Drosophila*. This family is composed of three members, Kv4.1, Kv4.2, and Kv4.3 being able to form Kv4 heterotetramers. In humans all three genes contains six exons, and splice variants could modify their activity (181). They associate with other proteins as Kvβ-subunits that assist them in the plasma membrane expression and enhance inactivation, while KChiPs enhances channel expression and delays inactivation. Kv4.1 and Kv4.2 are responsible for the somatodendritic A-type currents. For example, in different neuron types KV4 channels prolong the latency to the first spike in a train of action, potentials, slow repetitive spike firing, shorten action potentials, and attenuate back propagating action potentials (86). KChiP1 increases KV4.1 current densities, accelerates inactivation time course and recovery from inactivation, and shifts steady-state inactivation to more depolarized potentials (181). Coexpression of KChIP1 with Kv4.2 results in increased current densities, slowed onset of inactivation, and accelerated recovery from inactivation (448).

Classical delayed rectifier

This name was used by Hodgkin and Huxley (HH) to describe the giant squid axon mostly outward K^+-current that activated later than the Na^+ currents (208). This current does not show inactivation in the millisecond time scale. According to this classical view, these channels not only terminate the action potential, restoring the dominant potassium permeability of the resting membrane but they also shape it. Several members of the voltage gated K^+ channels underlie noninactivating currents. Most of the following description and references can be found well organized in the Gutman et al. compendium (181).

Unlike their *D*. Shaker counterpart, in the absence of β-subunits most members of the Kv1 channel family are not inactivating and only Kv1.4 inactivates with fast kinetics (195) (see Fig 14). Kv1 can coassemble with other Kv1 subunits only because they share the same T1 tetramerization domain (279, 308). They associate with the β-subunits, Kvβ1, Kvβ2, or Kvβ3, that confer inactivation to noninactivating subunits and play a role in channel membrane recruitment. Also, most Kv1.x channels associate to synaptic protein as PSD95, SAP97, or Dlg. Kv1.5 can also associate to *Src* tyrosine kinase.

A detailed pharmacological study comparing several delayed rectifiers including Kv1.1, Kv1.2, Kv1.3, and Kv1.5, found that all have submillimolar sensitivity to 4-AP and flacainide; tens of micromolar sensitivity to capsaicin, nifedipine, ditiazem, and resiniferatoxin (171). They have different sensitivity to external TEA, with EC50 ranging from 0.3 to 560 mmol/L in Kv1.1 and Kv1.2, respectively. Both, Kv1.1 and Kv1.2 have low nanomolar sensitivity to dendrotoxin (DTX). Kv1.2 and Kv1.3 have low nanomolar sensitivity to charybdotoxin (CTX) and noxiustoxin (NTX). Kv1.1 and

Kv1.3 have nanomolar and picomolar affinity to kaliotoxin (KTX), respectively. Also, Kv1.1, Kv1.3, and Kv1.6 have picomolar sensitivity to the sea anemone toxin, ShK (93, 249).

In rats, Kv1.1 expresses in brain, heart, retina, skeletal muscle (31, 552), and their malfunction is associated to episodic ataxia type 1 with myokymia (104). Kv1.2 is expressed in brain (mostly in pons, medulla, cerebellum, and inferior colliculus), spinal cord, Schwann cells, atrium, ventricle, islet, retina, and smooth muscle where participate in contractile tone regulation. Kv1.3 is expressed in brain (mostly in inferior colliculus, olfactory bulb, and pons), lungs, islets, thymus, spleen, lymph nodes, fibroblasts, B and T lymphocytes, pre-B cells, tonsils, macrophages, microglia, oligodendrocytes, osteoclasts, platelets, and testis. Because it could be a therapeutic target for immunosuppressant, its role in T-cell activation has been intensely studied. Kv1.3 inhibitors inhibit calcium signaling, cytokine production, and proliferation of T-cells *in vitro*, and T-cell-motility *in vivo* (444). Kv1.5 is expressed in aorta, colon, kidney, stomach, smooth muscle, whole embryo, hippocampus, and cortex (oligodendrocytes, microglia, and Schwann cells), pituitary, and pulmonary artery. Kv1.5 has properties similar to the ultra rapidly activating IK_{ur} current in the heart. It has potential use in management of AF via blockade of IK_{ur}. Information on Kv1.6, Kv1.7, and Kv1.8 is sparser.

Kv2.x channels are the counterparts of *Shab* in *Drosophila*. This family is composed of Kv2.1, the mayor delayed rectifier present in CNS neurons (372), and Kv2.2 expressed abundantly in localized GABAergic neurons (196). Although, many tissues express both types of channels, and an approximately 90% identity in the N-terminus, there is very little evidence indicating heteromultimerization among them. Expression of these two types of channel appears to be spatially segregated within cells (381, 550) and Kv2.1/Kv2.2 coexpression apparently does not form functional heterotetramers (346). Recently, Kv2.1/Kv2.2 multimerization has been described in neurons expressing an approximately 100-residue longer form of Kv2.2 (259). However, Kv2.1 form heterotetramers with Kv5, Kv6, Kv8, and Kv9 subunits, showing a very complex landscape of functional diversity (181). Kv2.1 function can be modulated by phosphorylation (372) and inhibited by hanatoxin binding to its voltage sensor apparatus (525). Some chronic pulmonary hypertension decreases the expression of Kv2 (181).

Kv3.x channels are the counterparts of the *Drosophila* Shaw channel While Kv3.3 and Kv3.4 produce A-type of currents, Kv3.1 and Kv3.2 are delayed rectifiers expressed prominently in the brain. Kv3 subunits form Kv3 heterotetramers. Because their fast activation and deactivation kinetics, Kv3 delayed rectifier channels are found in some neurons that are specialized to fire very short action potentials at high rates, such as those of the auditory system. They are found in cerebellum (in fast spiking neurons), skeletal muscle, arterial smooth muscle, and germ cells. They are blocked by micromolar 4AP and TEA and, in particular, Kv3.2 channels are block by verapamil and the toxin from the sea anemone *Stichodactyla helianthus* (ShK). Kv3.2 knockout mice are susceptible to epileptic seizures (181).

The Kv7 channels are also known as the KCNQ subfamily in humans. The *KCNQ1* (Kv7.1) gene was the first member of the KCNQ subfamily to be isolated. Mutations in this gene give rise to the most common form of long QT syndrome, LQT1. Kv7.1 in association with KCNE3 [minK-related peptide 2 (MiRP2)] and minK (KCNE1), a single TM domain β-subunit, are the major determinants of the cardiac I_{Ks} current, which is involved in the repolarization of ventricular action potential (24, 470). KCNQ1 mRNA is abundant in the heart, but also is found in the pancreas, kidney, lung, placenta, and ear.

Kv 7.2 (KCNQ2) and Kv7.3 (KCNQ3) have overlapping tissue distribution. Antibodies directed against Kv7.2 are able to coimmunoprecipitate Kv7.3, and vice versa. The heteromeric channel Kv7.2/Kv7.3 determine subthreshold excitability and corresponds to the M-channel found in neurons. They are sensitive to external pH (Fig. 15A and B) and are widely distributed throughout the brain, sympathetic and dorsal root ganglia (DRG), and expressed at high levels in hippocampus, chordate nucleus, and amygdala. Mutations in the *KCNQ2*/*KCNQ3* genes give rise to an idiopathic form of epilepsy (181)

KCNQ4 (Kv7.4) is expressed in outer hair cells (OHCs) and neurons of the auditory system and VSM. Kv5, Kv6, Kv8, and Kv9 channels are not functional alone; they coassemble with Kv2 subunits and modify their function.

The Eag family

The *Eag* channel family derives its name from a *Drosophila* behavioral mutant, ether-à-go-go, having enhanced neurotransmitter release at the neuromuscular junction. Known as the *KCNH* gene family in humans, it consists of three closely related subfamilies of genes defined by sequence homology, Kv10 (truly *Eag*), Kv11 (*Erg*), and Kv12 (127), where *Erg* stands for *ether-à-go-go related gene*, and *Elk* for *ether-à-gogo-like K-channel*. They all produce slowly activating currents (Fig. 15C).

The Kv10 family has two members, Kv10.1 and Kv10.2 having a restricted distribution. Kv10.1 has been found almost exclusively in brain, slightly in placenta and transiently in myoblasts, and in several tumor cell types, while Kv10.2 has been found in the CNS only (181). Kv10.1 has a potential as tumor marker and in cancer therapy (413).

Kv11 family is composed of three members, Kv11.1, Kv11.2, and Kv11.3, all capable to form Kv11 heteromultimers. Kv11.1 channels are ubiquitous; transcripts have been found in heart, brain, kidney, liver, testis, uterus, and prostate. The C-type inactivation of the ionic currents of the human counterpart, human ether-a-go-go-related gene (HERG) is orders of magnitude faster than the time course of activation (Fig. 15C). These properties are evidenced in characteristic outward going tails upon return to negative voltages. HERG underlies the cardiac Kir current known as I_{Kr} and is

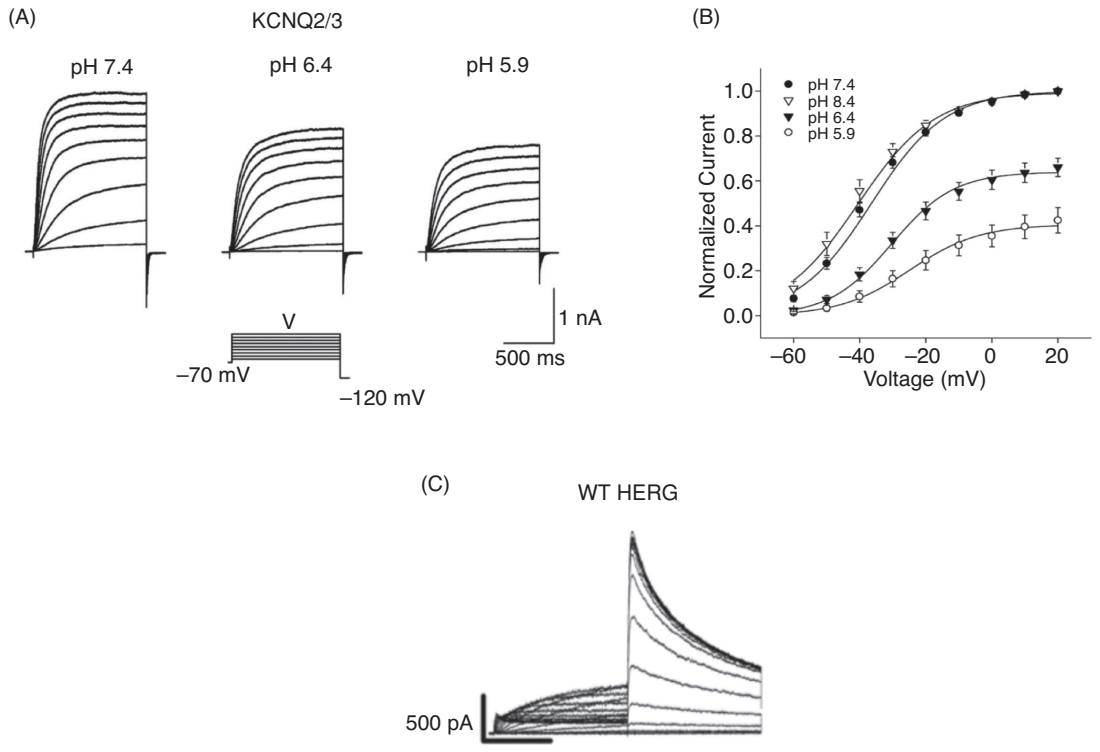


Figure 15 K currents from Kv7 and EAG families. Modulation of heteromeric KCNQ2/3 current by extracellular H^+ ions. (A) Whole-cell KCNQ2/3 currents from a HEK-293 cell in bathing solutions of differing pH were elicited by depolarizing voltage steps (1.5 s duration) from a holding potential of −70 mV. (B) Whole-cell KCNQ2/3 current activation curves in bathing solutions of different pHs (437). (C) Isochronal activation of human ether-a-go-go-related gene (HERG) channels. Membrane potential was stepped from −80 mV to a test potential between −70 and 100 mV, in intervals of 10 mV, for 2 s, followed by step to −50 mV. The HERG characteristic rapid rise in the tails of current account for a very fast recovery from inactivation and a slower inactivation (378).

responsible for ending the plateau phase of the cardiac action potential (471). Nonfunctional mutations or deletion produce type 2 long QT syndrome (LQT2) not linked to deafness. Patients are prompt to fibrillation and sudden cardiac death (181). Kv11.1 homotetramer are blocked by nanomolar concentrations of astemizole, ergtoxin, sertindole, dofetilide, cisapride, pimozide, terfenadine, halofantrine, and micromolar concentrations of CT haloperidol, imipramine, cocaine, and ketoconazole. Kv11.2 can be found in brain, uterus, and in some tumor cells as neuroblastoma and leiomyosarcoma. Kv11.3 can be found in brain (CA pyramidal neurons, lactotrophs, and rat pituitary), pituitary derived GH3 cells, and sympathetic ganglia. Kv11.3 is blocked by nanomolar concentrations of sertindole and pimozide (181).

Recently, K_v11.1 activators have gained interest as potential therapeutic agents mainly as a potential treatment of certain types of cardiac arrhythmias (111, 292). Two of these compounds have markedly different modes of action. NS1643 has been shown to increase K_v11.1 currents primarily by rightward shifting the inactivation curve and by slowing the fast inactivation process (76, 189). In contrast, RPR260243 almost exclusively acts by slowing the deactivation process of the channels (254).

Kv12 family is composed of three members, Kv12.1, Kv12.2, and Kv12.3 that are able to form Kv12-only heterotetramers (634). They are expressed primarily in the nervous system and produce a slowly activating and deactivating current. They contain a light, oxygen, or voltage (LOV) flavin mononucleotide and cyclic nucleotide-binding domains. Kv12.1 is expressed in brain, sympathetic ganglia, testis, colon, and lung. Kv12.2 is expressed in brain, (eye, cortex, amygdala, hippocampus CA1 and CA3, and dentate gyrus) peripheral nervous system, and lymphocytes. Blockade by 1-(2-chloro-6-methylphenyl)-3-(1,2-diphenylethyl thiourea) (CX4) or genetic deletion of Kv12.2 reduce the firing threshold in hippocampal pyramidal neurons. Also, Kv12.2$^{-/-}$ mice show persistent neuronal hyperexcitability, spontaneous seizures, and increased sensitivity to convulsants (624). Little is known about Kv12.3 except that appear to be expressed in brain, esophagus, lung, and pituitary grand (181).

Kinetic models consistent with Kv gating

The Hodgkin and Huxley model

To explain voltage-dependent ion permeability, HH proposed that it arises "from the effect of the electric field on the

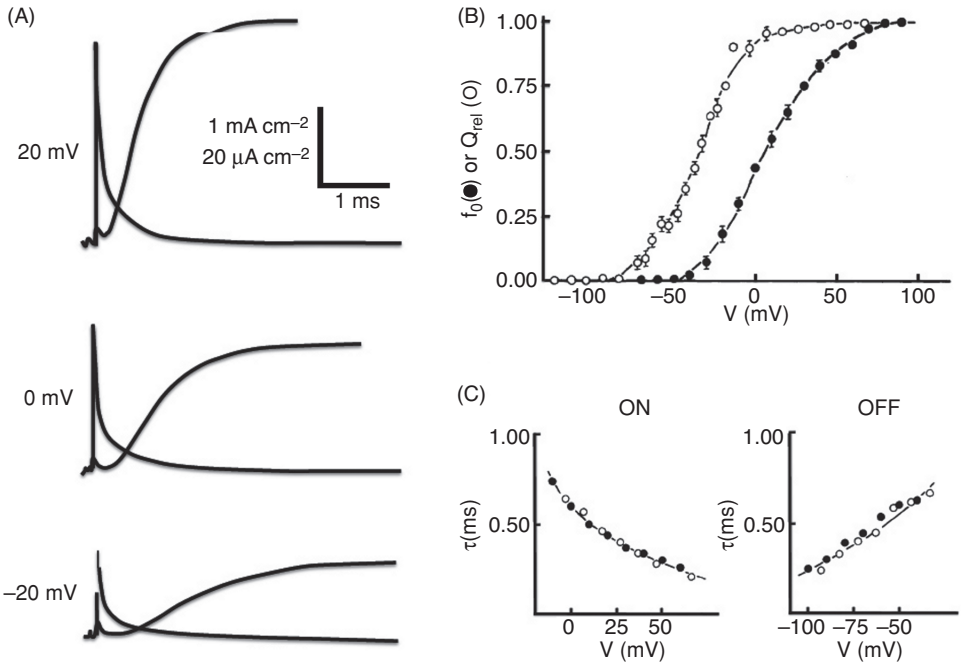


Figure 16 Gating currents elicited by the squid potassium channels. (A) Superimposed 10 ms traces of gating and ionic currents recorded at three different voltages taken a 20°C degrees. Na^+-gating currents are missed because at this temperature they are too fast for the recording system (modified, with permission, from reference 44). (B) Voltage dependency of the gating charge (open symbols) and the ionic conductance (filled symbols). (C) Kinetics of the gating and ionic currents (B and C modified, with permission, from reference 572).

distribution or orientation of molecules with a charge or dipole moment" (209). Currently, there is a consensus that voltage dependency in K^+ channels is mostly due to charge movement instead of displacement of dipoles. The probability of finding the charge in either side of the electric field (or the membrane) must follow a Boltzmann distribution, which is a function describing the probability (P_o) of finding a charged particle with valence z in a electric field of intensity V, such that:

$$P_o = \frac{1}{1 + e^{\frac{-zF(V-V_o)}{RT}}}$$

where F, R, and T have their usual meanings and V_o is the voltage at which $P_o = 0.5$. We must emphasize here that the effective valence z is actually the product of the actual valence times the fractional distance the charges move across the electric field.

HH applied a Boltzmann distribution to describe the K^+ conductance as function of the applied TM voltage (see, for example, the curve f_o vs. V in Fig. 16B). Notice that when V is sufficiently negative, equation becomes:

$$P_o = K e^{zFV/RT} \qquad (2)$$

where K is constant. In this limit HH found for that the K^+ conductance increased an e-fold increase every 4 mV. Their conclusion was that the particles controlling the K^+ conductance were endowed with at least six electronic charges that move across the electric field.

One key observation was that after a square voltage pulse from a negative voltage, where K^+ conductance was at rest (or closed), the activation of the K^+ currents followed a sigmoidal time course (Fig. 16A). In other words, there is a lag in the ionic currents after the voltage pulse is applied. This particular kinetic attribute suggested that the structure governing the K^+ conductance undergo several nonconductive steps before reaching the active state. On the other hand, after returning to the resting voltage, the relaxation of the currents did not show a delay and was well described with an exponential time course. Thus, the system governing K^+ conductance had several nonconductive states but only one or few conductive states.

Following HH, we can assume that four identical and independent charged particles control the K^+-permeability. The particle moves across the electric field between two positions, *active* and *resting*. The probability for the potassium channels to be in the active conformation is proportional to the joint probability that all four charged particles are in the active position. If n is the probability of each particle to be in the active position, $1 - n$ is the probability of being at resting. Thus the probability of finding K-channels conducting is proportional to n^4. Then, the reaction:

$$n \leftrightarrow 1 - n \qquad (3)$$

must be a simple first order chemical reaction such that in the presence of a perturbation (for example, a change in membrane voltage) reaches a new equilibrium according to:

$$\frac{dn}{dt} = -\beta n + \alpha(1-n) \tag{4}$$

where α and β are the backward and forward rate constants, respectively. The solution of this equation describes how the n-particle relaxes to a new equilibrium, n_∞, from the previous preperturbation equilibrium, n_0 and is given by:

$$n(t) = n_\infty + (n_0 - n_\infty)e^{-\frac{t}{\tau}} \tag{5}$$

where $n_\infty = \alpha/(\alpha+\beta)$ and $n_0 = \alpha_0/(\alpha_0+\beta_0)$. At $t = 0$, $n(t) = n_0$, the initial value, which relaxes exponentially to reach n_∞ as $t \to \infty$. The time constant of this exponential relaxation is $\tau = 1/(\alpha+\beta)$. Because four independent particles in the active position are needed to activate K-permeability, a general expression for the potassium current (I_K) is:

$$I_K = g_K n(t)^4 (V - E_K) \tag{6}$$

where g_K is the maximal K-conductance, V is the membrane potential, and E_K is the equilibrium potential for K^+.

Fitzhugh's expansion of the HH model

The expansion of the HH model, as recognized by Clay Armstrong in his seminal 1975 review (11), is due to Richard Fitzhugh an influential biophysicist that developed several conceptual and educational advances in our understanding of the HH model (142, 143).

If the activating particles distribute randomly, at a given membrane potential, the total number of nonconductive configurations and their proportion, is given by the binomial distribution and by the geometrical arrangement of the particles. If none of the geometrical configurations are equivalent, the number of all possible configurations having less than four active n particles ϕ_i is given by:

$$\sum_{i=0}^{3} \phi_i; \quad \text{where} \quad \phi_i = \frac{4!}{i!(4-i)!} \tag{7}$$

For four particles, the maximal number of nonconductive states is $\phi_0 + \phi_2 + \phi_2 + \phi_3 = 15$, producing a complex kinetic scheme. But if geometry is not important, the number of nonconductive states becomes reduced to four, having 0, 1, 2, or 3 active n particles, and yielding a more simple kinetics:

$$C_0 \underset{\beta}{\overset{4\alpha}{\rightleftarrows}} C_1 \underset{2\beta}{\overset{3\alpha}{\rightleftarrows}} C_2 \underset{3\beta}{\overset{2\alpha}{\rightleftarrows}} C_3 \underset{4\beta}{\overset{\alpha}{\rightleftarrows}} O_4 \tag{8}$$

where C and O represent closed and open states of the channel, respectively, and the subindexes represent the number of active n particles in each population. This kinetic scheme, which is in fact the expansion of the HH model (11), reproduces the basic kinetic and steady-state features of the potassium conductance in the squid axon. Due to the transit of the K^+ channel among several closed states, it reproduces the sigmoidal activation of the currents, and the monoexponential deactivation because there is only one open state (209).

The HH model made two additional predictions that were tested only 20 years later (12, 13, 41, 42). Because of the charged nature of the *voltage-sensing* particle it could be possible to detect the movement of the n particles as a nonionic current. With a high-enough number of channels on the membrane or with high-enough sensitivity, it would be possible to measure the current produced by the intramembrane charge displacement of the voltage sensing particles, the *gating currents*. The gating currents, I_g, can be predicted from the HH model assuming that each n particle has a charge z and that they are proportional to the rate of movement of N particles

$$I_g = Nze\frac{dn}{dt}$$

Because, most of the transitions in scheme 8 occur among closed states, upon positive voltage pulses, these gating currents should follow an exponential relaxation time course with a time constant equals to $1/\alpha$ preceding the activation of the ionic currents. On the other hand, upon returning to the resting voltage, the gating currents should be four times slower than the ionic currents because the channel closes with 4β while the n-particle returns with a rate constant β. These predictions were tested for K^+ currents about 30 years later (13, 44, 258).

For K^+ channels, the gating currents show a very fast rising phase followed by an exponential decay (Fig. 16A) and indicating that most of the sensing charge displacement occurs among closed states, the voltage activation of the gating charge (Q_{rel}) is shifted toward negative voltages compared to the K^+ conductance (f_o), (Fig. 16B). However, both activation and deactivation kinetics of the gating currents were similar to those of the ionic currents (Fig. 16C). These results indicated that leaving the deeper closed states is rate limiting for activation and leaving the open states could be also rate limiting for the deactivation and gating charge return (44, 572).

The ZHA kinetic model

After the molecular cloning of voltage gated K^+ channels during the late 1980s, the preferred model for structure-function studies on voltage gated ion channels was the Shaker K^+ channel. This protein is the alternative splicing product of a complex gene in *Drosophila*, extending approximately 130 kb (250, 412).

The tetrameric structure of potassium channels put forward for Shaker K-channels (311, 337) reinforced the idea of four gating particles, each one in each subunit. Aldrich and

co-workers proposed a kinetic scheme for Shaker K-channels, the ZHA model (220,613,614) is consistent with macroscopic currents, gating currents, and single channel recordings. The key observation on the channel behavior was that the effective valence was large, 12 to 13 electronic charges (e_o), but no single process, as activation or deactivation, showed a large voltage dependence. To describe the latency of the current activation required a minimum of eight transitions between closed states. Thus, the voltage-dependent activation must involve a large number of states, each one moving a small number of charges. The resulting scheme has some of the features of the original *n*-particle model from HH, but includes two voltage-dependent transitions per subunit (613).

$$\left.\begin{array}{l} C_0 \rightarrow C_1 \rightarrow C_2 \\ C_0 \rightarrow C_1 \rightarrow C_2 \\ C_0 \rightarrow C_1 \rightarrow C_2 \\ C_0 \rightarrow C_1 \rightarrow C_2 \end{array}\right\} \quad O$$

Each subunit displaces approximately 3 e_o in two transitions, suggesting three conformations for the voltage sensor (Eq. 9). This scheme introduces a concerted opening transition when the last voltage sensor reaches the C2 state. The rate constant describing the channel closing is 10-fold slower than the other backward rates departing from C2. This explains in a most economical manner why the kinetics of the OFF gating currents is similar to that of deactivation of the ionic currents as was observed by White and Bezanilla (572).

However, the ZHA model has the caveat of strictly tying the last forward transition of the voltage sensor to channel opening. There is ample evidence for the existence of an activated-not-open conformation present in several types of voltage gated K^+ channels (see, for example, reference 15). More complete kinetic models that incorporate the existence of activated nonopen state and a concerted opening transition have been developed by Sigworth and co-workers (483,627).

Structure-function relations in voltage-dependent K^+ channels

Gating in the Kv channels is conferred through the attachment of VSDs to the pore. The basic function of this domain is to perform mechanical work that allows the ion conduction pore to change its conformation between closed and open states. In voltage-dependent channels, the VSD converts the energy stored in the membrane electric field into mechanical work. There is strong evidence that the positive charges contained in S4 are the voltage-sensing elements (3, 490). Thus, Kv channel gating is essentially an electromechanical coupling between a voltage sensing unit and a pore unit.

The crystal structure of a mammalian voltage-dependent K^+ channel (Kv1.2), suggested to be in a relaxed state (see section on *VSD conformation during slow inactivation*), had initially been resolved at 2.9 Å and further improved to 2.4 Å using a chimeric Kv1.2-Kv2.1 channel. In the latter case, the channel was crystallized in complex with lipids. These structures showed that the helices of the ion conduction pore (S5-S6) related to the helices of the voltage sensor domain (S1-S4) in a special way. The voltage sensor domain of one subunit is located near the pore domain of an adjacent subunit (Fig. 12). The connection between the pore and the voltage-sensor domain is made by the S4-S5 linker helix, which runs parallel to the intracellular membrane surface.

Voltage sensitivity

The tetrameric organization of voltage-dependent K^+ was demonstrated early after the almost simultaneous molecular cloning of the *D*. Shaker K-channels (311, 337). Each monomer is formed by two well-defined structural and functional domains, the pore domain and the VSD (see Fig. 17A) (238, 307, 523). The pore domain is structurally related to the Kir channels family. As in the KcsA K^+ channel, this protein module should contains two TM α-helices and a reentrant loop composed of a four-turn pore helix flanking a selectivity filter lined by the carbonyls groups of six residues unfolded in an extended conformation (115). The operation of the pore main access gate is under the control of the VSD, which is a separate structural domain formed by four TM segments [named S1 to S4 (238, 307, 458).

There are several lines of evidence indicating that the VSD of voltage-gated K^+ channels is a separate structural domain *per se*: *First*. The VSD from the bacterial (*A. pernix*) voltage-gated K channels, KvAP, can be synthesized, purified, and folded separately showing similar crystallographic structure to the channel-attached domain (238, 458). *Second*, it can be added to pore domain only K^+ channels, such as KcsA, transferring VSD-gated voltage sensitivity (326) to the chimeric channel *Third*, there are functionally different membrane proteins consisting of only a voltage-sensor domain. For example, a voltage-gated proton channel (161, 401, 442, 476) and a voltage-sensitive phosphatase discovered in the ascidian *Ciona intestinalis*, Ci-VSP, which consist in a VSD functionally linked to a inositide phosphatase. This protein displays channel-like "gating" currents and directly translates changes in membrane potential into the turnover of phosphoinositide (215, 382, 401). The physiological activity persists after functional detachment of the phosphatase domain (559).

When Numa and co-workers first cloned a voltage-gated ion channel (398), they proposed that the unusually charged fourth TM segment (S4), hosted the molecular determinant for the voltage sensitivity. In voltage-gated K^+ channels, S4 contains a highly conserved sequence array of 6-8 basic amino acids periodically spaced by two hydrophobic residues. With individual charge-neutralizing mutations of charged residues in the VSD of Shaker K^+ channels, only E293 an acidic residue in S2 (G1 in Fig. 17A), and R262, R365, R368, and R371 (R1 to R4, respectively in Fig. 17A) in S4 contributed significantly to the gating charge or to the voltage sensitivity. Individual neutralization of each of these charged residues led

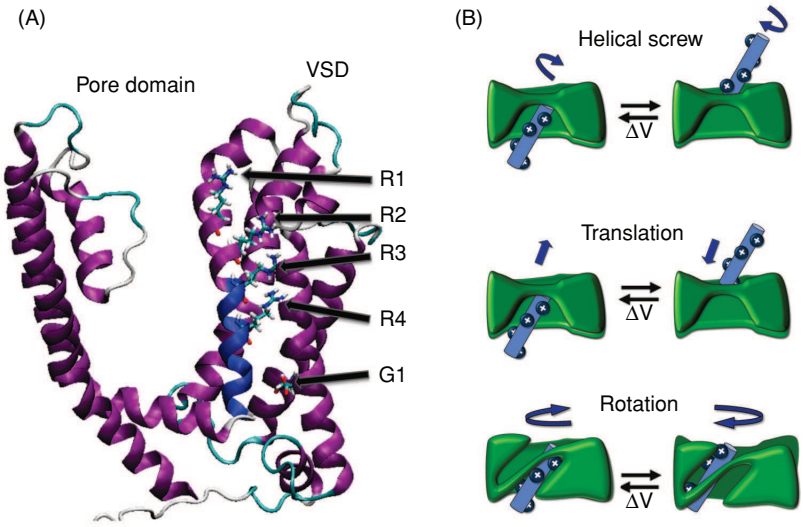


Figure 17 Structural determinants for the voltage sensitivity in voltage-gated K^+ channels. (A) Structure of a single monomer depicting the voltage-sensor domain (VSD) and the pore domain. Arginines R1, R2, R3, and R4 (corresponding to Shaker R362, R365, R368, and R371) are represented in stick form. (B) Possible trajectories for the gating charges (for more details see text).

to large decreases (~4 e_o each) in the gating charge and in the effective valence of the voltage dependence (z in Eq. 1) (3, 490). This agreement indicates that most, if not all, the charge transferred during activation is energetically coupled to channel opening.

However, the simple arithmetical addition of the contribution of each individual charge neutralization reaches over 20 e_o, a figure much larger than the total number of 12 to 14 e_o charges per channel determined by either gating currents (3,490) or by the limiting slope analysis (160, 229, 482, 614). This paradox can be solved if it is assumed that neutralization of some of the charges not only changes the total number of gating charges but also is modifying the local electric field. This disparity also indicates that each charge does not contribute independently to the voltage dependence and their contribution must depend on the specific protein sequence nearby the voltage-sensing residues. For example, the introduction of charged side chains into conserved hydrophobic positions in the S4 reduces dramatically the effective gating charge (160).

Physical displacements in the VSD

The individual contribution of each of the S4 arginines R362, R365, R368, and R371 (named R1-R4 in Fig. 17A) of the Shaker K^+ channel to the gating charges is close to 4 electronic charges (e_o) (3, 490). A straightforward interpretation to these results, imply that each one of the four arginines side chains move across most of the electric field. If the electric field decays along the thickness of the membrane, each voltage-sensing arginine should move 30 to 40 Å. Following an strategy designed in Richard Horn's lab for the sodium channel, a few labs measured activation-dependent internal and external solvent accessibility of cysteine residues introduced to replace R1 to R4, one at a time (293, 600, 609). Chemical modification of residue 362 by membrane impermeant thiol reagents was possible from the extracellular side in the active state and, to a much lesser extent, in the closed state. For residues 365 and 368 changes in accessibility were more dramatic; they were internally accessible in the closed state and accessible to thiol reagent from the external side in the open state. Thus, these results not only revealed significant movements of S4, but also a short hydrophobic septum in the closed state, since 362 was accessible from the external side as 368 was it from the internal side (i.e., only 6 amino acid residues, which if conforming a α-helix implies a septum of ~9 Å). Thus, water crevices must surround the voltage sensor very deep into the protein, focusing the electric field in a short stretch of low dielectric material (293). The elegant histidine substitution studies of Bezanilla's group (511-513) gave further support to the structural model that considered the S4 contained in water-lined crevices separated by a short hydrophobic septum. Histidines introduced in R2 and R3 transport protons down the proton gradient each time the voltage sensor moves from the resting to the activated state indicating that R2 and R3 traverse the full length of the electric field. Histidines replacing R2 and R4, on the other hand behaves as voltage-dependent proton channels, which allow proton fluxes only when the voltage sensor is in the resting and the active state, respectively. The fact that replacement of R1 and R4 by histidines form proton pores in both the open and the closed state is a strong evidence of the existence of a short hydrophobic septum in the resting and active state of the voltage sensor.

Because the size of the gating charge decreases at low ionic strength, part of the electric field must fall across these water crevices (230). From this reduction, an intracellular conical cavity of 20 to 24-Å depth and 12-Å aperture, and a smaller extracellular cavity of 3-Å depth and the same aperture could be estimated, leaving a septum with an expected thickness of 3 to 7 Å. Consistent with this figure, using a series of permanently charged methanethiosulfonate (MTS) reagents with alkyl tethers ranging from methyl to hexyl, Ahern and Horn (5) found that short adducts ($<3CH_2$) added to R362C could be dragged across the electric field during activation to carry charge across it; however, charged adducts with six CH_2 or longer linkers could not be dragged across the septum, suggesting that these linkers were long enough to stretch with the voltage-sensor movement without shuttling the charge across the field. Thus, the low dielectric septum must be only 4 Å across (5).

Consistent with a very short septum, amino acid replacement in some of the voltage-sensing positions make the voltage sensor behave as cationic pore at negative voltages (in the resting conformation) (72, 512, 542, 543). The histidine scanning mutagenesis studies and these results indicate that a single amino acid replacement can disorganize entirely the dielectric septum transforming it into an ion channel.

The trajectory of the voltage-sensing charges

From the previous description, a small "vertical" movement should be necessary to shuttle the sensing charges across the electric field. In fact, Bezanilla's lab made measurements with luminescence resonance energy transfer (LRET) of distance changes between the voltage sensors of each Shaker subunit and between voltage sensors and a pore-bound scorpion toxin during activation. They proposed a small vertical displacement of 2 Å or less (91, 155, 433) (see Fig. 17B). On the other hand, the KvAP structure (238, 240, 457) suggested that S4 together with the second half of S3 (S3b) formed a helical hairpin structure located rather intracellular that MacKinnon and colleagues named the "paddle." They attached a biotin molecule, through a 17 Å linker, to paddle residues and then probed for heir activation-dependent internal and external accessibility to streptavidin. The accessibility pattern to streptavidin suggested that the paddle would traverse most of the membrane thickness, that is, 25 to 35 Å. (240). Alternatively, S4 could also slide up in a helical screw trajectory along S3 (78, 182) (Fig. 17B top). By cutting short the Shaker K-channel S3-S4 linker to restrict S4 movement (163, 357) it was found that S4 require to slide 3 to 5 Å with respect to S3 in a rotational trajectory (162, 164). However, a disulfide bond between Shaker residues 325 in S3 and 360 in S4 can be formed in the closed state, while a bond between 325 and 366 can be formed in the open state, a result consistent with a helical trajectory of 9-16 Å of S4 (63). Discrepancies may arise from the use of different channels (bacterial vs. mammalian) as well as from the use of different experimental approaches [see (39, 524)].

The molecular determinants of the hydrophobic septum have been further elucidated by substituting residues I241 and I287 in S1 and S2, respectively by histidines in the Shaker K^+ channel (72). Mutants I241H and I287H generate inward currents at negative applied voltages indicating that these residues are part of the hydrophobic plug. Replacement of I241 and I287 by cysteines showed that under oxidizing conditions and at hyperpolarized voltages, these residues are able to form disulfide bonds and metal (Cd^{2+}) bridges positioning in an unambiguously manner the position of the S4 segment relative to S1 and S2. Importantly, these results open for the possibility of predicting the trajectory followed by the S4 segment in going from the closed to the open state. To satisfy these constraints, the S4 rotates ($\sim 180^\circ$) and undergoes a vertical movement of about 6.5 Å (72).

The environment surrounding the voltage-sensing charges is aqueous

S4 is an unusually charged TM segment, having a strictly conserved sequence array of six to eight basic amino acids periodically spaced by two hydrophobic residues (see supplementary material in reference 299).

Some of S4 basic residues seem to be stabilized by a network of negatively charge residues in S2 and S3. Intragenic suppression strategy with charge reversal mutations in Shaker suggested activation-dependent electrostatic interactions between E283 (S2) and R3 and R4, and between K374 in S4 with E293 in S2 and D316 in S3 (540, 541). The other charged arginine side chains could be stabilized by hydration shells protruding intro the core of the membrane (5, 243, 244, 278, 549) or by counter charges provided by phosphate groups of the polar head of phospholipids (200, 316, 318, 338, 443, 481, 524, 593). The counter charges mechanism must be specific for *basic* residues; in contrast, hydration could stabilize charges independently of their sign. Consistent with this latter expectation, S4 tolerates additional charged side chains, negative and positive, added in a number of positions in S4 (4, 160). These results argue in favor of hydration as the charge stabilization mechanism. This mechanism would shape the protein-lipid-water interfaces, providing a molecular explanation for the formation of the aqueous crevices surrounding S4 (160, 244, 278, 549).

The K^+ selective pore domain

The K^+ selective pore is located in a structurally homologous locus of the protein as voltage-gated Na^+ and Ca^{2+} channels, and share a common mechanism of ion transport too: they can hold several permeant ions in single file (125, 199, 385, 445). K channels are endowed of a highly K^+ selective pore that allows fluxes of K^+ ranging from 10^6 to 10^8 ions/s in physiological conditions (in terms of conductance, it is equivalent to $\sim$3 pS to $\sim$300 pS). Voltage-gated K^+ channels constitute one of the most diverse membrane protein family (467) but all of them encoded an extremely conserved signature sequence

of seven amino acidic residues, TTVGYGD (193) that forms the structure of the ion selectivity filter.

Potassium channels conduct K^+ ions with high selectivity over other cations. In general, they prefer K^+ ions hundreds times over the Na^+ ions having only an approximately 0.4 Å smaller radius. This high selectivity was expected if oxygen atoms inside the pore replace K^+ hydration shell with a separation between oxygen so critical that Na^+ does not fit comfortable (40). When the crystal structure of a bacterial K channel KcsA at 3.2 Å resolution became available from the MacKinnon lab (115), it showed a snapshot of several permeant ions in single file inside the conduction pathways as was anticipated in 1955 by Hodgkin and Keynes for the giant axon (210). The structure of this ion channel showed two zones that K^+ ions must transit in their trajectory trough the pore; the selectivity filter, containing two cations, and the internal vestibule or "cavity," having one cation beneath the entrance of the selectivity filter (Fig. 18A). MacKinnon and colleagues proposed that the oxygen atoms of the peptide backbone carbonyl groups, in perfect 4-fold symmetry, stabilized dehydrated K^+ ions by acting as water "surrogate," as Bezanilla and Armstrong had proposed earlier (40). The transit of the ions in the selectivity filter could be restricted to jumps between well-defined binding sites (zones of larger electron densities in the crystallographic data), while in the cavity, cations would have to diffuse from the internal entrance to the deep end to reach the cavity-binding site.

In a surprising example on how a static/stable structure of the selectivity filter determined at 2 Å resolution (629) revealed details of a dynamic process as ion conduction, this structure shows in detail a remarkable machinery appearing to be optimized not only to conduct ions but also to exquisitely discriminate between K^+ from other cations (Fig. 18B). The structure revealed seven K^+-binding sites in single file in the pore with alike electron densities (i.e., energetically similar). The two antipodal K^+, at the external end of the selectivity filter and at the cavity, were fully hydrated with eight water molecules around the pore's axis of symmetry, four on top and four on the bottom of the K^+, suggesting that the energetic cost of dehydrating K^+ ions inside the pore is close to zero. The second K^+, counting from the external site at the external entrance shows partial dehydration, as if during the snapshot it was being stripped from its solvating water as it enters the pore. Because the distance between the binding sites is too small (~3.5 Å) to overcome electrostatic repulsive interaction between sites neighboring K^+, it is unlikely that, in addition to the cavity site, all six binding sites are simultaneously occupied by K^+ ions. Instead, the similarities in electron densities could be revealing two alternating and energetically equivalent ion configurations within the

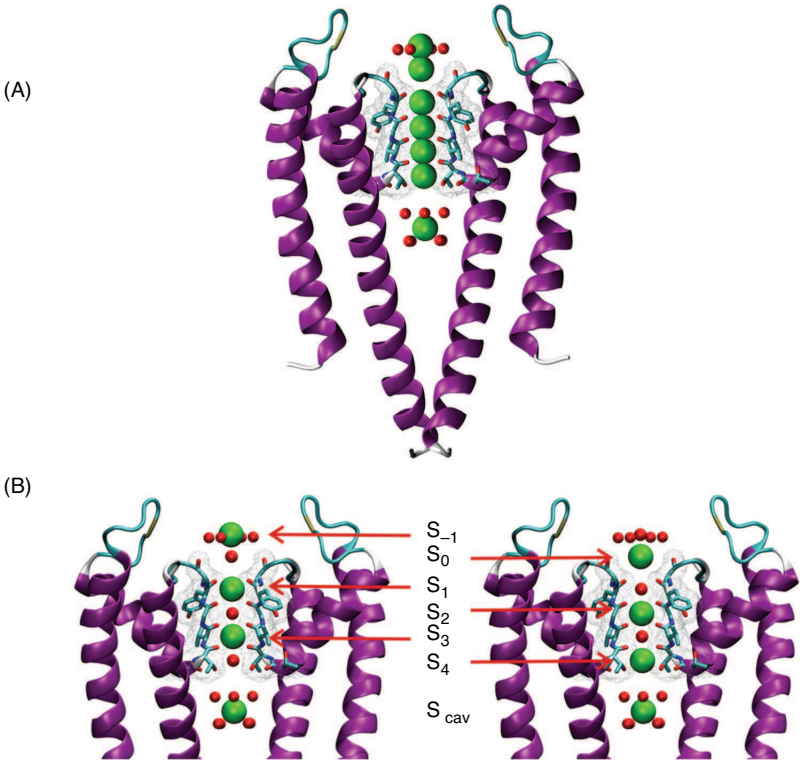


Figure 18 Structural design of the K^+ conduction system. (A) Ions in the pore of the KcsA bacterial channel (PDB_ID: 1K4C). All possible K^+-binding sites are shown. Hydration water molecules are shown in red with a Van der Waal radius of 0.5 Å. (B) Ion conduction is due to two alternating and energetically equivalent configurations in ion occupancy (for more details see text).

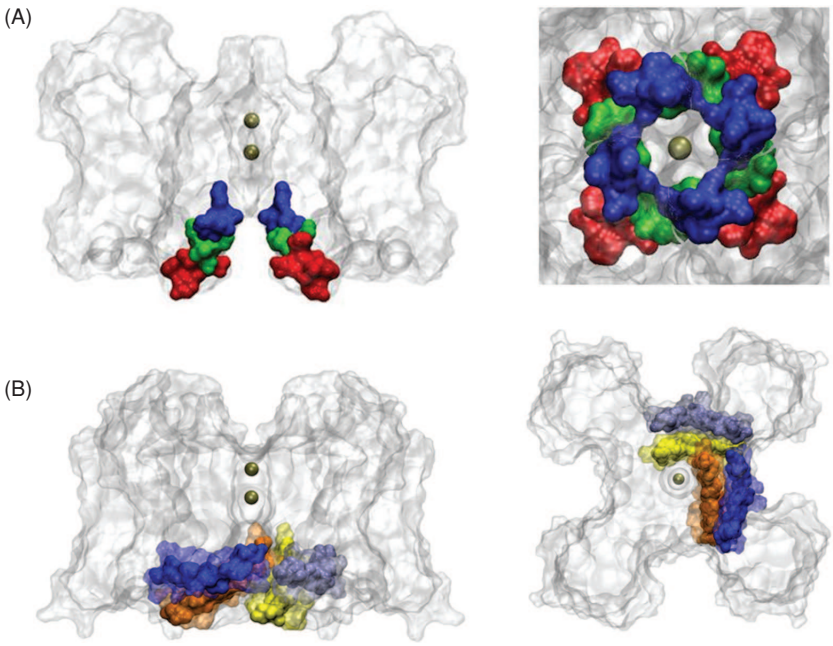


Figure 19 Mechanical movements of the voltage-sensitive pore opening. (A) Side and enlarged bottom views of the residues that change in accessibility during the opening of the Shaker activation gate (residues 470-474; in blue), that do no change in accessibility during gating (residues 481-486, in red), and residues that may form the gate (residues 475-479; in green). After reference 313. (B) Allosteric surface proposed for the interaction between the S4 and S5 linker (in blue and gray) with the S6 C-terminal half of two adjacent subunits (in yellow and orange).

selectivity filter, each having only three K^+ ions. One configuration occupies the sites −1, 1, and 3 (s_{-1}, s_1, and s_3 in Fig. 18B), while the other configuration fills sites 0, 2, and 4. Thus, ionic conduction in the selectivity filter is pictured as concerted transitions between these two conformations, both energetically equivalent to diffusion (375). The occupancy of s_4 favor s_{-1}, s_1, s_3 configuration because of electrostatic repulsion with the ion in s_3, in an electric equivalent of the transference of kinetic energy in the Newton swinging balls, in which the strike of the swinging ball to the last ball in the row expels the first one almost instantaneously (369).

Coupling between VSD and the K-selective pore

The pioneering work of Clay Armstrong revealed that only open channels allowed the entrance of large tetraalkylammonia ions into the pore from the intracellular side (9). Moreover, this type of ions could be trapped inside the pore by forcing the blocked channel to close (10). These classical experiments revealed for the first time the existence of an internal gate able to hinder the passage of ions through K^+ channels.

Using internal thiol reagent to modify cysteine residues that were introduced in several locations of Shaker's S6, Gary Yellen's lab showed that chemical modification in position 470 to 474 was possible by activation and inhibited by tetrabuthylammonium (TBA). Meanwhile, cysteine residues located at 481 to 486 were always highly accessible and could not be protected by TBA (107, 211, 313). Thus, the intermediate residues, 475 to 480, would form the access gate to the pore. Other work extended the gate between 473 and 481 (184) (see Fig. 19A).

The movement of the voltage sensor that makes possible the opening of the pore appears to require physical interaction between residues 475 and 480 in S6 with residues in the S4 and S5 linker (326, 327). In fact, the structure of Shaker mammalian ortholog, Kv1.2, shows a surface of intimate contact between these two helical segments, in the same, and neighboring, subunits, suggesting an allosteric communication between the VSD and the pore domain (see Fig. 19B) (317). Such a picture is in agreement with current kinetic models as those by proposed by Aldrich and Sigworth groups (483, 613), if we assume they represent the late stages in the activation pathway (see Section "*The ZHA Kinetic Model*"). This structure and that of the Kv1.2/Kv2.1 chimera shows all voltage sensors in the active position and the pore open. In the closed state, this interaction surface probably persist because the open probability in Shaker K^+ channels maintains a tight coupling to the voltage sensor, not showing hints of becoming less voltage dependent, even at open probabilities as low as 10^{-8} (160, 229, 482). Asymptotic reduced voltage dependence at low Po is the expected outcome of an allosteric model (218). Thus, the allosteric binding energy between the S4 andS5 linker and the C-end of S6 remains high in the closed-resting state, being at least 11 kcal/mol.

Inactivation mechanisms

N-type inactivation

At the beginning of the nineties, both the Aldrich's and Yellen's labs proposed what is the classical view of potassium channel inactivation. They described two types of inactivation processes in Shaker, the N-type and the C-type inactivation, each having different molecular bases. The N-type inactivation occurs when a movable 22-residue segment localized at the N-terminus of the protein blocks the pore by binding to the internal entrance of the pore in the open conformation (108, 219). Removal of part of the N-terminus of Shaker abolish N-type inactivation and the addition of the isolated 22-residue peptide back into the internal solution restores the inactivation in a dose-response manner (14, 612).

C-type inactivation

The removal of the N-type inactivation to Shaker uncovers another, slower, inactivation process reminiscent of the one observed in the squid axon (43), the so-called C-type inactivation (219). Structural determinants of this inactivation appear to be localized toward the external entrance of the selectivity filter (see Fig. 1 in reference 404), and toward the N-terminus of the sixth TM segment of the protein (221). In the conventional view, the C-type inactivated state is produced by a localized constriction of the external mouth of the channel, which thereby interrupts K^+ ion conduction. Such conformational change is antagonized by the extracellular addition of K^+ ions or tetraethylammonium (TEA) (26, 103, 324, 373, 603). Based on crystals of KcsA obtained in different K^+ concentrations, several structural propositions have emerged to account for such conformational change in the selectivity filter (87, 628, 629).

Other inactivation types

At present, other slow inactivation processes have been described for Shaker, Kv1.5, Kv2.1, Kv3.1 and Kv4.2 K-channels (113, 159, 266, 287). An inactivation process having an opposite voltage dependence to that of C-type inactivation, rendering U-shaped voltage-dependent channel availability. This slow inactivation is not antagonize by external K^+ or external TEA but is delayed by internal TEA, suggesting the presence of an intracellular molecular determinant intervening in its development. In agreement with this, mutations at the internal mouth of the pore severely alter the slow inactivation rate (104, 212, 265). Moreover, during deactivation or slow inactivation, Kv1.4 extrudes similar volumes of water toward the cytosolic side, suggesting comparable conformational changes (235). For Shaker and Kv4.2 a mechanism has been proposed similar to the ultraslow inactivation in Na-channels or the so called voltage desensitization present in HCN channels that imply the re-closing of the activation gate (113, 159, 469, 498). Thus, it wouldn't be surprising if several members of the voltage-gated ion channel family were endowed of a common repertoire of non conducting conformations.

VSD conformation during slow inactivation

The gating charge-voltage (Q-V) curves from slow inactivated channels are shifted to more negative voltages (~ -60 mV) as compared with the Q-V curves obtained from non slow-inactivated channels (159, 402). Thus, slow inactivation correlates with the appearance of a highly stable conformational state of the voltage sensor. Such a conformational change induced by voltage appears to be an intrinsic property of the VSD, since the shift in the Q-V curve that is seen in slow-inactivated channels can be also observed when gating currents are measured using the isolated VSD (560). Periodicity analysis suggests a S4 transition from a mostly 3_{10} helical packing at resting to mostly α-helical at positive voltages (a relaxed state). This latter packing being the observed in the structure of Kv channels, crystallized in the absence of electric field.

The slo (KCa) Family of K^+ Channels

Function and localization

This family, encoded by the *slo* genes, is characterized by K^+ channels having an unusually large conductance (466). In particular, Slo1, that with a 250 pS single-ion conductance in 100 mmol/L symmetrical K^+, has also been dubbed "big" potassium (BK) channels and also maxi-K channels. The first member of this family was cloned from the *Drosophila* mutant *slowpoke* (*Slo*) (2, 21) and was found to code for a voltage- and Ca^{2+}-activated channel Four genes encode the Slo family of ion channels in mammals (Fig. 20A): *Slo1 (KCa1.1;* KCNMA1 in humans*)*; the mammalian *slo* orthologue was cloned using a low-stringency DNA hybridization of a mammalian cDNA using the *Drosophila slo* cDNA (69). Slo1 is activated by Ca^{2+} and voltage; *Slo2 (KCa4)* cloning was possible thanks to the genomic sequencing in *C. elegans* that revealed a gene coding for a channel able to be activated by internal Ca^{2+} and Cl^- (605). In mammals two *Slo2* paralogs, *Slo2.1* (*KCa4.2,* KCNT2, *Slick*) and *Slo2.2* (*KCa4.1,* KCNT1, *Slack*), were found but in contrast to the *C. elegans* Slo2 channel, in mammals Slo2 is activated by Na^+ and Cl^- (47, 605). *Slo3* (*KCa5.1,* KCNU1) was identified by performing a computer search that lead to the identification of an expressed sequence tag (EST) with homology to part of the C-terminus of mSlo1 (484). Slo3 proved to be activated by voltage and internal alkalization.

This family of ion channels, because their ability to sense changes in the intracellular ion concentration (H^+, Na^+, and Ca^{2+}) is unique since establishes a link between the ionic metabolism of the cell and its membrane conductance.

Slo 1

The gene *Slo1* was cloned from the *Drosophila* mutant Slowpoke, which has flight problems, mate song defects and

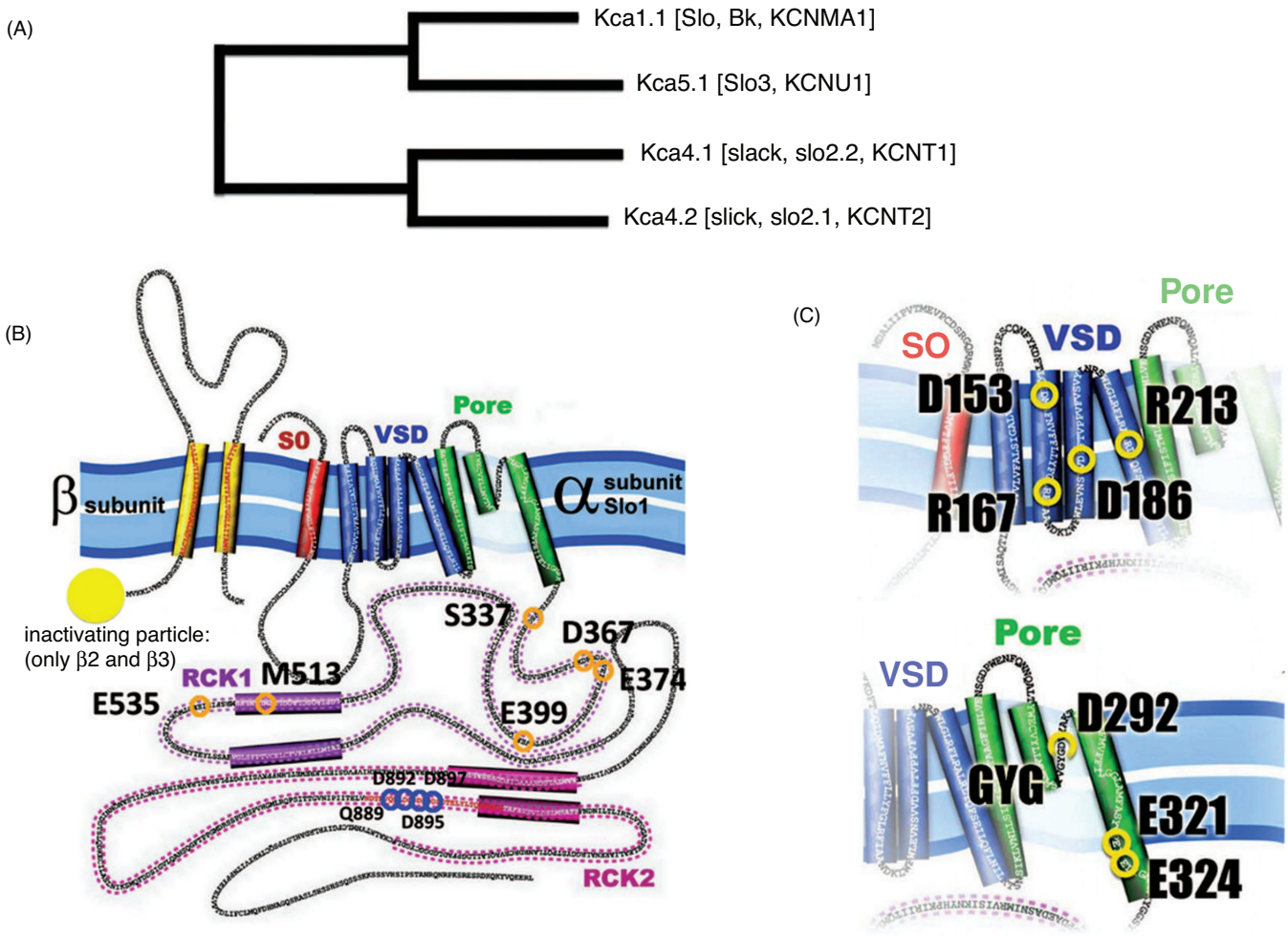


Figure 20 Phylogenetic tree of Slo channels family in mammals and membrane topology of the α- and β-subunits of Slo1 channels. (A) The four genes present in Slo channels families: *Slo, Slo2.1, Slo 2.2,* and *Slo3*. (B) The α-subunit of Slo1 contains seven transmembrane segments divided in two domains [voltage-sensor domain, (VSD) and pore region] that is normally associated to β-subunits consisting of two transmembrane segments. β2 and β3 have an inactivating particle on their N-terminus able to interact with the channel internal vestibule and block the passage of K^+ through the channel. The α-subunit contains a long C-terminus domain in which two regulators of K^+ conductance domains (RCK1 and RCK2) are present. Spread throughout in the BK C-terminus are located the binding sites for Ca^{2+} and Mg^{2+} (for more details on the divalent cation-binding sites see Section "*Carboxy terminus*"). (C) (Top) The α-subunit has a voltage-sensing domain formed by the S0 to S4 segments. Four charged residues contribute to the channel voltage membrane sensitivity, D153, R167 in S2, D186 in S3, and R213 in S4. (Bottom) The pore region formed by S5, the pore helix, the pore loop, and the S6 transmembrane. Three amino acid residues have been identified in the BK pore as partially responsible for the channel high conductance, D292, E321, and E324.

altered response to heat shock. *Drosophila* muscles of Slowpoke lack a calcium-activated potassium conductance present during early larval stages (127). This gene codes for a protein with homology to voltage-dependent potassium channels, but in addition it has an extra N-terminus segment (S0; Fig. 20B) and in addition to the six TMs segments it has four hydrophobic segments in the C-terminus domain (S7-S10). The S0 segment let the N-terminus facing the extracellular side of the membrane.

When patch clamp and bilayer experiments were performed to record the Slo1 single-channel activity, it was evident that the channel open probability increased when confronted to a membrane depolarization or to an increase in the intracellular Ca^{2+} concentration (Fig. 21A) (296, 356, 409). This features a study case protein due to its capability of coupling both chemical and electrical stimulus to generate a change in membrane conductance, made of this channel.

Electrophysiological recordings in native cells have shown Slo1 channels with different calcium sensitivities. However, the Slo1 channel is coded by a single gene in mammalian genomes. This channel diversity is possible due to alternative processing of introns, which produce at least 11 splice variants expressed in different tissues and cell types (553). This feature is conserved among evolution, and is observed in mammals, reptiles, birds, and insects (2, 69, 248, 289, 291, 360, 453, 553, 616). When expressed in heterologous expression systems, channels formed by these splice variants present different calcium sensitivities and gating

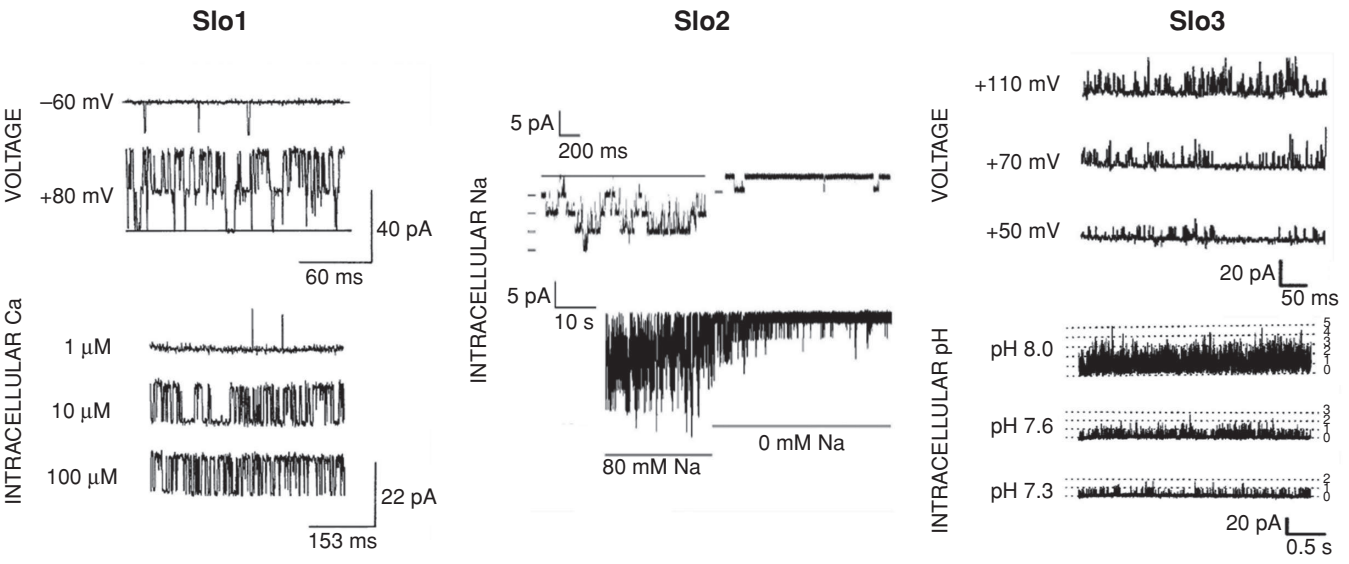


Figure 21 Polymodal activation of Slo channels. (A) Slo1 channel single-channel activity increases its open probability in response to an increase in the membrane voltage. Upper trace was taken at −60 mV. Openings are downward deflections in the current. Lower trace was taken at 80 mV. Upward deflections are opening events. The opening of two independent channels can be appreciated in this current record. Open probability also increases with increasing intracellular calcium (1, 10, and 100 μmol/L) at a fixed voltage (+60 mV). (B) Slo2.2 channels single-channel activity increases with high intracellular sodium. Perfusion using 80 mmol/L intracellular sodium elicited four conductance levels, which are reduced to just one with nominal 0 sodium concentration (top). (Bottom) The same type of experiment performed at a compressed time scale. (C) Single-channel activity of cloned Slo3 increases with the alkalinization and depolarizing voltages. Upper, single-channel activity increases at positive potentials. Bottom, single-channel recordings at +80 mV at several intracellular pHs.

kinetics, resembling the ones found in native cells. Alternative splicing is responsible in part for the great variety of calcium sensitivities found for Slo1 channels.

Several of these splice variants are produced by "insertions" at the C-terminal and one of the most studied variants is expressed under activation of the hypothalamic-pituitary-adrenal (HPA) axis under stress conditions, reason why it was called STREX (591). Two splice variants produce dominant negative subunits, which retain the channel in subcellular compartments (98, 553, 616). One of these variants corresponds to an insertion of 33 aminoacids in S0 (SV1 subunit) produce a natural dominant negative subunit that reduces the level expression of Slo1in myometrium.

Diversity of Slo1 channels is vast and it appears as a consequence of metabolic regulation, splicing and/or modulatory β-subunits. The main physiological function of this channel ubiquitously found in a variety of different tissues is to damp excitatory stimuli, like for example, an increase in cytosolic Ca^{2+} or a membrane depolarization (90, 295, 296, 356, 407).

β-subunits of Slo1 channels

Since β-subunits of Slo1 channels escort these channels in most tissues where they are present—the exception is skeletal muscle—and dramatically modify their gating properties, it is convenient to discuss here how these auxiliary subunits modify the gating properties of Slo1 channels.

Regulatory α-subunits share a putative membrane topology, with two TM segments connected by a 120-residue extracellular "loop" and with NH2 and COOH terminals oriented toward the cytoplasm (see Fig. 20B). At present, four αâ-subunits have been cloned in mammals [α1-α4; (32, 60, 267, 365, 555)]. Sequence similarities are major between α1-α2 and α2-α3, respectively. α4 is the most distantly related of all α-subunits.

Changes in biophysical properties of Slo1 channels induced by SLO1 α-subunits

The Slo1 β1-subunit induces an increase of the apparent Ca^{2+} sensitivity, a decrease of the voltage dependence of the Ch, and slowing of the macroscopic kinetics (407, 546, 547) (Fig. 22A and B). Slo1 β1-subunit also modifies the pharmacological properties of the channel (Orio et al. 2002). This subunit is mainly expressed in VSM, but is also found in urinary bladder and in some brain regions. β2 increases the Ca^{2+} and voltage sensitivity of Slo1 channels and slows the kinetics of the channel (60, 407) (Fig. 22A and B). Moreover, this subunit induces fast and complete inactivation (586). The N-terminus of the β2-subunit (residues 1–45) blocks the BK channel via interaction with a receptor site in the α-subunit, which becomes accessible once the channel is in the open state (Fig. 22A, third line). β2 also induces an instantaneous outward rectification that suggests that the β2 external loop approaches the Slo1 pore as to alter the Slo1 ion conduction characteristics (99). It is worth noticing that the N-terminus of β2 prevents the surface expression of this subunit and hinders the surface expression of the α-subunit via an endocytic mechanism (333, 615). This subunit is present in kidney, spleen, adrenal

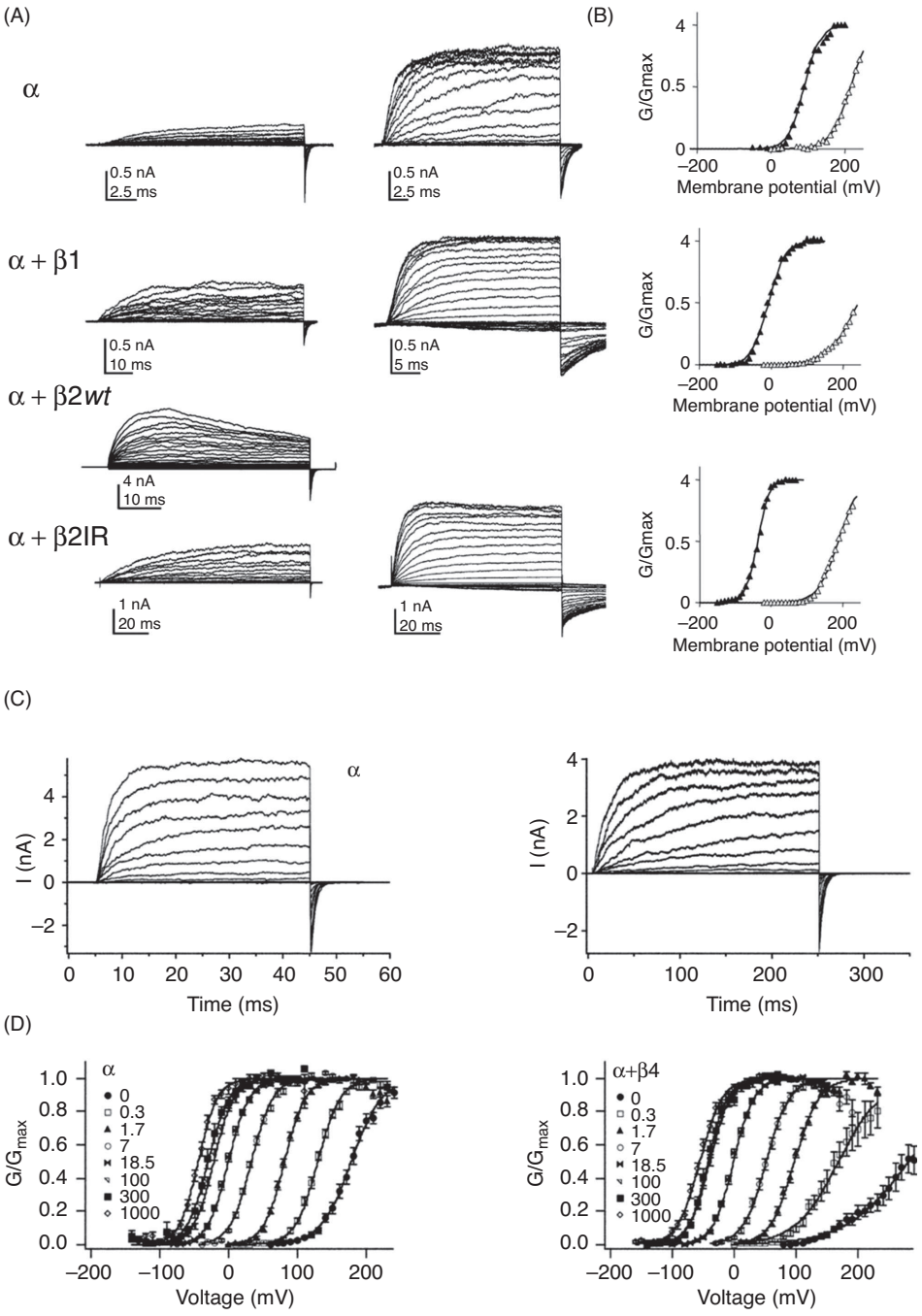


Figure 22 Functional differences between β-subunits. (A) Macroscopic currents were elicited by voltage pulses between −200 and +200 mV at 5 nmol/L (left) and 2.8 μmol/L (right) intracellular calcium. All currents were recorded in the inside-out configuration. Notice the change in the activation and the deactivation kinetics when β1 and β2IR (β2 inactivation removed) are coexpressed with the α-subunit. Current records in the third line were obtained by coexpressing the α with the β2-subunit. Notice that currents inactivate. (B) Voltage activation curves obtained from tail currents (the currents measured at the beginning of the repolarizing pulse; −60 mV) of recordings showed in A at 5 nmol/L (open symbols) and 2.8 μmol/L intracellular calcium (filled symbols) (modified, with permission, from reference 406). (C) Macroscopic currents of α + β4 channels (upper), and the activation curves at different calcium concentrations (lower). Notice the slower activation and deactivation kinetic produced by the β4-subunit. (D) Comparison of the voltage activation curves at different Ca^{2+} concentrations between channels formed by expressing the α-subunit alone (left) or by expressing α + β4 (adapted, with permission, from reference 564).

chromaffin cells, DRG, and brain (58, 309, 563). β3a–c induce channel inactivation to Slo1 currents and also produce an outward rectification of the open channel currents. The inactivation process is faster than β2-induced inactivation albeit incomplete. The β3b-subunit induces a small and consistent decrease in activation time constants at all Ca^{2+} concentrations, and it does not affect channel deactivation. β3b-subunit confers a non-linearity on instantaneous current-voltage properties that is regulated by the extracellular segment of this subunit (619). This subunit is expressed in adrenal chromaffin cells (587). The human β4-subunit has a complex Ca^{2+} concentration-dependent effect on Slo1 channel current. This subunit decreases apparent Ca^{2+} sensitivity at low Ca^{2+} concentrations but induces an increase in the apparent sensitivity at high Ca^{2+} concentrations (183). Human β4 also slows down activation and deactivation kinetics (32, 60) (Fig. 22C and D). This subunit is expressed exclusively in the brain, and is responsible for some of the features of neuronal Slo1 channels as low affinity for scorpion toxins and ethanol sensitivity, (352, 365, 555).

Pharmacology

Slo1 channels are blocked by the scorpion toxin CTX (370) and by the highly selective Slo1 scorpion toxin iberiotoxin (IbTX) (74, 153). These scorpion toxins are pore blockers and the group of Miller (414, 415) identify the positively charged side chain of lysine 27 in CTX as the BP. Slo1 channels are also very sensitive to external TEA (K_D ~250 μmol/L), sensitivity that is due to the presence of a ring of phenylalanines in the neighborhood of the external aspect of the selectivity filter (495, 558).

A number of Slo1 channels openers have been identified including the synthetic benzimidazolone derivatives (NS1619) and the natural modulator dihydrosoyasaponin (reviewed in reference 151). In this regard, we should mention that the compound NS11021 (1-(3,5)-bis-trifluoromethyl-phenyl-3-[4-bromo-2-(1H-tetrazol-5-yl)-phenyl]thiourea) is an Slo1 channel activator with better specificity and ten times higher potency compared to NS1619, one of the most broadly applied Slo1 opener (36).

Tissue distribution and function

Brain

In the CNS Slo1 channels are present in most regions of the mammalian brain and by colocalizing with VDCC they are important in the modulation of neurotransmitter release (Fig. 23A) (131, 156, 449). Colocalization of Slo1 channels with VDCC appears to be essential for Slo1 channel activation since to raise the channel open probability to reasonable values ($Po \geq 0.5$) at membrane voltages in the range −50 to 0 mV requires values of Ca^{2+} concentration 10 μmol/L or more (60, 135, 428) (Fig. 23A). We note here that Slo1 channels form macromolecular complexes with VDCC channels of the L-, P/Q-, and N-type and that this type of complexes can be reconstituted as a functional Ca^{2+} nanodomain is *Xenopus* oocytes (37, 38, 174). In this type of domains, VDCC channels are able to activate Slo1 channels in the physiological voltage range (Fig. 23B). However, in different neurons, Slo1 channels are fueled by different types of VDCC. N-type of VDCC are involved in the activation of Slo1 channels in hippocampal neurons (351) but P/Q- and T-type of VDCC control the activity of Slo1 channels in Purkinje neurons (123).

In the mammalian brain the Slo1 protein can be found as α-subunits alone or forming α/β4 complexes and to a lesser extend as α/β2 complexes (e.g., reference 206). In particular, clusters of channels formed by α/β4-subunits are expressed most exclusively in nerve terminal compartments (584).

In neurons, Slo1 channels serve functions like, for example, the repolarization of the action potential (222, 290, 517) and giving origin to the fast phase of the afterhyperpolarization following an action potential (1). The different roles played by Slo1 channels in the nervous system are possible because they show pre- and postsynaptic localizations being likely to found them in soma, dendrites, axons, and synaptic terminals. For example, in neurons from the hippocampus and cerebellum, the Slo1 α-subunit shows a distribution to the axons and presynaptic terminal (477).

In amygdala neurons, Slo1 is responsible of the repolarization and broadening of action potentials without affecting afterhyperpolarization (AHP) (130). In this cell type, the fast afterhyperpolarization (fAHP) is driven by voltage-dependent potassium channels sensitive to 4-AP and DTX but in other cells, as cerebellar Purkinje neurons, Slo1 is responsible only for the AHP (123). In this case, the pronounced AHP induced by Slo1 allows voltage-dependent sodium channels to recover from inactivation and fire the next action potential. Spike broadening during a train of action potentials is a common phenomenon in several neuronal types, and appears as a consequence of cumulative inactivation of voltage-dependent channels that leads to a slower repolarization (6, 150, 335). In hippocampal pyramidal neurons, trains of action potentials show a frequency-dependent spike broadening, which has been attributed to the progressive decrease in Slo1 currents due to Slo1 channel fast inactivation (493). This decrease in the Slo1 current reduces the amplitude of the AHP and the repolarization rate, causing that any successive action potential will have a smaller AHP and a slower repolarization.

During high-frequency (100 Hz) firing periods, Slo1 currents are responsible for the fast repolarization that allows the high spike frequency (177). This Slo1-induced increase in excitability is counterintuitive since in general is thought that potassium channels are involved in *decreasing* the cellular excitability. In this case, Slo1 channels are able to provide a fast repolarization and an AHP large enough to remove the inactivation of sodium channels.

Using $\beta4^{-/-}$ mice it was possible to show that this subunit is involved in decreasing excitability in the hippocampus dentate gyrus, thus protecting against hyperexcitability that can lead to temporal lobe epilepsy (59). β4 knockout

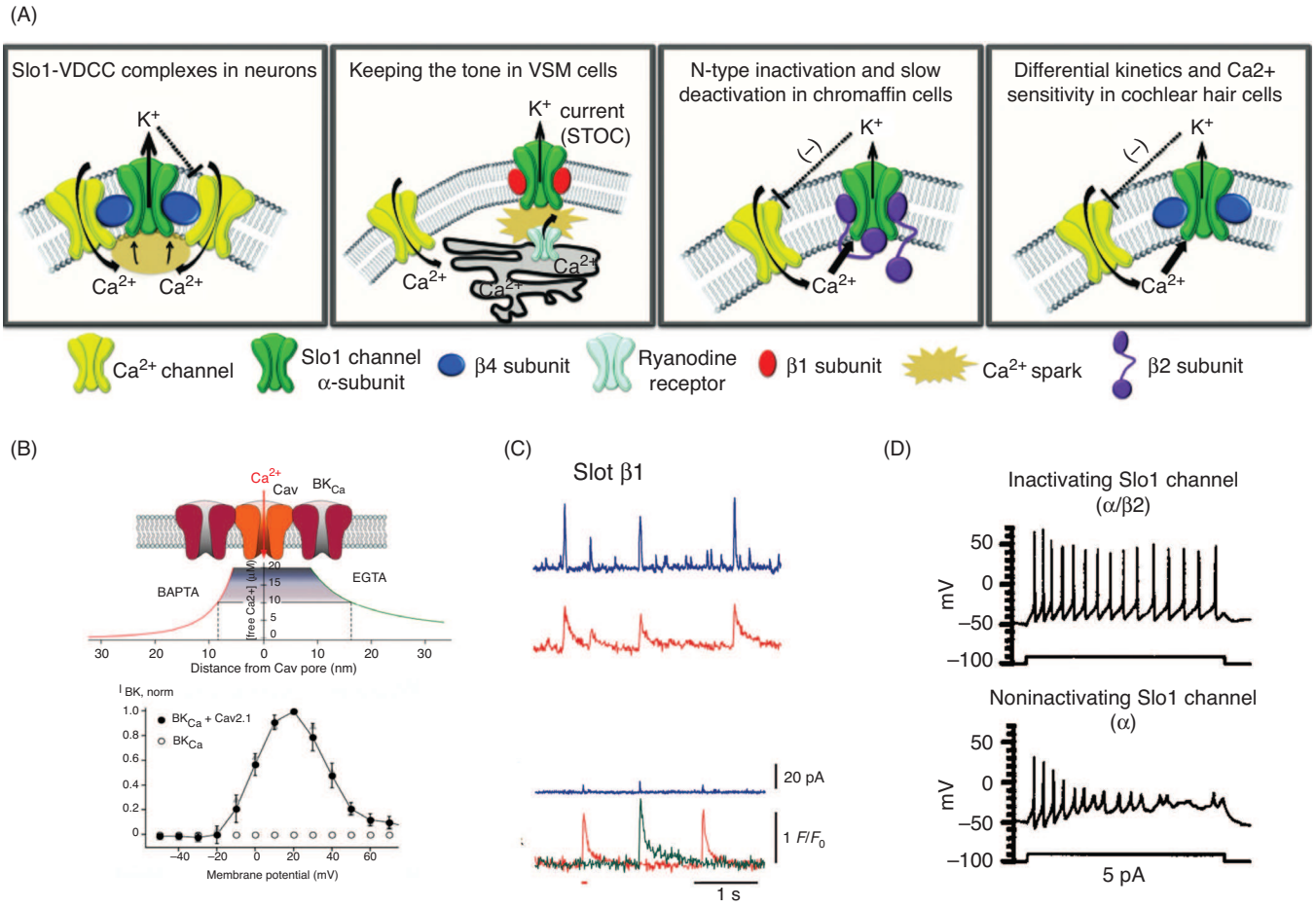


Figure 23 Physiological roles of Slo1 channels. (A) Proposed physiological roles of Slo1 channels. α- and β1-subunits are shown as cartoons. (Adapted, with permission, from reference 407.) (B) Thanks to the close proximity of Slo1 (BK_{Ca}) and voltage-dependent Ca^{2+} channels (VDCC), the increase of Ca^{2+} concentration induced by the opening of VDCC (up to 10 μmol/L in the neighborhood of Slo1 channels) promotes the opening of Slo1 channels (top). (Bottom) Current-voltage relationship obtained in an oocyte expressing only Slo1 (open circles) and coexpressing Slo1 and VDCC. The colocalization of these two channels allows an increase in the K^+ current that decreases when the potential approaches the reversal potential for Ca^{2+} indicating that K^+ currents were elicited by the increase in internal Ca^{2+} concentration induced by the VDCC opening. (Adapted, with permission, from reference 131.) (C) In vascular smooth muscle cells, β1-subunits confer the required Ca^{2+} sensitivity for effective coupling between Ca^{2+} sparks and spontaneous outward currents. [Adapted, with permission, from reference 61.] (D) In chromaffin cells, slowed Slo1 deactivation kinetics allows β2-subunit-expressing cells to fire a train of action potentials. (Adapted, with permission, from reference 508.)

mice lack any tonic or clonic behaviors but show paroxysmal synchronous discharges originated in the hippocampus and spreading to the cortex. Action potentials in $\beta4^{-/-}$ mice were shorter, have an AHP decay faster than those of wt mice and showed very little spike frequency adaptation, all features that allow a higher spike frequency. Addition of the specific blocker paxilline (168) does not affect wt cells, but produce a strong reduction in firing frequency in $\beta4^{-/-}$ cells, as well as returning action potential width, AHP decay time and interspike interval to wt levels. This result means that under normal conditions, Slo1-β4 channel complex in dentate granule cells is not active and it became active in $\beta4^{-/-}$ animals, possible because the β4-subunit decreases the calcium sensitivity so much that it never opens under physiological conditions. The Slo1 channel became active in $\beta4^{-/-}$ animals, where sharpens the action potential and support abnormal high-frequency firing.

A mutation in the Slo1 α-subunit has been linked to generalized epilepsy and paroxysmal dyskinesia (119). This is a gain-of-function mutation that promotes an enhanced Slo1 channel activity compared with that of the wild-type channel at the same calcium concentration and voltage. As discussed previously, this apparently counterintuitive result can be explained by the fact that activation of the Slo1 channel induces a faster action potential repolarization and thereby reduced neuronal refractory period. This mutation has helped much in the elucidation of the mechanism that mediates the coupling between Ca^{2+} binding and channel opening (see section on Slo1 channel structure).

It is important to mention here that chronic application of ethanol modulates Slo1 channel function and distribution in neuronal terminal. Chronically applied ethanol also induces a reduction in channel density, membrane clustering, and an increase in channel internalization (reviewed in reference 548).

On the other hand, single-channel experiments, cell and behavioral experiments taking advantage of β4 knockout mice strongly suggest that the β4-subunit is the molecular determinant of alcohol tolerance (352).

Smooth muscle

In VSMCs, Slo1 channels provide the adequate regulation of the contractile tone (297). Local Ca^{2+} increases, called Ca^{2+} sparks, generate spontaneous transient outward currents (STOCs), which are generated by Slo1 channels (Fig. 22A and C). This hyperpolarizes the membrane and promotes relaxation (233). In these cells highly Ca^{2+}-sensitive Slo1 channels are formed mostly by α- and β1-subunits. The physiological relevance of β1-subunits in modulating the Ca^{2+} sensitivity of the Slo1 channel was shown with β1-subunit knockout mice (61,431). The cerebral artery myocytes of these mice exhibited a decrease in the Ca^{2+} sensitivity of the Slo1 channels and a low Ca^{2+} spark-STOC coupling (Fig. 23C). This decreased coupling is responsible for an elevated arterial tone, which leads to an increment in arterial tone and blood pressure.

Role in secreting cells

By acting on target organs such as liver, adrenal gland, and gonads, hormones secreted by electrically excitable cells in the brain are crucial in the regulation of a number of physiological processes including reproduction and stress response. In this regard, adrenal chromaffin cells are a widely studied cell type. Rodent chromaffin cells fire spontaneously and their electrical activity is associated with basal release of catecholamines (386, 630). In this type of cells, L-type VDCC are tightly coupled to Slo1 channels and the action potential firing is modulated by the interaction between these two type of channels (435). In chromaffin cells, Slo1 channels can be either fast inactivating (BKi) or noninactivating (BKs) (Fig. 23D). In the former case, inactivation is induced by the amino terminus of the β2-subunit (N-type inactivation). Cells expressing BKi currents showed a higher firing frequency than BKs, due to a slower channel deactivation rate that produced an AHP able to remove the inactivation of sodium channels and make the cell fire at high frequencies (508). Slo1 channels formed by α/β2 complexes are most closely coupled to VDCC most likely the ones affecting the pacemaker currents (348,407,586,587).

In β-cells, due to the presence of the Slo1 β2-subunit, Slo1 currents activate rapidly and then inactivate and, suggesting that Slo1 channels colocalize with VDCC channels (505). In human β-cells activation of Slo1 channels decreases spike amplitude and addition of iberiotoxin increases insulin secretion by 70% (57). Slo1-knockout mice, on the other hand, are normoglycemic but show a markedly impaired glucose tolerance due to reduced glucose-induced insulin secretion. The glucose-stimulated β-cells from Slo1-knockout mice show broadened action potentials with an afterhyperpolarization greatly reduced (120).

Kidney

The α-subunit of the Slo1 and all the β-subunits subtypes have been found in the nephron (169, 170, 582). In the distal nephron, Slo1 channels are localized in the apical membrane of the principal cells where they mediate flow-stimulated kaliuresis. β1-knockout mice show a reduced fractional excretion of K^+, decrease glomerular filtration rate, and augmented excretion of Na^+ in response to acute volume expansion (432). Recalling that Kir1.1 underlies baseline luminal K^+ secretion (see Kir section), the K^+ secretion is ablated in the Kir1.1 knockout mouse by the administration of iberiotoxin, a result that strongly suggest that Kir1.1 and Slo1 are responsible for most of the K^+ secretion in distal tubules. As discussed previously, lack of the β1-subunit leads to hypertension, and this appears to have its origin in an increase vascular tone as well as a renal origin (169, 170).

Cochlea

In the frog, chick, and turtle auditory systems, which have been used as models of study of this sense, frequency tuning is performed almost exclusively by the hair cells (16). Each different hair cell has a characteristic tuning frequency. In these animals, electrical resonance is achieved through the interplay of L-type VDCC and Slo1 channels operating, as, for example, in the turtle, at frequencies from 30 to 600 Hz (137). The opening of L-type VDCC induced by depolarization increases internal Ca^{2+} concentration, which in turn activates Slo1 channels. Activation of Slo1channels hyperpolarizes the cell, closing Ca^{2+} channels, and promoting the membrane potential oscillation. Subsequent oscillations are damped, because fewer Slo1 channels are recruited in each cycle (17,137). The number and type of Slo1 channels control the resonant frequency of a particular hair cell. Higher frequencies are present in cells containing a large number of Slo1 channels with faster activation kinetics. The origin of this wide range of Slo1 gating kinetics is not completely clear at present but most probably is accomplished by differential expression of distinct splice variants of the Slo1 α-subunit, together with an expression gradient of α-subunit (137,248,291,441,453). α1-subunits add to the system a level of variability that cannot be achieved only with a splice variant expression gradient. It is of interest to note here that, as the frequency range gets wider, more diversity in the Slo1 channel is needed. Thus Fettiplace and Fuchs (137) modeled the electrical tuning in the turtle with five Slo1 splice variants, but in the chicken basilar papilla (150-4000 Hz), they needed a minimum of nine Slo1 splice variants. The main problem in attributing the tonotopic gradient to a differential expression of Slo1 channel splice variants is that they differ only slightly in their gating kinetics (371). The recent results of Miranda-Rottmann et al. (371) argue in favor of the hypothesis that the tonotopic gradient is mainly established on the basis of the gradient in expression of the α1-subunit and that is this gradient the responsible for the slowing down of Slo1 channels toward the low-frequency apex of the cochlea.

Mitochondria

BK channels are also found in mitochondria (mitoK_{Ca}) where they at present in the inner membrane and contribute to K^+ uptake (114, 592). Experimental evidence indicates that BK channels inmitochondria are involved in the protection of cardiomycytes from hypoxia and apparently inhibition of the α1-subunit mRNA expression contributes to cardioprotection after exposure to chronic hypoxia (28, 56).

Slo2

The Na^+-activated potassium channel (K_{Na}) was originally described in the cardiomyocytes in the 1980s (251), and subsequently they were identified in brain (117, 118). Due to its fast diffusion rate and the lack of large changes in the bulk concentration, Na^+ is not commonly thought as a cellular messenger. However, in dendritic domains closer to synaptic inputs, the Na^+ concentration after a short spike train can increase up to 40 mmol/L and up to 100 mmol/L after high-frequency stimulation similar to the one used to produce long-term potentiation (452). In the axon initial segment, the site of action potential initiation in most central neurons, Na^+ channels are found at a high density. The opening of these Na^+ channels promotes a raise in Na^+ concentration of the order of 3 to 30 times compared to that of the soma (144,272).

The two main routes of Na^+ entry to the cell are voltage-dependent Na^+ channels and glutamate-activated channels of AMPA and NMDA type (48). The K_{Na} channels may serve role of damping the excitatory signal mediated by Na^+ and glutamate-activated channels helping to avoid the deleterious consequences of the raise in internal Na^+.

The molecular identity of K_{Na} channels remained elusive until 2003, year in which two independent groups found that mammalian *Slo2* genes code for high-conductance potassium channels sensitive to intracellular sodium (47,606) (Fig. 21B). Actually, Slo2 was originally cloned in *C. elegans*, where it codes for a Ca^{2+}- and Cl^--activated K^+ channel, mainly expressed in body-wall muscle (605).

In mammals the two *Slo2* paralog, *Slo2.1* and *Slo2.2* code for proteins that give origin to tetrameric channels sensitive to internal Na^+ and Cl^- (466). These channels are also known as Slick (sequence like an intermediate conductance K^+ channel, Slo2.1) and Slack (sequence like a calcium-activated K^+ channel, Slo2.2). Similar to Slo1, these channels have a large single-channel conductance [60-180 pS (247,466)] and Slo2.2 can coassemble with Slo1 channels to produce channels with biophysical properties different to those of the parent channels. Moreover, both Slo2 channels can for heteromeres in heterologous expression systems, with kinetics and unitary conductance different to homomeric channels (96).

Expressed in heterologous systems, Slo2.1 shows a fast activation, low intrinsic voltage dependence, and an EC50 for Na^+ of 89 mmol/L. Slo2.1 shows a basal activity in the absence of Na^+ and is inhibited by intracellular ATP. Slo2.2 macroscopic currents show an instantaneous activation and a slow activating component, the EC50 for Na^+ is 41 mmol/L and does not show a basal activity in absence of sodium. The chloride dependence is more pronounced in Slo2.1 than in Slo2.2.

In excised patches some of the native K_{Na} are characterized by a fast and strong rundown in single-channel activity (124). In DRG neurons the fast rundown in K_{Na} activity can be reverted by increasing the Na^+ concentration suggesting that the lost of a diffusible factor responsible for the channels Na^+ sensitivity (124,535). A putative NAD+ binding is present in Slo2.1 and Slo2.2 and addition of NAD+ increases the open probability of native K_{Na} and Slo2.2 channels, indicating that lost of this diffusible factor is the cause of rundown in these channels.

Slo2.2 has several putative PKA and PKC phosphorylation sites. PKA is involved in internalization of channels and PKC increases the activity of Slo2.2 and decreases it of Slo2.1 (400,474). As Slo1, Slo2.2 has several splice variants from which Slack-A and Slack-B are the most frequently found (64).

Na-sensitive channels have a widespread expression in brain (46, 49) and several studies had addressed the roles of K_{Na} channels during action potential repolarization and AHP (reviewed in reference 48). In motoneurons from lamprey spinal cord, it has been reported the existence of both transient and persistent K_{Na} current activated by sodium influx (198). The transient K_{Na} current follows the action potential time course. There is a second persistent component, which disappear when sodium is replaced by lithium. In mammalian neurons only the persistent component has been observed (67). In lamprey motoneurons, the transient K_{Na} current appears at the peak of the action potential before the Kv current, contributing to the early repolarization and setting the spike peak and limiting the duration of the action potential. The K_{Na} component on the AHP is evident after a single-action potential, but is more prominent after spike trains and burst firing (562). The role of the sustained component is unclear at present. In the same cell type Na^+ influx through AMPA receptors also activated K_{Na} current acting as a negative feedback mechanism, decreasing the magnitude of the excitatory postsynaptic potentials and thus decreasing the excitability (384). In newborn rat motoneurons as well as in neocortical interneurons a K_{Na}-dependent slow AHP was observed after a train of action potentials (146, 460). Under voltage-clamp conditions lithium replacement induces a decrease in the sustained outward potassium current, consistent with the idea that a persistent K_{Na} is responsible for the slow AHP observed in neocortical interneurons. The fact that the K_{Na}-dependent slow AHP in lamprey motoneurons is evidenced after a single-action potential, suggesting that either K_{Na} channels are closer to the sodium influx source or the channel has a high sodium affinity (146,460).

In several neuronal types, K_{Na} channels are abundantly expressed as evidenced by the high probability to find it in single-channel studies or the big macroscopic current elicited in whole cell recordings (124, 400, 595). In a recent study,

Budelli et al. (67) found that Tetrodotoxin (TTX) application decreases the outward potassium current in 40% to 60%. The potassium current eliminated in this way was not inactivating and depends on the activity of persistent sodium channels. Selective elimination of Slo2.1 and Slo2.2 by RNAi dramatically decreases the effect of TTX.

Slo3

What is unique in Slo3 channels is that they are only found in mammals and remarkably they are only expressed in testis, specifically in developing spermatocytes and mature sperms (473, 484). Slo3 appears to play an important role in sperm capacitation, a process by means of which sperms become competent in fertilizing the ovule. The distinctive feature of Slo3 channel when expressed in heterologous expression systems is that its activity increases by intracellular alkalization (Fig. 21C). Other key features of Slo3 gating are: (i) maximal Po increases with increasing pH but to a maximum value of 0.3 and (ii) activation and deactivation kinetics can be fitted to two exponentials (Slo1 is fitted with only one) (625). Slo3 share with Slo1 the high sensitivity for Ba^{2+}, TEA, IbTx, and ChTx (537). In the selectivity filter, this channel has a phenylalanine instead of the canonical tyrosine found in most of the potassium channels, which confers a low-permeability discrimination between potassium to sodium (P_K/P_{Na} ~5-10, ~100 times less than Slo1) (473, 484).

By swapping C-termini between Slo1 and Slo3 it was found that the C-terminus of Slo3 is responsible for proton sensitivity (590). Slo3 is more related to Slo1 than to Slo2, it has seven putative TM domains (with an S0). This high rate of change is a characteristic of genes involved in reproductory functions, possible creating mechanisms involved in the speciation process (522). Bovine and mouse channels (bSlo3 and mSlo3) show differences in kinetics, voltage dependence, and pH sensitivities; features that were mapped to the C-terminus, one of the domains with the lowest sequence homology between the two channels (473).

In mouse sperm, an outwardly rectifying potassium conductance was identified (Ksper) with some of Slo3 features as its pH dependency and pharmacology (355, 387). A potassium conductance and intracellular alkalinization are needed for the phenomenon of capacitation to occur (387). In sperms, the resting membrane potential is driven by intracellular pH through Ksper channel (387). At pHi = 6 the Ksper is closed and the membrane potential is approximately 0 mV, while at pHi = 7 the channel is open which drives the resting potential to −54 mV. These results show that a proton-inhibited K^+ conductance is central in setting the membrane potential in sperms. In $Slo3^{-/-}$ mice several defects are evident under capacitation conditions such as impaired motility and failure to undergo achrosomal reaction, resulting in infertile animals (475).

Recently, Yang et al. (596) reported the association of Slo3 and β4-subunit, which was thought exclusively associate to Slo1. In heterologous expression systems, β4-subunit increased Slo3 macroscopic currents by increasing the number of channels in the membrane without affecting other parameters as single-channel conductance or open probability. Both subunits are present in mouse testis, which suggest that this interaction can occur in native cells.

Allosteric models account for most of the Slo1 channel gating properties

In this section, we will emphasize some of the highlights of the two-tiered allosteric model that is commonly used to explain the Slo1 channel activity (reviewed in reference 340). In the absence of Ca^{2+}, several closed (4-5) states and several open states (2-3) were necessary to explain the Slo1 single-channel activity (392, 532). Given the large number of closed and open states present in the absence of Ca^{2+}, the correlation between adjacent intervals (361) and the fact that the channel is a tetramer (see later), Slo1 channel gating in the absence of internal Ca^{2+} is consistent with the 10-state model indicated in Figure 24A. One of the predictions of this model is that even in the absence of voltage sensor activation, described by the equilibrium constant *J,* the channel can open through the reaction described by the equilibrium constant *L*. This prediction was confirmed by Horrigan and Aldrich (216) who found that in the absence of Ca^{2+} and at very negative voltages, the channel can open, albeit with a very low, but measurable, *Po* (about 10^{-6}) and a low voltage dependence, z_L, not related to the voltage sensors. On the other hand, a detailed analysis of the gating currents in the absence of Ca^{2+} suggests a two-state model, in which the voltage sensors transit between resting and activated (66) states, suffices to explain the voltage sensor movement (216). The simple behavior the gating charge-voltage [Q(V)] curves which are well described by a Boltzmann function, the monoexponential kinetics of the fast component of the gating current, and the lack of a gating current rising phase also are consistent with the kinetic model proposed in Figure 24A in which the voltage sensors act independently. In the allosteric model described in Figure 24A, for each voltage-sensor activated, the equilibrium constant for channel opening, *L*, is multiply by an allosteric factor *D*, so the opening process is facilitated as more voltage sensors are activated. The observation that even when all voltage sensor are resting, *Po* can be increased by augmenting intracellular Ca^{2+} is the basis for postulating the allosteric kinetic model depicted in Figure 24B under the assumption that there is only one Ca^{2+}-binding site per channel subunit (217). In this case, for each Ca^{2+}-binding site occupied the equilibrium constant *L* is multiply by an allosteric factor *C*. Figure 24A and B define the key feature of Slo1 channels: neither Ca^{2+} nor voltage are strictly necessary for channel activation and Ca^{2+}-binding and voltage-sensor activation can act independently to enhance channel opening. Thus, we are in the presence of three processes, Ca^{2+} binding, voltage-sensor activation, and channel opening, which are independent equilibriums that interact *allosterically* with each other. In support of the model shown in Figure 24B, Niu and

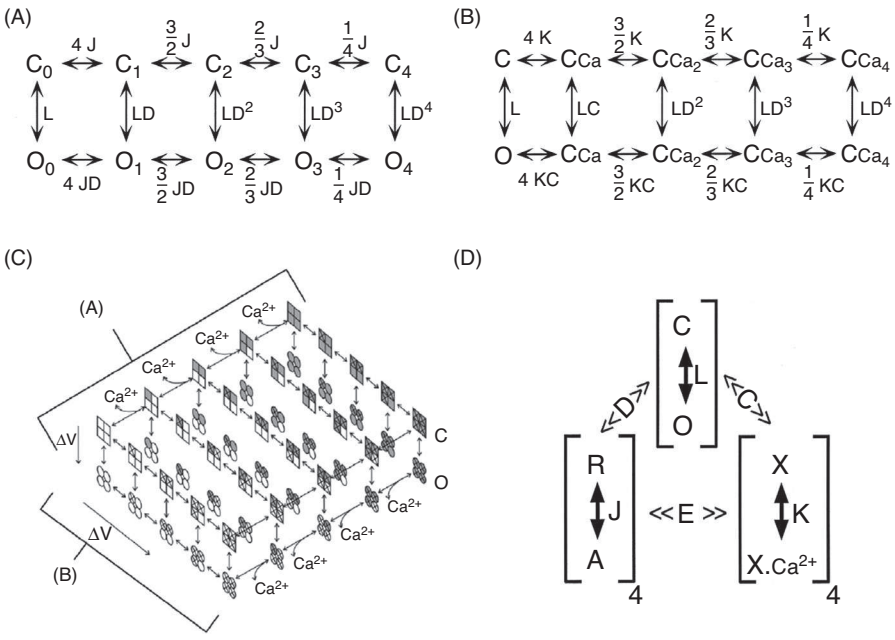


Figure 24 Allosteric models for Slo1 activation by voltage and Ca^{2+}. (A) Allosteric scheme for channel activation by voltage. *J* is the equilibrium constant governing the equilibrium between resting and active configuration of the voltages sensor. *D* is the allosteric factor and *L* is the intrinsic equilibrium for channel opening. Notice that the channel can open when all voltage sensors are in their resting configuration. (Adapted, with permission, from reference 217.) (B) Allosteric kinetic scheme for activation by $Ca2^{+}$. *K* is the equilibrium constant for calcium sensor activation and C is an allosteric factor. (C) The combination of A and B produces a two-tiered 50-state kinetic model. [Adapted, with permission, from reference 218.) (D) The complete allosteric model taking into account that Slo1 channels are tetramers and including some interaction between the voltage sensor and Ca^{2+} binding (allosteric factor *E*). In this type of mechanism neither voltage, nor Ca^{2+} binding is strictly coupled to channel opening, these three processes are independent equilibria that interact allosterically with each other. (Adapted, with permission, from reference 406.)

Magleby (396), using channels with 1, 2, 3, or 4 Ca^{2+} bowls, determined that the Hill coefficient increased in a stepwise fashion as the number of bowl increased from 1 to 4. This observation is consistent with models like the one shown in Figure 24B in which the Ca^{2+} binding to each of the sites is independent, and cooperativity arises as a consequence of the action of the allosteric factor *C*.

The best compromise between simplicity and reproduction of the voltage and calcium channel dependence in a wide range of voltages and Ca^{2+} concentrations, including very low *Po*s, is probably the 50-state two-tiered gating mechanism shown in Figure 24C (89, 455, 456). If some allosteric coupling (*E*; Fig. 24D) between Ca^{2+}-binding and voltage-sensor movement is included, the model increases to 70 states (217). The beauty of this model is that it is possible to set experimental conditions to determine some of the different parameters unequivocally. For example, in the absence of Ca^{2+} and at very negative voltages, channel gating kinetics is determined by the transition

$$C \overset{L}{\longleftrightarrow} O$$

and

$$Po = \frac{O}{O + C} = \frac{1}{1 + L^{-1}}$$

since

$$\mathrm{L} \ll 1, \quad Po \approx L = L0e^{(z_L FV/RT)}$$

Thus, under these experimental conditions, we are able to determine two parameters: *L0* and *zL*. This exercise allows us to arrive at another important conclusion: for the Slo1 channel, the limiting slope is actually determined by the *lesser* voltage-dependent transition and does not reflect the voltage-sensor charge effectively coupled to channel activation (6, 502).

Slo1 channel structure

The Slo1 channel is a homotetramer of its pore-forming α-subunit is a member of the Kv channels superfamily. As in all other Kv channels, the S4 TM segment is part of an intrinsic voltage sensor (89, 110, 336). Gating and ionic currents in Slo1 channels can be elicited by membrane depolarization in the absence of calcium, suggesting that this is a voltage-dependent channel (217,514). This divalent cation, by binding to sites contained the regulatory domain for K^{+} conductance (RCK) domains contained in the Slo1 C-terminus, acts as a modulator able to decrease the necessary energy to open the channel, promoting a leftward shift in the open probability (*Po*) vs. voltage relationships (reviewed in (340)).

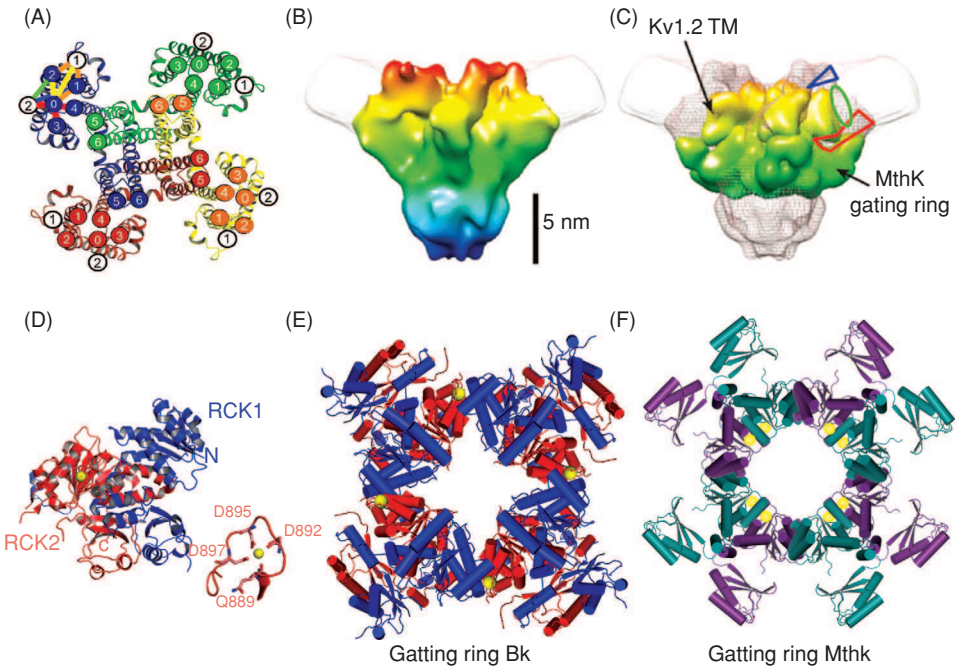


Figure 25 Structural organization of the Slo 1 channel and the crystal structure of the gating ring. (A) Transmembrane segments location using the cysteine cross-linking technique. Kv1.2/Kv2.1 chimera S1 to S6 with superimposed, labeled circles, uniquely colored for each subunit. White numbered circles correspond to TM1 and TM2 of the β1-subunit. (Adapted, with permission, from reference 565.) (B) Slo1 20 Å structure resolved with electron cryomicroscopy. The large protrusion at the periphery of the voltage sensor has been suggested to correspond to S0 and the external N-terminus. (C) Superimposed to the Slo1 structure shown in C is the structure of the transmembrane (TM) domains of Kv1.2 and the gating ring of the MthK channel (adapted, with permission, from reference 565). (D) Slo1 channel RCK1 and RCK2 domains of one subunit showing the position of the Ca^{2+}-binding site (calcium bowl) in the RCK2 domain. Calcium (yellow ball) is coordinated by D892/D895/D897/Q889 (modified, with permission, from reference 583). (E) Slo1 gating ring at 6 Å resolution. The ring is viewed down the 4-fold symmetry axis with RCK1 in blue and RCK2 in red. Calcium ions are shown as yellow spheres. (F) The open gating ring structure from the MthK channel viewed down the 4-fold axis of symmetry. Notice that a Ca^{2+} binds to the assembly interface in the Slo1 gating ring whereas two Ca^{2+} ions bind to the flexible interface in the MthK gating ring. (Modified, with permission, from reference 607.)

Transmembrane segments: S0, the voltage sensor and the pore

The Slo1 α-subunit contains seven TM segments; an extra one compared with others voltage-dependent K^+ channels (Kv), and a long C-terminus (364) (Fig. 21B). The minimal molecular component necessary and sufficient for Slo1 activity is its pore-forming α-subunit, and functional channels are formed as tetramers of this protein (495). Tetramerization is driven by an association segment (Slo1-T1 segment) located between the S6 and the α-helix denominated S7 in the intracellular C-terminal region (438). The additional TM segment S0, places the N-terminus toward the extracellular side and adds an extra intracellular linker between the S0 and the S1 compared to Kv channels (364). The exact position of S0 is unknown, but the experiments of Liu et al. (312), using disulfide cross-linking, indicates that S0 lies in close proximity to the S3-S4 loop. S0 is centrally positioned among the extracellular ends of S1 to S4 TM segments (Fig. 25A). A tryptophan scanning mutagenesis study of S0 suggests that the middle and the N-terminus of this TM segment are in direct contact with the voltage sensor domain (S1-S4) and that this interaction modulates the equilibrium between resting and active states of the channel voltage sensor (274, 489). We note here that, the physical association between the α1-subunit and the auxiliary β1-subunit requires the presence of S1, S2, and S3 segments. However, the functional coupling between these two subunits, that is manifested as an apparent increase in the Slo1 Ca^{2+} sensitivity and the Slo1 channel modulation mediated by 17β-estradiol (556) but not in the changes in gating kinetics, is determined by the Slo1 N-terminus residues (376).

The Slo1 structure recently resolved by electron cryomicroscopy at 17-20 Å, shows a large protrusion at the periphery of the VSD, which as has been suggested should to correspond with the additional helix S0 and the extracellular ~ 40 N-terminal residues of Slo1 α-subunit (565) (Fig. 25B and C). As with others Kvs, the α-subunit contain a positively charged TM domain (S4) with one residue directly implicated in the voltage sensing, the R213 [see Fig. 20C (110, 336)]. Unlike other Kvs, a large portion of the gating charge

movement is contributed by residues D153, R167 in S2 and D186 located S3 [Fig. 20C; (336)]. Voltage clamp fluorometry, on the other hand, revealed voltage-dependent conformational changes of the S3-S4 region of R207Q mutant of the Slo1 channel (410, 478) using the same technique found evidence of cooperativity between S2 and S3. Charge neutralization in one segment modifies the effective valence of the other and vice versa, a result explained by Pantazis et al. (410) assuming changes in the dielectric (dynamic field focusing) induced by the creation of aqueous crevices. In Kv channels the VSD is defined as the structure comprised by S1-S4 (238). Most probably, the architecture of the Slo1 VSD would be affected by the presence of the S0 segment and the results of Pantazis et al. (411) appear to confirm this hypothesis.

The pore domain of the channel is assigned to the region contained between S5 and S6 segments, which include the signature sequence of K^+ channel TVGYG. The external aspect of pore determine the block properties by charibdtoxin (ChTx), iberiotoxin (IbTx), and tetraethylamonium (TEA) (339, 370, 379, 495, 558). In general, the architecture of the conduction machinery of Slo1 channels is not different from that of other K^+ channels but multiple alignments show that the external loop (turret; Fig. 20C) between S5 and the pore helix of Slo1 channels contains several residues more than the other K^+ channels analyzed (75, 152). This difference in the turret length between Slo1 and Kv channels determines the specificity for only one subfamily of K^+ channel toxins, alpha-KTx1.x, of the Slo1 channel (152).

Experiments to determine the structural motifs by the high conductance in Slo1 channels (~250 pS) has shown a ring of residues in the inner vestibule entrance in the pore (E321 and E324) that allow to concentrate the K^+ ions in the inner vestibule trough electrostatic mechanisms doubling the conductance for outward currents with respect to low conductance Kv channels [Fig. 20C (58)]. Also, in the external vestibule near to the selectivity filter, the residue D292 would contribute to concentrate K^+ ions, increasing the conductance of inward currents (190).

Carboxy terminus

Some K^+ channels can be activated by a raise in the cytosolic Ca^{2+} and in two cases, the K^+ channels from the archeon *Methanobacterium thermoautotrophicum* (MthK) (236) and the SLO1 channel, it has been established that the Ca^{2+}-binding sites are contained in RCK domains. The structure of the RCK domain of a six TM domain K^+ channel from *E. coli* solved at 2.4 Å resolution has a Rossmann-fold topology, a very common structural motif found in enzymes and ligand-binding proteins. Rossmann-fold secondary structures are organized into two linked α-α-α-α-α units and were first identified in a number of NAD^+-dependent dehydrogenases. This is the type of structure present in the MthK and in the *Drosophila,* mouse and human Slo1 channel (Fig. 25D). The intracellular C-terminus domain, comprising two-thirds of the protein, contains four hydrophobic segments (S7-S10) and the Ca^{2+}- and Mg^{2+}-binding sites. As we show later, the C-terminus of Slo1 channels consists of two tandem RCK domains (Figs. 20B and 25E). The RCK domain in the SLO1 channel was initially unveiled by MacKinnon's group (239) by multiple sequence alignment of the SLO1 channel with prokaryotic K^+ channels and other proteins known to possess the RCK domain structure. We should mention here that based on the primary sequence, C-terminus domains structured as two RCK domains in tandem have been proposed for the K^+ channels Slo2 and Slo3 (466).

The sequence and predicted secondary structure of the cytoplasmic domain comprised by amino acid residues 339 to 516 in Slo1 that includes the S7 domain, are homologous to a RCK1 domain as that found in a number of K^+ channels (239). The existence of a second RCK domain (RCK2) contained in the distal part of the C-terminus received support in a structure-based alignment study of the C-terminus of the Slo1 and prokaryotic RCK domains. The structure proposed for Slo1 RCK2 (residues 712 to 999) includes the calcium bowl, and has the characteristic Rossman-fold topology of RCK domains. In addition, the putative RCK2 undergoes a Ca^{2+}-induced change in conformation associated with a α-helix to β-folded structural transition; deletion of the calcium bowl impairs this transition (610).

Recently, two groups determined the x-ray structure of the human SLO1 C-terminus at a 3 and 3.1 Å resolution, respectively (583, 607) The structures obtained confirmed two tandem RCK domains in each SLO1 α-subunit and the deduced tetrameric structure indicated that the SLO1 C-terminus forms a 350 kDa gating ring at the intracellular membrane surface. This study also confirmed that the Ca^{2+} bowl located within the second (RCK2) of the tandem RCK domains forms a Ca^{2+}-binding site. This site is located on the outer perimeter of the gating ring, in a region denominated the assembly interface (Fig. 25D and E). Thus, as is the case of the MthK channel, the resulting structure of the SLO1 gating ring is an octamer of RCK domains but different to the MthK channel where each subunit of the tetramer contributes one RCK domain, and another is assembled from solution, both RCK domains in the SLO1 channel are intrinsic to the α-subunit. This structural difference may give origin to the different places to which Ca^{2+} is bound in these two gating rings. In the MthK, Ca^{2+} binds on the "flexible" interface where a cleft between two RCK domains creates the Ca^{2+} binding site (Fig. 25F).

Coupling between Ca^{2+}-binding and pore opening

One important question is how the gating ring extracts the free energy of Ca^{2+} binding to open the SLO1 channel gates. It has been proposed that the RCK1-S6 coupling system is contained in the linkers, which behave as a passive spring that applies force to the gates in the absence of cytoplasmic Ca^{2+} to modulate voltage-dependent gating (397). An internal

Ca^{2+} increase changes the force and increases further the Slo1 channel open probability. We notice here that the crystal structure of the MthK-gating ring obtained in the absence of Ca^{2+} and comparison with the structure of the open MthK channel allowed to visualize the open and putative closed conformations of the Ca^{2+} binding domain (601). Calcium binding to each of the RCK domains induces an expansion of the gating ring that in turn can exert a lateral force on the pore opening the channel.

More recently, a clinical problem has come into our help to solve the structures involved in the allosteric coupling between Ca^{2+} binding and Slo1 channel opening (599). A mutation in the neighborhood of the N-terminus of the Slo1 RCK1, D434G, has been associated with human syndrome of generalized epilepsy and paroxysmal dyskinesia. This mutation is inside a region that encompasses the secondary structures βA-αC, hence denominated the AC region, contained in the N-terminus of the SLO1 RCK1 domain and enhances Slo1 channel activity in a manner not related to Ca^{2+} binding. The results indicate that this mutation increases Ca^{2+} sensitivity by augmenting the flexibility of the AC region strongly suggesting that it is or it is part of the coupling system that allows the transformation of chemical energy (Ca^{2+} binding) into mechanical energy (pore opening).

Location and structure of divalent binding sites in the SLO1 RCK domains

Partial deletion or point mutations of the aspartates contained in the calcium bowl in RCK2 produced Slo1 channels that were less sensitive to Ca^{2+} (reviewed in references 90 and 295). Amino acid residues Q889, D892, D895, and D897 in the calcium bowl coordinate the Ca^{2+} ion [(607) Fig. 25D]. The fact that disruption of the Ca^{2+} bowl did not completely eliminate the Slo1 channel sensitivity was a clear demonstration that there was more than one high Ca^{2+}-affinity site. The second high-affinity Ca^{2+} sensor was identified on the proximal tail region embedded within the upstream RCK1 domain including residues D367, M513, and E535 (23,583,589,622). Apparently, the Ca^{2+} bowl speeds up channel activation at low Ca^{2+} concentrations whereas the second high-affinity site (D362/D367) modulates both activation and deactivation at $[Ca^{2+}]$ more than 10 μmol/L (620). Surprisingly, the binding of Ca^{2+} to the high-affinity site contained in the RCK1 domain is voltage-dependent whereas at the Ca^{2+} bowl is not (526).

Additional research identified a third lower-affinity divalent cation-sensing domain in the RCK1 able to bind Mg^{2+} as well as Ca^{2+}. Mg^{2+} is coordinated at the interface between the voltage-sensor domain and the RCK1 domain to activate Slo1 channels (597). Potential residues contributing to Mg^{2+} coordination are E374 and E399 in RCK1 and D99 in the S1-S2 linker and N172 in the S2-S3 loop. Notably, E374 and E399, and D99 and N172 may come from neighboring subunits to form the Mg^{2+}-binding site. The proximity between the Mg^{2+} site and the voltage sensor, on the other hand, enables the electrostatic interaction between the bound Mg^{2+} and R213 contained in the S4 segment that in turn affects the displacement of the voltage-sensor giving an elegant mechanistic explanation to the Mg^{2+} Slo1 channel activation.

C-terminus and ion-binding sites in Slo2 and Slo3

For nematode Slo2 both Ca^{2+} and Cl^- are required to induce robust macroscopic K^+ currents but channel activation is much weaker in the presence of only one of these ions. This is qualitatively similar to what is observed for Slo1, that either Ca^{2+} or voltage is able to open the channel. For the case the *C. elegans* Slo2 channels, it has been postulated the existence of a "chloride bowl" composed of positive residues involved in chloride binding (605). Mutations of several of these positive residues to neutral residues produce channels with reduced sensitivity to Ca^{2+} and charge reversion produced channels insensitive to Ca^{2+} and Cl^-. However, chimeras between the chloride bowl of Slo2.1 and Slo2.2 (which have different chloride sensitivity) showed no differences with the parental channel Cl^- sensitivity, suggesting that the anion site is not located at this position (47). The fact that Ca^{2+} or Cl^- alone are unable to generate macroscopic currents and mutations in chloride bowl affect the sensitivity for both ions, suggests that both ions act synergistically to open the channel (605).

The sodium-sensing site in Slo2.2 has been recently map to the RCK2 domain, by homology to the sodium site found in G-protein-sensitive inwardly rectifying K^+ (GIRK) channels (622). Several putative sequences were found in Slo2.2 and finally D818 located in the RCK2 domain was the residue implicated in sodium sensitivity.

For Slo3, the proton-binding site is also located in C-terminal region, evidenced by chimeric channels between Slo1 and Slo3 as explained earlier (590). An allosteric model similar to that proposed for Slo1 channels has been proposed for Slo3 (625).

Small Conductance K^+ (SKCa, KCa2) Channel Family

KCa2 channels diversity and localization

Small conductance calcium activated potassium channels were originally discovered in red cells. SK channels are so named because they have a small conductance of approximately 10 to 14 pS (50, 416) Figure 26. SK channels are potassium channels that are activated by an increase in intracellular calcium. They were first cloned by Kohler et al. (271) and they are divided in three subtypes, KCa2.1 (SKCa1), KCa2.2 (SKCa2), and KCa2.3 (SKCa3), encoded by the genes *KCNN1*, *KCNN2*, and *KCNN3*, respectively (Fig. 27A). This family also includes an "intermediate conductance" channel KCa3.1 (IKCa1; Figs. 1 and Fig. 27A) encoded by the gene KCNN4. SKCa1-3 are neuronal and sensible to the bee venom apamin. The intermediate conductance, IKCa1, channel

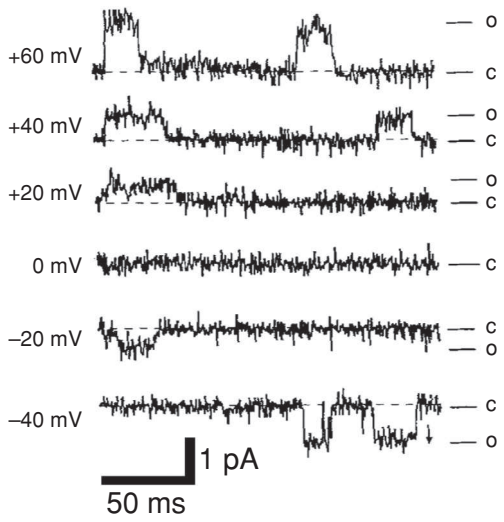


Figure 26 KCa2 channels activation: single-channel currents. Single-channel current from arterial chemoreceptor cells. The inside-out patch containing one observable open channel during 200-ms depolarizations from −80 mV to the indicated membrane potentials. Solutions: 130 mmol/L K, 0.01 mmol/L Ca^{2+}//130 mmol/L K, 10 mmol/L EGTA. (Adapted, with permission, from reference 149.)

is present mainly in non-neural cells and is not sensitive to apamin. The gene coding for KCa2.1 channel (KCNN1) has 12 exons, with 32 theoretical transcripts, 20 of which have been observed in mouse. Some splice variants can promote the binding of calmodulin to the channel [(621); see later]. The *KCNN4* gene also show alternative processing, producing three splice variants, one of which is expressed in VSM and the other two in endothelial cells (25). In distal colon epithelium, the *KCN4* gene is present in both apical and basolateral membranes. KCa2.1 and KCa2.2 are located in the CNS and KCa2.2 is also located in sensory cells, microglia, and cardiomyocytes. KCa2.3 is located in neurons and glia.

There are also two known isoforms of KCa2.3 channels, one isoform that is insensitive to traditional SK channel blockers and the other that behaves as a dominant negative, preventing the surface expression of all the KCa2.3 subunits (544, 575). The physiological roles of these splice variants are yet to be determined. KCa2 channels are thought to assemble as tetramers because of their similarity with voltage-gated potassium channels (Fig. 27B and C). In expression systems, human KCa2.1 and rat KCa2.2 channels can form functional homomultimers (271), whereas the rat KCa2.1, because of the inability of the C-terminus to mediate trafficking, is unable to reach the cell membrane (35, 105). The 32 splice variants found for KCa2.1 channels encode for at least 16 KCa2.1 polypeptides in the mouse brain. Differences reside in the C-terminus sequence, S6 domain, the calmodulin-binding domain and two predicted binding sites for PDZ[1] domain-containing proteins (499). KCa2.2 subunits can contain either a long or a short N-terminus (518), or lack S3, S4, and S5 TM domains, leading to nonfunctional channels (383).

KCa2.1 and KCa2.2 subunits are primarily expressed in the neocortex, hippocampus, amygdala, cerebellum, and brainstem, whereas KCa2.3 subunits are highly expressed in the midbrain, thalamus, cerebellum, and hypothalamus (see Fig. 29). The calcium sensitivity and wide subcellular distribution confers KCa2.2 channels with the ability to act as feedback regulators in many neuronal processes, including repetitive action potential firing, dendritic calcium rises, spine calcium rises, and endocannabinoid signaling. KCa2.1 and KCa2.2 channels tend to be more important in controlling dendritic integration, synaptic transmission, and synaptic plasticity, whereas KCa2.3 channels appear to be more important in controlling repetitive firing patterns (see Fig. 29).

Calmodulin confers Ca^{2+} sensitivity to KCa2 channels

KCa2 channels have six TM segments and a P loop region (between S5 and S6) containing the characteristic signature sequence GYGD of most K^+ channels, and intracellular N- and C-termini (Fig. 27B and C). Transmembrane segments of KCa2 channel subtypes are highly homologous and most of the divergence between these channels resides in their C- and N-terminal domains. Although the S4 segment contains two arginines (Fig. 27C), KCa2 channels are voltage independent.

KCa2 channels are highly sensitive to calcium, being activated in the submicromole per liter range (271, 416, 588), and low concentrations of intracellular calcium (EC_{50} of 300-700 nmol/L) induce very fast activation (515). Interestingly, the deactivation time constant is in the orders of tenths of milliseconds and is responsible for the long-lasting changes in membrane potentials, as for example, the medium after hyperpolarization (mAHP) of CA1 hippocampal neurons (488) (Fig. 29a).

In contrast with Slo1 channels that have calcium-binding sites in the α-subunit, KCa2 channels form a stable complex with calmodulin (CaM), a protein that act as the calcium sensor in nearly all eukaryotic cells [Fig. 28; reviewed in Mayle et al. (359)]. In the case of KCa2 channels it is the binding of calcium to calmodulin that leads to channel opening. CaM mediates calcium signaling by protein-protein interactions with other proteins in presence of calcium. CaM has four EF calcium-binding motifs, two located in the N-terminus, and the other two in the C-terminus [reviewed in Weatherall et al. (568)]. Mutant KCa2.2 channels with disrupted C-terminal sites did not show changes in calcium sensitivity (256) indicating that only the two N-terminal EF motifs are necessary for calcium sensitivity. The association of CaM with KCa2 channels is a target of pharmacological agents as the KCa2 activator 1-ethyl-2-benzimidazalinona (1-EBIO). This compound increases the affinity for Ca^{2+} in heterologously expressed channels by one order of magnitude, allowing

[1] PDZ is an acronym combining the first letters of three proteins—post synaptic density protein (PSD95), Drosophila disc large tumor suppressor (Dlg1), and zonula occludens-1 protein (zo-1)—which were first discovered to share the domain.

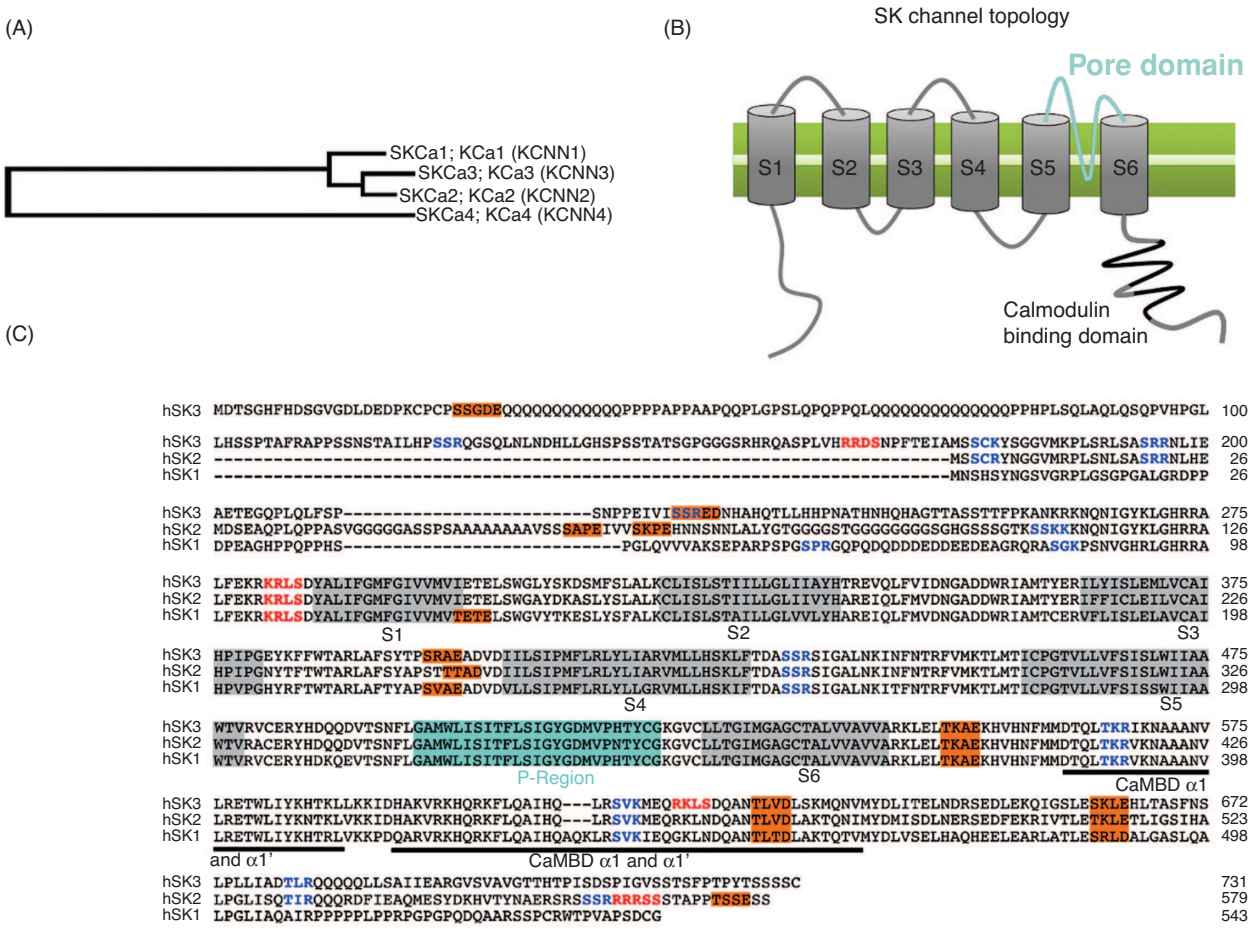


Figure 27 Topology of KCa2 channels and family dendogram. (A) Dendogram of the human SK channels genes constructed using t coffee and ClustalW. Genebank accession numbers: NC_000019 (KCNN1), NC_000005 (KCNN2), NC_000001 (KCNN3), and NC_000019 (KCNN4). (B) Proposed topology for KCa2 channels, showing a canonical six-transmembrane segments organization (S1-S6) whence S5 and S6 form the ion-conduction pathway (shown in cyan) and the S4 segment. The intracellular Ca^{2+} regulation is given by the calmodulin-binding domain (CaMBD) located in the C-terminus (black segment). (C) Sequence alignment of the human SK channels (hSK1, hSK2, and hSK3). The transmembrane segments, S1 to S6, are boxed in gray. The pore region (P-Region) is boxed in cyan. The CaMBD is indicated by black bars. Orange boxed amino acids and red residues show different phosphorylations sites conserved along the family. (Adapted, with permission, from reference 424.)

channel activation at Ca^{2+} concentrations as low as 50 nmol/L (423). The main effect of 1-EBIO is to slow down the deactivation without affecting the activation. The effect of EBIO on the calcium sensitivity disappears if the N-terminal EF motifs of CaM are mutated, suggesting that this drug affect the CaM-KCa2 channel interaction.

Once activated, potassium currents through KCa2 channels shows inward rectification (271), which in KCa2.2 channels has been attributed to a voltage-dependent block by divalent cations that bind within the selectivity filter (506, 507).

Crystal structure, channel trafficking, and assembly

Crystallographic evidence suggest that four CaM molecules are bound to the channel, within a region in the SK channel that has no homology with CaM-binding regions in other proteins (486). This CaM-binding domain (CaMBD) is located adjacent to S6, and it has a short and a long α-helix connected by a loop (Fig. 28). In the crystal structure of CaM-CaMBD complex, the α-helices of two CaMBD run antiparallel to each other, making contact with two CaM molecules. Crystallographic and biochemical evidence suggest that in absence of Ca^{2+}, CaM-CaMBD complex are monomers, which dimerizes when calcium is bound (486). It has been hypothesized that when calcium is bound, dimerization of CaMBD produces a conformational change that allows S6 to rotate and open the channel gate (588).

CaM also is important for the sorting of KCa2 channel to the plasma membrane. In IKCa1, the expression of isolated CaMBD prevents the assembly of CaM to the channel, and result in retention of the protein in intracellular organelles that can be overcome by CaM overexpression (246). In the absence of free CaM, channels do not multimerize, causing retention

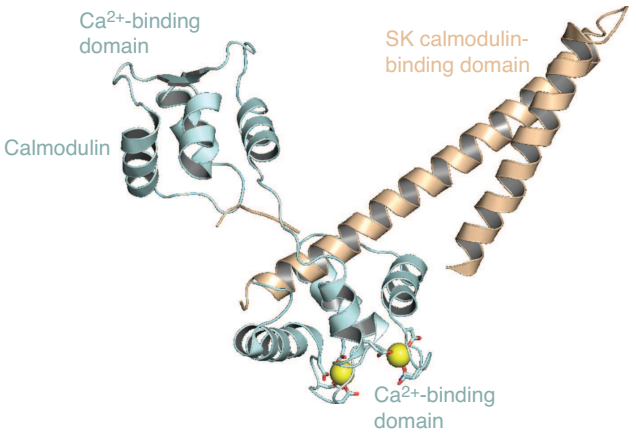


Figure 28 KCa2 channel C-terminal calmodulin-binding domain. Calmodulin protein and KCa2 C-terminal calmodulin-binding domain complex was crystallized at a 1.6 Å resolution (PDB: 1G4Y). Calmodulin protein is shown in cyan with two of the four calcium bowls occupied by Ca^{2+} (yellow balls). The center of the calmodulin molecule is in contact with the KCa2 C-terminal domain (pale brown) (486).

at subcellular locations. In the crystal structure, CaM and CaMBD form saline bridges between residues R464/L467 in KCa2.2 Channels with the double mutation R464E/L467E, have a low affinity for CaM, consistent with these residues being located at the CaM-CaMBD interface (486). This low CaM affinity can be overcome by overexpression of CaM or a CaM mutant unable to bind Ca^{2+} (300). The double mutant R464E/L467E does not express in the membrane by itself but it does when coexpressed with CaM, suffering a robust rundown after patch excision. This rundown is due to CaM washout, and can be rescued if an excess of recombinant CaM is perfused in the bath. This evidence suggests that CaM is essential for channel multimerization at subcellular compartments. However, the channel can be present as tetramers in the plasma membrane in the absence of CaM, but proper function requires of the presence of the Ca^{2+}-binding protein.

Rat KCa2.1, KCa2.2, and KCa2.3 channels can form functional heteromultimers in expression systems (35,374), while *in vivo*, immunoprecipitation, expression, and pharmacological studies suggest that KCa2.2 and KCa2.3 channels form both homomultimers (422, 463) and heteromultimers (518). KCa2.1 and KCa2.2 channel proteins show distinct subcellular distributions in rat brain regions such as the neocortex and hippocampus, suggesting that they may form homomultimeric channels in these regions (463, 464).

Localization of the KCa2 channel activation gate

The location of the activation gate in KCa2 channels appears to be different to that of Kv channels. Accessibility of MTS reagents to cysteines engineered in Kv channels showed that the K^+ access to the selectivity filter is controlled by the bundle crossing formed by the intracellular end of the sixth TM domain (S6) of each of the four channel subunits (313). Cysteine residues in the S6 are modified by MTSET at a faster rate in the open than in closed states, as observed for Kv channels. However, the smaller molecule 2-(aminoethyl) MTS (MTSEA) also modifies a residue located just below the selectivity filter at the same rate irrespective of the channel state (65). This evidence suggests that the gate is located in or very close to the selectivity filter. The state-dependent accessibility changes of S6 can be explained as rotation of the TM helix due to the conformational change that calcium binding to CaM imposes to the channel structure.

Physiological roles

The most explored role for SK channel is its involvement in the mAHP following an action potential. Due to the activation of VDCC during the rising phase of the action potential several types of calcium-activated conductances develop. The fAHP in CA1 neurons is carried by BK channels [(1, 290, 461); see section on Slo channels]. The mAHP is also Ca^{2+}-dependent and inhibited by nanomolar concentrations of apamin and it can last tenths to hundred of milliseconds, depending on the neuronal type (186, 427, 434). This long hyperpolarization is responsible for long interburst events as well as determining the firing frequency within a train and its origin resides in a very slow deactivation compared with the channel activation (175, 176, 341).

Potassium channels are involved in the repolarization of action potentials, where there are three phases: the fAHP controlled by Kv and Slo1, the medium AHP which is sensitive to apamin, and the slow whose molecular identity is unknown. The activation of SK channels depends on calcium influx from VDCC during the rising phase of the action potential, and in some system also from intracellular calcium stores.

In several neuronal types as CA1 pyramidal cells, the fAHP is carried by Slo1 channels and is sensitive to IbTX and low TEA concentration (175, 493). The mAHP is also calcium dependent but inhibited by nanomolar concentration of Apamin and can last tenths to hundred of milliseconds, depending on the neuronal type (Fig. 27A) (reviewed in references 54 and 129). This long hyperpolarization is responsible for long interburst events as well as determining the firing frequency within a train (79). The mAHP decays over several hundred milliseconds, consistent with the slow deactivating kinetics observed in heterologous systems (588) (reviewed in references 129 and 515). mAHP is present in cortical structures as neocortex, hippocampus, amygdala; and also in other structures as substantia nigra, hipothalamic nucleus and, *globus pallidus*, *locos ceruleous*, among others (reviewed in reference 129). A prototypical role of SK activation is mAHP in CA1 neurons, where apamin decreases the number of action potentials and decreases the extent of AHP in short trains, without affecting other properties as spike frequency adaptation (516, 554). By using KO animals of the three neuronal SK channels, it was observed that only SK2 $^{-/-}$ animals show elimination of mAHP in CA1 pyramidal neurons (509). However, more recent evidence shows that mAHP is mediated by M and H currents (175, 176). The possible explanation for

this discrepancy is that previous studies were performed under voltage-clamp conditions, in which a long (10-50 ms) is used to elicit mAHP, while the recent publications reported current-clamp recordings, in which action potentials last 1 to 2 ms. This difference in depolarization duration can account for an increased calcium influx in voltage-clamp experiments. In this context, is possible that under low-frequency stimulation H and M currents account for mAHP, while SK becomes relevant under higher frequencies where calcium is bigger, or under a calcium spike.

The distal dendrites of CA1 neurons show regenerative events called plateau potentials, which are local membrane depolarizations that no propagate to adjacent branches (570). This potential is generated by calcium entry trough dendritic VDCC. Dendritic SK and Kv4 channels are responsible for maintaining this compartmentalization (70). Local apamin in the distal dendrites increases the plateau potential duration and calcium influx (Fig. 29A); however, do not prevent compartmentalization. Kv4 channels decrease the amplitude of plateau potentials, preventing its propagation to the adjacent branch. Thus, SK conductance controls duration and Kv4 the amplitude of depolarization inhibiting compartmentalization, thus both acting coordinately to regulate synaptic integration.

SK channel block increases the LTP induction after high-frequency stimulation, and improve the performance of spatial learning tasks (509). It is possible that NMDA receptors and KCa2 channels are closely located at dendritic spines, a hot spot for LTP induction, where KCa2 channels decrease the magnitude of depolarization evoked for NMDA channel activation.

Dopaminergic (DA) neurons of the midbrain have a pacemaking behavior with a slow (0.6-4.3 Hz) firing rate at physiological conditions (576). Blocking of KCa2 channels leads to an increase, while activation by 1-EBIO produce a decrease in firing frequency. Firing precision is high in this neuronal type, with a low coefficient of variation (CV) and single Gaussian fit of interspike interval (ISI) duration histogram (Fig. 29B). Increasing the number of blocked channels by increasing the concentration of blockers, leads to a decrease in firing precision that is reflected as an increase in the CV and the inability of fit the duration histogram with a single Gaussian (576). Biophysical and pharmacological analysis, single-cell mRNA, and protein-expression profiling strongly suggest that KCa2.3 channels mediate the calcium-dependent afterhyperpolarization in DA neurons (228,576).

mAHP is blocked when inhibitors of T-type VDCC are presents, suggesting that these types of Ca^{2+} channels are the calcium source needed to activate KCa2 (577). Inhibition of T-type channels decreases mAHP with the same IC_{50} value estimated for VDCC. In addition, KCa2 current follows the time course of the cumulative inactivation of T-type channels. All these evidences strongly suggests that KCa2 channels are functionally coupled to T-type VDCC. As observed when KCa2 channels are blocked, T-type channel blockage also decreases the precision of firing, seen as an increase in the CV. In a subset of cells with a high basal CV, blockage of T-type channels leads to an increase in burst firing. Therefore, T-type VDCC stabilizes peacemaking firing and reduce the probability of neurons entering into a burst-firing mode.

In dopaminergic neurons from young animals there is a calcium release from intracellular stores that produces spontaneous miniatures outward currents (SMOCs) through KCa2 channels (88). L-type calcium channel blockers inhibit the large-SMOC and depletion of intracellular calcium stores by ryanodine or cyclopiazonic acid (CPA) eliminates the SMOCs, suggesting that Ca^{2+} influx through VDCC activates a calcium-induced calcium release (CICR), which in turn activatesKCa2 channels.

Metabotropic activation of SK, lasting even minutes, has been reported in several cortical structures, all of them mediated by second messengers cascades (reviewed in reference 129).

DA projections in several brain areas are involved in motor functions, working memory, reward, and goal-directed behaviors. Since KCa2 channels control repetitive firing and suppress burst generation in dopaminergic midbrain neurons, these channels play an important role in controlling the amount of dopamine released by these cells.

Cerebellar Purkinje neurons are the only cell type that sends projections out of the cerebellar cortex. This neurons show tonic firing which is maintained by several types of ion channels: transient and resurgent sodium channels, fast activating potassium channels, T-type calcium channels, hyperpolarization activated ion channels, and calcium-activated nonselective cationic conductances (30,353,440,527). Block of Kca2 channels with apamin in tonically firing Purkinje neurons produce a burst-firing behavior, and an increase in CV (Fig. 29C) (580). There is a population of cells that fire in a trimodal pattern consisting of firing, bursting, and silent periods (578). In this group of cells apamin reduces the duration of tonic and bursting periods, without affecting the silent period (580). The calcium entry needed for opening SK channels come through P/Q-type calcium channels (579). In a mice model of cerebellar ataxia that expresses a mutated P/Q-type calcium channel, the precision of firing of Purkinje cell is decreased (561). This is restored by activation KCa2 channels with 1-EBIO, suggesting that the role of P/Q-Type VDCC is to provide a calcium source that leads to the opening of SK channels (579).

By using an action potential as the command waveform in voltage clamp mode, it is possible to record the membrane currents in dissociated Purkinje neurons (527). Analyzing short bursts, during the first ISI the Kv current decays faster than calcium-dependent potassium currents, which do not change much during this period. In successive spikes, Kv current decreases due to cumulative inactivation; however, since Slo1 and SK channel activity is strongly coupled to the activation of VDCC, KCa current remain stable during Purkinje neuron burst activity, being the most important potassium conductance at the end of the ISI. Slo1 currents, as described in previous section, is active in the falling part of action potential, and undergoes a decrease in magnitude after successive

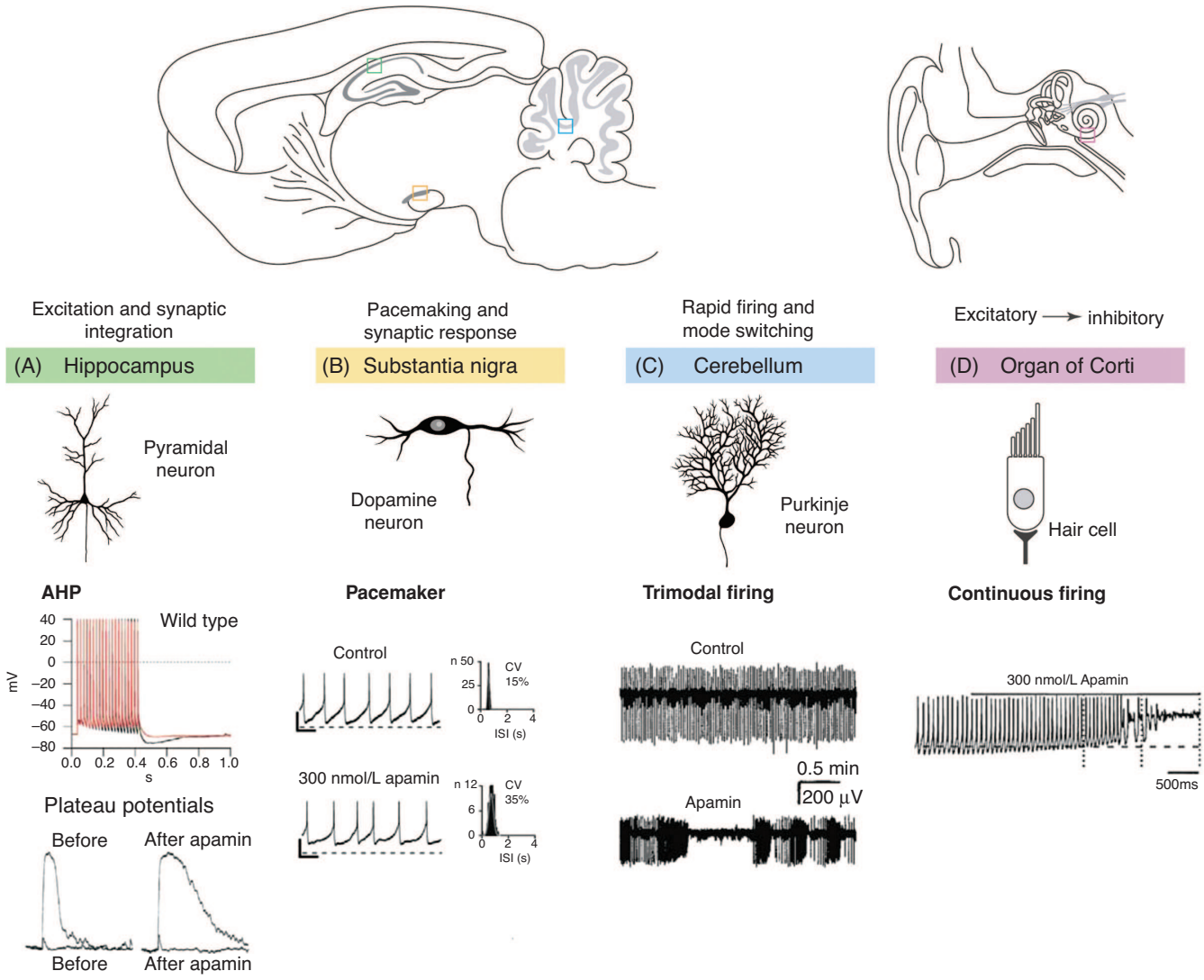


Figure 29 Physiological functions of KCa2 channels. Schematic representation of SK channel function in central nervous system (A) afterhyperpolarization (AHP): CA1 pyramidal neuron whole cell current clamp recording. Twenty action potentials were elicited at 50 Hz in control (black) or apamin (red, 100 nmol/L) bath solutions. The control trace shows the development of an interspike AHP and a posttetanus AHP that is blocked by apamin. Plateau potentials: apamin prolonged the duration of the plateau potential but did not affect the amplitude. (B) Substantia nigra. Pacemaker: perforated-patch current-clamp recording of a dopamine neuron in control or apamin (300 nmol/L) bath solutions. On the left is a 4 s trace representative of a 5-min recording. On the right, the interspike interval (ISI) frequency distribution is plotted for each recording. Apamin significantly decreased the pacemaker precision as shown by the increase in the coefficient of variation (CV). (C) Cerebellum. Trimodal firing: extracellular field recordings of individual cerebellar Purkinje neurons the tonic activity of the cells changed to random bursting when 100 nmol/L apamin was bath applied. (D) Auditory hair cells. Continuous firing: whole cell patch current-clamp recording from inner ear hair cells in the acutely dissected organ of Corti of a P5 rat. Voltage responses induced by a continuous 30 pA depolarizing current from the resting potential of –59 mV are shown. Bath application of 300 nmol/L apamin gradually abolished the evoked action potentials, indicating that KCa2 channel activity is necessary for continued firing. (Modified, with permission, from reference 54.)

action potentials, probably due to inactivation (440). In contrast, KCa2 current increases with successive action potential, possibly due to a calcium increase, which is responsible for the burst termination (527). KCa2 channels blockage with apamin produces a robust increase in burst duration, reinforcing the idea of SK channel as regulators of firing behavior.

In auditory OHCs the IPSPs are due to acetylcholine release. In this cell type the nicotinic acetylcholine receptors (nAChR) contain the α9-subunit, which confers calcium permeability to these type of channels (126). KCa2 channels are strongly coupled to nAChR, and the kinetics of IPSPs is determined by KCa2, but not calcium diffusion. Inner hair cells (IHCs) also receive cholinergic afferents but only during early postnatal stages. During this period, a Ca^{2+}-dependent and apamin sensitive potassium conductance is present (349). Apamin increases the firing frequency and reduces the extent of AHP, leading finally to a steady depolarization (Fig. 29D). This means that Kv channels are not sufficient to maintain firing, in contrast to cerebellar Purkinje cells where apamin does not suppress neuron electrical activity.

Pharmacology of SK channels

SK_{Ca} channels are blocked by different pharmacological agents, including the bee toxin apamin (50,68,450,463,464), tubocurarine, quaternary salts of bicuculline such as bicuculline methiodide and bicuculline methochloride (245,491), the scorpion toxin scyllatoxin (77, 101), NS8593 (519), dequalinium, UCL1848, and a number of bis-quinolinium cyclophanes (73,97,121). More recently, the reversible blockers *N*-methyl-laudanosine (NML) and methyl-noscapine (167, 480), bis-quaternary isoquinoliniums (165), and lipophilic tetrahydroisoquinoline derivatives (166) have been developed. There are also a number of KCa2 channel openers available. EBIO, which enhances the calcium sensitivity and open probability of SK_{Ca} channels, dichloro-EBIO (DCEBIO), and NS309 (403, 423). Finally, buffering intracellular calcium with high concentrations of 1,2-bis(o-aminophenoxy)ethane-N,N,N′,N′-tetraacetic acid (BAPTA) or Ethylene glycol tetraacetic acid (EGTA) also blocks activation of SK channels (462,487).

Apamin-binding site

Blockade of KCa2 channels by apamin allowed their initial characterization and provided insights into subunit composition due to the differential sensitivity of K^+ channel subunits to apamin (50,68,173,450). KCa2 channels are blocked by nanomolar concentrations of the honeybee toxin apamin. KCa2.2 is blocked with the highest affinity (27-140 pmol/L), KCa2.1 has the lowest affinity (0.7-12 nmol/L), and SKCa3 has an intermediate affinity (0.6-4 nmol/L) (424). These differences in toxin sensitivities have been used to distinguish between channel types in native systems. Point mutations in the extracellular vestibule of KCa2.1 to the residues present in KCa2.2 increase the affinity for apamin of KCa2.1 to the same levels of KCa2.2 channels. The use of chimeras between several KCa2.1/2.2 channels, allowed the identification of the extracellular S3-S4 loop as one of the molecular determinants of apamin sensitivity. This finding gives an economical explanation to the fact that some scorpion toxins can strongly displace ^{125}I-apamin, without affecting channel ion conduction (492). The binding site for apamin is located in both the pore region, between S5 and S6, and on a serine residue located in the extracellular region between S3 and S4. The lower sensitivity of KCa2.1 channels to apamin compared to KCa2.2 channels is due to replacement of this serine residue with a threonine on the KCa2.1 subunit.

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