New Disguises for an Old Channel: MaxiK Channel β-Subunits

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Ca2+-activated钾离子(K+)通道中的大型转导器（MaxiK或BK通道）控制一系列生理过程，包括平滑肌张力、神经分泌和听觉。尽管被编码由单个基因（Slowpoke），MaxiK通道的多样性巨大。调节β-亚单位、剪接和代谢调节创造这种多样性的必要性在于许多生理功能。

Molecular properties of MaxiK channels

The minimal molecular component necessary and sufficient for MaxiK activity is its pore-forming α-subunit, and functional MaxiK channels are formed as tetramers of this protein. First cloned from Drosophila, the gene encoding for MaxiK was called Slowpoke or Slo, and after the description of the Slo2 and Slo3 channels (see below) it was renamed Slo1. The presence of a positively charged fourth transmembrane segment makes the MaxiK channel a member of the S4 superfamily. Most members of this superfamily have six transmembrane segments, called S1 to S6, but MaxiK channels have a seventh transmembrane segment at the NH2 terminus, called S0. Thus, the NH2 terminus of the protein is placed in the extracellular side of the membrane (Fig. 1). The intracellular COOH-terminal domain comprises two-thirds of the protein and contains four hydrophobic segments and several alternative splicing sites (Fig. 1).

The pore domain of the channel is assigned to the region contained between S5 and S6 segments, which includes the signature sequence of K+ channels (TVGYG). As in all other voltage-dependent K+ channels, the S4 segment is (or is partially) an intrinsic voltage sensor, which is the actual trigger for MaxiK activation (8). Gating and ionic currents in MaxiK channels can be elicited by membrane depolarization in the absence of Ca2+, suggesting that this is a voltage-dependent channel. The divalent cation acts as a modulator able to decrease the necessary energy to open the channel, as can be inferred from the leftward shift in the open probability vs. voltage (Popen-V) relationships (Fig. 2).

Recently, a tetramerization domain has been identified for the MaxiK channel in a hydrophilic region located between the S6 and S7 hydrophobic segments (10). This is the only hydrophilic region capable of self-association, forming stable tetramers in solution. In functional assays with truncated channels, this domain proved to be necessary for a dominant negative feature, suggesting its involvement in tetramerization.
This region was named BK-T1, resembling the T1 domain of voltage-dependent K+ channels, which is also involved in tetramerization. However, these domains are different both in amino acid sequence and localization.

The region from the S8-S9 linker to the end of the protein is called the “tail” and can be expressed as a separable domain. Its coexpression with the rest of the channel (the “core”) produces functional channels, whereas neither of the parts alone forms functional channels. The Ca2+-binding site has been located to this large intracellular domain, between the hydrophobic segments S9 and S10 (8). This region, frequently called the “Ca2+ bowl” (Fig. 1), is highly conserved in all cloned MaxiK channels and contains an Asp-rich (-QDDDDDD-) sequence motif, emerging as a very good candidate for a Ca2+-binding site. A study using chimerical channels between Slo1 and Slo3 confirmed the localization of the Ca2+ sensitivity to a region comprising the end of the S9-S10 linker and part of the S10 hydrophobic segment (13). On the other hand, direct 45Ca2+-binding studies were performed by using a fusion protein consisting of the last 280 amino acid residues of the Drosophila Slo1 (dSlo1) channel in an overlay assay (1). By replacing all Asp residues with the uncharged residue Asn, they showed that the Ca2+ bowl motif accounts for only 56% of 45Ca2+ binding. This implies the existence of more than one Ca2+-binding site per tail domain: a low-affinity and a high-affinity site (the latter being the Ca2+ bowl).

The Slo family

The MaxiK channel is not the only member of its family. Another two members have been described: Slo2 and Slo3 (12, 20). The Slo2 gene was cloned from the worm Caenorhabditis elegans, and Slo3 was identified from a testis cDNA library.

Slo2 needs the presence of internal Cl− to be activated by Ca2+, and the sensitivity to these two ions is strictly coupled. Slo2 lacks a S0 domain and an apparent intrinsic voltage sensor since the S4 domain is uncharged (Fig. 1). Surprisingly, Slo2 is a voltage-dependent channel, albeit with a smaller voltage dependence than Slo1. The Slo2 gene has a mammalian ortholog called Slack.

Slo3 shares the same membrane topology with Slo1 and is also voltage dependent. However, Slo3 is regulated by intracellular pH instead of internal Ca2+; increasing pH increases Po.

Sources of MaxiK channel diversity

It is not only changes in membrane potential and Ca2+ concentration that result in modulation of MaxiK channel activity. There is evidence of changes in MaxiK channel activity by phosphorylation and/or interaction by G proteins, by mechanical stretch, and by various endothelium-derived vasoactive substances (8, 17). All of these modulatory mechanisms allow fast integration of multiple stimuli in many tissues, including neurons, VSMCs, and cochlear hair cells. The Drosophila α-subunit (dSlo) can interact with two different accessory proteins, known as dSlip1 and Slob. Both are soluble proteins that can physically interact with MaxiK channel by its intracellular face. Whereas Slob increases the channel Po, dSlip1 seems to decrease the number of MaxiK channels in the plasma membrane.

Alternative splicing creates channels with different kinetics and Ca2+ sensitivity. Most splicing sites are located in COOH-terminus of the Slo1 protein, and several sites reside between hydrophobic domains S8 and S9 (8). However, differences between splice variants are modest when compared with the effect of coexpression with β-subunits. It is interaction with these accessory proteins that creates really different MaxiK channels, which, with the other regulatory mechanisms, can be finely tuned to perform their physiological roles.

The β-subunits

Regulatory β-subunits share a putative membrane topology, with two transmembrane segments connected by a 120-residue extracellular “loop” and with NH2- and COOH terminals oriented toward the cytoplasm (Fig. 1). The loop has three or four putative glycosylation sites. At present, four β-subunits have been cloned in mammals (2, 7, 9, 15, 18).

Sequence similarities are major between β1–β2 and β2–β3, respectively. β4 is the most distantly related of all β-subunits. β-Subunit orthologs have not been described in Drosophila or in the worm C. elegans, suggesting that this protein is a “novel” acquisition in evolution.

The first β-subunit was identified as a protein associated with
The next cloned β-subunit was identified by searching homologues to the β1-subunit in human expressed sequence tag (EST) databases. This new subunit is expressed preferentially in chromaffin cells and brain and was dubbed β2 (18). The most notorious difference from the β1-subunit is an NH2-terminal domain that contains a hydrophobic region followed by positively charged residues. This type of sequence is characteristic of inactivation peptides that can occlude the conduction pathway of Shaker K+ and of MaxiK channels. Consequently, coexpression of α- and β2-subunits produces inactivating currents, such as those seen in some chromaffin cells (see below). Removal of the NH2-terminal domain, either by trypsin or molecular biology techniques, results in a β-subunit that does not inactivate the channel, so the currents are sustained and more suitable for kinetic and Ca2+ sensitivity comparisons. Ca2+ sensitivity and gating kinetics of channels formed by α- and β2-subunits are similar to those of channels formed by α- and β1-subunits (18). In contrast to the β1-subunit, this subunit confers low CTX affinity compared with channels formed only by α-subunits (18).

The β3-subunit was cloned from human EST databases and was detected in testis, pancreas, and spleen (19), and it is biochemically more related to β2 than to β1 (15). There are four splice variants (β3a–d), whose differences are in the NH2-terminal region. Each splice variant confers different inactivation properties to the MaxiK channel. Whereas the β3a and β3d subunits confer similar inactivation properties, β3b induces a faster and incomplete inactivation process that becomes evident only at large depolarizations (19). It is unclear whether or not the β3d-subunit interacts with the α-subunit since coexpression of α- and β3d-subunits does not produce changes in the Ca2+ activation curves or in the gating kinetics of the MaxiK channel.

The β4-subunit, also cloned from human EST databases, is expressed mainly in brain. Its coexpression with the α-subunit decreases the apparent Ca2+ sensitivity of the MaxiK channel (2, 9). Although this subunit slows down channel activation in kinetics in a manner similar to the β1-subunit, the deactivation kinetics is very fast (similar to that observed in absence of the β-subunit; see Fig. 2) (2). These results indicate that the functional coupling of this subunit with the α-subunit is different from that induced by the other β-subunits. The β4-subunit decreases the CTX binding strength. If the external loops of the β1- and β4-subunits are exchanged (chimeras β1β4 and β4β1), the phenotypes obtained regarding toxin binding correspond to their respective loops (e.g., chimera β1β4 has a toxin sensitivity corresponding to the β4 subunit). These results suggest that the loops of the β-subunits determine the characteristic of toxin binding. Also, because CTX is a pore-blocking toxin, it is suggested that the extracellular loop of β-subunits (at least β1 and β4) faces the pore and is very close to it (9).

β-Subunits therefore alter the Ca2+ sensitivity and gating kinetics of MaxiK channels, greatly contributing to MaxiK channel diversity. On the other hand, they modify the MaxiK channel pharmacological properties, changing toxin binding and acting as receptors for drugs. Most importantly, they allow the MaxiK channel to play important physiological roles, as we will see below.
Physiological role of β-subunits

In most native cells, MaxiK channels are functionally coupled to VDCC, an association that makes MaxiK channels function as negative feedback for VDCC activation and Ca\(^{2+}\) entry into the cell. VDCC activation leads to inward Ca\(^{2+}\) currents, which then promote membrane depolarization and accumulation of intracellular Ca\(^{2+}\). Both events then promote MaxiK channel activation, leading to a hyperpolarization that closes VDCC.

To have a significant effect on MaxiK channel activity, intracellular Ca\(^{2+}\) concentrations must be >10 \(\mu\)M. Those elevated intracellular Ca\(^{2+}\) concentrations can indeed be reached in small “compartments” inside the cells, the Ca\(^{2+}\) microdomains, where VDCC and MaxiK channels are often tightly colocalized. Space and time characteristics of such compartments depend on the entry and exit of diffusing free Ca\(^{2+}\) and Ca\(^{2+}\) buffer properties (binding rate, mobility, etc.).

Not only VDCCs from the cell membrane are coupled with MaxiK channels. Ryanodine receptors from the sarcoplasmic reticulum are very close (<20 nm) to MaxiK channels in the plasma membrane. This association, confirmed by structural and functional evidence, is the basis for the proposed role of MaxiK channels in the control of vascular smooth muscle contraction. Below we discuss the negative feedback imposed by MaxiK channels in smooth muscle, chromaffin cells, and cochlea.

Smooth muscle

In VSMC, MaxiK channels provide the adequate regulation of the contractile tone. Local Ca\(^{2+}\) increases, called Ca\(^{2+}\) sparks, generate spontaneous transient outward currents (STOCs), which are generated by MaxiK channels. This hyperpolarizes the membrane and promotes relaxation (discussed in Ref. 6). As mentioned earlier, in these cells highly Ca\(^{2+}\)-sensitive MaxiK channels are formed mostly by α- and β1-subunits. The physiological relevance of β1-subunits in modulating the Ca\(^{2+}\) sensitivity of the MaxiK channel was shown with β1 knockout mice (3). The cerebral artery myocytes of these mice exhibited a decrease in the Ca\(^{2+}\) sensitivity of the MaxiK channels and a low Ca\(^{2+}\) spark-STOC coupling (Fig. 3). The absence of the β1-subunit also promoted an increment in arterial tone and blood pressure.

Chromaffin cells

Adrenal chromaffin cells are excitable cells that release neurotransmitters such as catecholamines in response to electrical stimulation. In these cells, MaxiK channels are important for the rapid termination of the action potential. Even though four different subtypes of VDCC (L, N, P, and Q types) are found in these cells, MaxiK channels are functionally coupled only to L- or Q-type VDCC. In rat chromaffin cells, there is a cell population that has inactivating MaxiK currents (MaxiKi) and a population that has activating MaxiK currents (MaxiK) and a population that has activating MaxiK currents (MaxiK).

FIGURE 3. Proposed physiological roles of MaxiK channel β-subunits, depicted as cartoons (A) and as examples on the impact of β-subunits on channel electrophysiology (B). In vascular smooth muscle (VSM) cells, β1-subunit confers the required Ca\(^{2+}\) sensitivity for effective coupling between Ca\(^{2+}\) sparks and spontaneous outward currents. In chromaffin cells, slow MaxiK deactivation kinetics allow subunit-expressing cells to fire repetitively. In auditory outer hair cells, a combination of MaxiK splice variants and β1-subunit expression gives rise to a variety of MaxiK channel kinetics, allowing each cell to electrically tune to a characteristic frequency. See text for further details. B, left: reproduced with permission from Ref. 3. B, middle: reproduced with permission from Ref. 14. B, right, reproduced with permission from Ref. 5.
ulation with noninactivating MaxiK currents (MaxiK) (17). In the MaxiK channels, the β2-subunit is expressed. As a consequence, MaxiK channels in these cells show rapid inactivation and slow deactivation kinetics (18). Because of the much slower deactivation of the MaxiK channel, the afterhyperpolarization phase is prolonged. This relieves Na+ channel inactivation and allows repetitive firing. Thus while MaxiK, are tonically firing cells, MaxiK, are phasically firing cells (Fig. 3) (14).

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. Each different hair cell has a characteristic tuning frequency. In these animals, electrical resonance is achieved through the interplay of L-type VDCC and MaxiK channels operating, as for example in the turtle, at frequencies from 30 to 600 Hz (5). The opening of L-type VDCC induced by depolarization increases internal Ca2+ concentration, which in turn activates MaxiK channels. Activation of MaxiK channels hyperpolarizes the cell, closing Ca2+ channels and promoting the membrane potential oscillation. Subsequent oscillations are damped, because fewer MaxiK channels are recruited in each cycle (Fig. 3) (5). The number and type of MaxiK channels control the resonant frequency of a particular hair cell. Higher frequencies are present in cells containing a large number of MaxiK channels with faster activation kinetics. The origin of this wide range of MaxiK 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 a β-subunit (5, 11). In fact, a number of MaxiK channel splice variants with different activation kinetics and Ca2+ sensitivities have been identified in different places in the cochlea (5). In chicken, an ortholog of the β1-subunit that presents an expression gradient across the cochlea has been identified (11). As mentioned earlier in this review, the β1-subunit increases Ca2+ sensitivity and slow deactivation kinetics. β-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 MaxiK channel is needed. Thus Fettiplace and Fuch (5) modeled the electrical tuning in the turtle with five MaxiK splice variants, but in the chicken basilar papilla (150–4,000 Hz), they needed a minimum of nine MaxiK splice variants.

Coda

In this review, we have tried to convey to the physiologist the importance of a voltage-dependent K+ channel with a probability of opening also controlled by cytoplasmic Ca2+. This tetrameric channel, formed by a protein coded by a single gene (Slo2), attains its large diversity essentially through three mechanisms: alternative splicing, metabolic modulation, and forming a molecular complex with β-subunits (β1–β4). Of course, one or more of the above-mentioned mechanisms acting at the same time can also obtain more multiplicity of MaxiK channels. In particular, the biophysical properties of MaxiK channels are drastically modified by the most studied and well-characterized β1-subunit. This subunit, by decreasing the energy necessary to open the channel and by slowing down channel deactivation, sets the tone in smooth muscle (a fact firmly demonstrated with the help of β1-subunit knockout mice). Extraordinary in its beauty is the molecular mechanism used by turtles, frogs, and chicks to generate in the cochlea the fundamental resonance frequencies. In those animals, gradients of spliced MaxiK channels and β1-subunits across the cochlear epithelium talk to VDCC to produce the different oscillatory voltage responses in the hair cells.

As we discussed, in many tissues the physiological role for β2-, β3-, and β4-subunits can be inferred from the impact of these subunits in the electrophysiology of the channel. However, the real physiological impact will not be known until more detailed studies in native cells are undertaken. For example, the β3-subunit has been detected in testis, but the MaxiK currents in this tissue have not been described in detail. The implication of β2- and β3-subunits in spleen and pancreas, where β3 is located at secreting β-cells (15), is also not clear. In these cells, macroscopic MaxiK currents have been described, but their physiological role remains obscure. We are confident that all of the present unknowns regarding this field will be understood in the near future, unveiling new mechanisms of how the electrical activity of the cell is coupled to its metabolism.

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