Perspectives on: Conformational coupling in ion channels

Conformational coupling in BK potassium channels

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Large conductance calcium- and voltage-dependent BK potassium channels (aka BKCa, MaxiK, Slo1, KCa1.1, and KCNMA1) are expressed in a wide variety of tissues throughout the body and are activated by both intracellular Ca2+ and membrane depolarization. Owing to these properties, BK channels participate in diverse physiological processes from electrical excitability in neurons and secretory cells, and regulation of smooth muscle tone to tuning of auditory hair cells (Vergara et al., 1998; Ghatta et al., 2006). The response to voltage and Ca2+ allows BK channels to integrate electrical and calcium signaling, which is central to their physiological role. Understanding how BK and other multimodal channels are regulated by and integrate diverse stimuli is not only physiologically important but also relevant to the topic of conformational coupling. As a voltage- and ligand-dependent channel, BK channels contain both voltage-sensor and ligand-binding domains as well as a gate to regulate the flow of K+ through the pore. Coupling of conformational changes in one domain to another provides the basis for transducing voltage and ligand binding into channel opening and, therefore, defines, together with the functional properties of the gate and sensors, the signal transduction properties of the channel. The goal of this perspective is to provide an overview on the role and molecular basis of conformational coupling between functional domains in BK channels and outline some of the questions that remain to be answered.

BK channel structure

The BK channel is a member of the superfamily of voltage-gated channels that assembles as a homotetramer of pore-forming Slo1 (α) subunits. Each subunit contains seven transmembrane segments (S0–S6), including an S5–S6 pore gate domain (PGD) and voltage-sensor domain (VSD) that is likely to include S0–S4 segments (Liu et al., 2008) with charged voltage-sensing residues in S2, S3, and S4 (Fig. 1 A; Ma et al., 2006). In addition, a large C-terminal cytoplasmic domain (CTD) consisting of two homologous regulator of K+ conductance domains (RCK1 and RCK2) contains binding sites for Ca2+ and other ligands (Hou et al., 2009). The CTDs form a tetrameric gating-ring structure whose conformation changes upon Ca2+ binding. Crystal structures of the isolated BK channel gating ring and related prokaryotic Ca2+-activated K+ channel MthK have been solved in the presence and absence of Ca2+ (Jiang et al., 2002; Ye et al., 2006; Wu et al., 2010; Yuan et al., 2010, 2012). The atomic structure of the transmembrane domain has yet to be determined but is assumed to be homologous with that of voltage-gated potassium (Kv) channels, consistent with a low resolution cryo-EM structure of the entire channel (Wang and Sigworth, 2009). Although BK channels formed from Slo1 alone are fully functional, each channel may also coassemble with up to four regulatory subunits of which several subtypes exist (B1–4 and γ1–4; Brenner et al., 2000; Yan and Aldrich, 2012). Regulatory subunits tune BK channel function in different tissues, contain one or two transmembrane segments, occupy sites adjacent to the VSD (Liu et al., 2010), and act in part to regulate voltage-dependent gating (Bao and Cox, 2005; Yan and Aldrich, 2010).

BK channel function

The response of BK channels to voltage and Ca2+ is illustrated in Fig. 2 by plotting steady-state open probability (P0; Fig. 2 A) and Log(P0) (Fig. 2 B) versus voltage at different [Ca2+]i (0–100 µM) for heterologously expressed Slo1 channels (Horrigan and Aldrich, 2002). The P0-V relation in 0 Ca2+ (∼0.5 nM) shows channels can be fully activated in the absence of Ca2+ binding, but only at voltages approaching +300 mV. Calcium, to a first approximation, shifts P0-V to more negative voltages (Fig. 2 A), allowing the channel to activate in a physiological voltage range. However, plotting the data on a log scale reveals that Ca2+ does not simply shift the curve but rather increases Log(P0) in a nearly voltage-independent manner until P0 saturates (Fig. 2 B). This response indicates that BK channels are activated independently by voltage- and Ca2+-sensors.
The energetics of conformational coupling

The structures of BK and homologous channels provide important clues concerning the molecular basis of conformational coupling, as discussed below. However, many features of coupling can only be resolved through structure-function analysis using site-directed mutagenesis. A prerequisite to such analysis is to quantify coupling interactions represented by allosteric factors C, D, and E in the HA model. Mutations that alter channel activity may perturb sensors, the gate, or their coupling. Therefore, it is crucial to distinguish changes in coupling from changes in the function of sensor or gate. One way to do this is by fitting steady-state data over a wide range of voltage and Ca\(^{2+}\) as in Fig. 2 (A and B) to determine all parameters in the HA model. However, a more direct and model-independent approach to measure coupling is to determine the energetic effect on one domain of forcing coupled domains into defined conformations (e.g., all activated or deactivated) under extreme stimulus conditions (see also Chowdhury and Chanda in this issue). For example, the total coupling between all Ca\(^{2+}\) sensors and the gate \(\Delta \Delta G = 5.0 \text{kcal mol}^{-1}\) can be determined by comparing Log\((P_o)\) in 0 Ca\(^{2+}\) and saturating 100 µM Ca\(^{2+}\) at extreme negative voltages where voltage sensors are in the resting state, and voltage-sensor/gate coupling \(\Delta \Delta G = 7.6 \text{kcal mol}^{-1}\) can be determined by comparing Log\((P_o)\) at extreme negative and positive voltages in 0 Ca\(^{2+}\) (Fig. 2 B; Horrigan and Aldrich, 2002).

In general, the HA model predicts that channels can occupy many different open and closed states, defined by the number of voltage- and Ca\(^{2+}\)-sensors activated in each channel. But under extreme stimulus conditions, where all voltage- or Ca\(^{2+}\)-sensors are either activated or deactivated, gating reduces to a single closed and open state. For a two-state process, the free energy...
difference between closed and open (\(\Delta G_{CO}\)) can be defined in terms of the equilibrium constant (\(P_o/1-P_o\)) for the C-O transition (i.e., \(\Delta G_{CO} = kT \ln \left( P_o / (1-P_o) \right) \)). Thus, changes in \(\log (P_o)\) in Fig. 2 reflect the energetic effects of voltage- and \(Ca^{2+}\)-sensor activation on the gate. Similarly, a weak coupling between voltage- and \(Ca^{2+}\)-sensors (\(\Delta \Delta G_{CO}^{Ca} = 0.5 \text{ kcal mol}^{-1}\)) has been measured by comparing the effects of 0 \(Ca^{2+}\) and saturating \(Ca^{2+}\) on voltage-sensor activation measured with gating currents while the gate is closed (Horrigan and Aldrich, 2002).

Although measurement of \(Ca^{2+}\)-sensor/gate coupling as in Fig. 2 B is relatively straightforward, measurement of voltage-sensor/gate coupling is subject to several challenges (Fig. 3). The relationship between gating and voltage-sensor/gate coupling is illustrated in Fig. 3 A by expanding the HA model to show the four combinations of states that the gate (C and O) and voltage-sensor (R and A) can assume in a single subunit (RC, RO, AC, and AO) together with the equilibrium constants between them. The equilibrium constant for the C-O transition increases from \(L\) when the voltage sensor is in the resting state (Fig. 3 A, #1) to \(LD\) when a voltage sensor is activated (Fig. 3 A, #2). Thus the voltage-sensor/gate coupling factor \(D\) can be determined by comparing \(P_o\) at extreme voltages (Fig. 3 B, #1 and 2), with the expectation that \(P_o/(1-P_o)\) will increase by a factor of \(D^4\) when all four voltage sensors are activated. One challenge is the large dynamic range of these measurements, which span a seven-order-of-magnitude change in \(P_o\) and require both macroscopic and unitary current recordings in the same patch and a high level of expression that cannot always be achieved with mutant channels. A related challenge is that \(P_o\) in 0 \(Ca^{2+}\) approaches saturation near unity at \(+300 \text{ mV}\) as voltage sensors become fully activated (Fig. 2 A). As \(P_o\) approaches unity, determination of the equilibrium constant \(P_o/(1-P_o)\) becomes problematic and coupling energy can therefore be underestimated, especially in the presence of \(Ca^{2+}\) or with mutants that are easier to open than the WT because \(P_o\) may saturate before voltage sensors are fully activated. Finally, the C-O conformational change, as in many ion channels, has a weak intrinsic voltage dependence (\(L(V)\)) that must be taken into account when comparing \(P_o\) at extreme voltages (Figs. 2 B and 3 B, dashed lines).
concerning the molecular basis of these interactions. Where in the channel do they occur? What are the identity and nature of amino acid interactions involved? When do the interactions occur during channel activation? These questions are broad because many potential sites of domain/domain interaction exist, the conformational changes that these domains and their interfaces undergo during gating are not all understood in detail, and insight provided by the structure of BK or homologous channels is in many cases limited. For example, although voltage-sensor/gate coupling is likely to be mediated in part by interfaces between the VSD and PGD as in Kv channels, there is also a unique interface between the VSD and CTD in BK channels that may contribute to this process. Intracellular Mg$^{2+}$ is a BK channel activator that is coordinated by residues in both VSD and CTD and interacts electrostatically with the voltage sensor, indicating (together with cross-linking experiments) that these domains come in contact (Yang et al., 2007, 2008). The primary functional effect of Mg$^{2+}$ is to enhance voltage-sensor/gate coupling, suggesting that VSD/CTD interaction could provide a basis for this process (Horrigan and Ma, 2008). VSD/CTD interaction must also mediate coupling between voltage and Ca$^{2+}$ sensors. However information about the VSD/CTD interface is incomplete. Structures of BK and MthK channel CTDs and the Kv channel VSD help identifying residues that may lie at this interface. But the complete BK channel structure including the VSD/CTD interface has yet to be determined, and neither MthK nor Kv channels contain a homologous interface.

Molecular mechanisms of conformational coupling

Although the energetics and biophysical mechanisms of sensor/gate and sensor/sensor coupling in BK channels are well defined, many fundamental questions remain concerning the molecular basis of these interactions. Where in the channel do they occur? What are the identity and nature of amino acid interactions involved? When do the interactions occur during channel activation? These questions are broad because many potential sites of domain/domain interaction exist, the conformational changes that these domains and their interfaces undergo during gating are not all understood in detail, and insight provided by the structure of BK or homologous channels is in many cases limited. For example, although voltage-sensor/gate coupling is likely to be mediated in part by interfaces between the VSD and PGD as in Kv channels, there is also a unique interface between the VSD and CTD in BK channels that may contribute to this process. Intracellular Mg$^{2+}$ is a BK channel activator that is coordinated by residues in both VSD and CTD and interacts electrostatically with the voltage sensor, indicating (together with cross-linking experiments) that these domains come in contact (Yang et al., 2007, 2008). The primary functional effect of Mg$^{2+}$ is to enhance voltage-sensor/gate coupling, suggesting that VSD/CTD interaction could provide a basis for this process (Horrigan and Ma, 2008). VSD/CTD interaction must also mediate coupling between voltage and Ca$^{2+}$ sensors. However information about the VSD/CTD interface is incomplete. Structures of BK and MthK channel CTDs and the Kv channel VSD help identifying residues that may lie at this interface. But the complete BK channel structure including the VSD/CTD interface has yet to be determined, and neither MthK nor Kv channels contain a homologous interface.

A complementary approach to measure voltage-sensor/gate coupling is to determine the effect of channel opening on voltage-sensor activation. The equilibrium constant for the R-A transition increases from J when channels are closed to JD when channels are open (Fig. 3 A, #3 and 4). The equilibrium constant J is determined from the charge distribution for closed channels (Qc-V; Fig. 3 C). Qc can be measured by integrating ON gating currents (Fig. 3 B, inset) because voltage-sensor activation in BK channels is rapid and occurs while most channels remain closed. The equilibrium constant JD is determined from the charge distribution for open channels (Qo-V; Fig. 3 D). Qo cannot be determined from gating currents because BK channels close rapidly. However, Qo can be estimated in a model-independent fashion from the log-slope of the Po-V relation \(q_a = kT \ln(P_o)/\Delta V\), as shown in Fig. 3 D (Horrigan and Aldrich, 2002). The Qo-V and Qc-V relations have the same shape but are shifted relative to each other by a voltage directly proportional to coupling energy for a single voltage sensor \(\Delta V = kT \ln(D)/z_j = \Delta G_{ctd}/4z_j; Ma et al., 2006\). This method yields similar results as in Fig. 3 B and avoids challenges relating to the voltage dependence of L(V), or Po saturation. However, gating currents are difficult to measure in BK channels and require an even higher level of expression than in Fig. 3 B.

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Figure 3. The energetics of voltage sensor/gate coupling. (A) Voltage sensor/gate states in a single subunit. Numbers refer to data in B, C, and D used to determine the indicated equilibrium constants. (B) Po-V determines L (1) and LD (4). Dashed lines indicate the predicted voltage dependence of PO with all voltage sensors either in the resting or activated state and zl = 0.3 e. (C) Normalized Qc-V for closed channels determined from ON gating currents (inset) is fit by a Boltzmann function with zJ = 0.58 e and defines J (3). (D) Qo-V relation for open channels defines JD (4). Qo is estimated by fitting the foot of the qa-V relation \(qa = kT \ln(P_o)/\Delta V\) with a Boltzmann function. The shift between Qo and Qc relations defines the coupling factor D.
Because most domain/domain interactions involved in conformational coupling remain to be identified, it is useful to consider what properties such interactions must have. In general, coupling may occur through linkers that directly connect two domains or through noncovalent interactions at domain/domain interfaces. In BK channels, Ca2+-sensor/gate coupling is thought to be mediated by the S6-RCK1 linker connecting CTD to PGD (Jiang et al., 2002; Niu et al., 2004). However multiple domain/domain interfaces are also involved in coupling, as noted above. Structural information has helped to identify where these interfaces are and to locate potential interaction partners. However, elucidating the basis of conformational coupling is more complex than simply identifying domain/domain interactions. Coupling is necessarily a state-dependent process that depends on the conformations of two coupled domains. To understand the possible interaction mechanisms, it is useful to consider the energetics of coupling in the context of a gating cycle such as that described by voltage-sensor/gate coupling in Fig. 3 A.

The coupling energy between a single voltage sensor and gate \( \Delta G_{kT}^{CD} = kT \ln(D) \) can be expressed in terms of the free energies of the four states involved (AC, AO, RC, and RO):

\[
\Delta G_{kT}^{CD} = \left[ \Delta G_{kT}^{RC} - \Delta G_{kT}^{AO} \right] = \left[ \left( G_{c}^{RC} - G_{o}^{RC} \right) - \left( G_{c}^{AO} - G_{o}^{AO} \right) \right] = (1)
\]

\[
G_{c}^{RC} - G_{o}^{RC} - G_{c}^{AO} + G_{o}^{AO}
\]

Therefore, the change in coupling produced by changes in the free energy of each state is:

\[
\Delta \Delta G_{kT}^{RA} = \left[ \Delta G_{kT}^{AC} - \Delta G_{kT}^{AO} - \Delta G_{kT}^{RC} + \Delta G_{kT}^{RO} \right]
\]

Eq. 2 indicates that coupling is enhanced \( \Delta \Delta G_{kT}^{RA} > 0 \) by decreasing \( G_{c}^{RC} \) or \( G_{o}^{AO} \) (stabilizing the RC or AO state) or by increasing \( G_{c}^{AO} \) or \( G_{o}^{RC} \) (destabilizing the AC or RO state). Coupling could also be enhanced by changing the free energy of multiple states, provided the net contribution (Eq. 2) is positive. However, interactions that are state independent or depend on the conformation of only one domain (e.g., \( \Delta G_{kT}^{AC} = \Delta G_{kT}^{RC} \) or \( \Delta G_{kT}^{AO} = \Delta G_{kT}^{RO} \)) will have no effect on coupling (i.e., \( \Delta \Delta G_{kT}^{RA} = 0 \)).

This analysis has several important implications for elucidating mechanisms of conformational coupling. First, to identify coupling interactions by structural methods requires that structures be solved in four conformations defined by two domains and have sufficient resolution to observe state-dependent changes in interaction. In practice, because changes in interaction energy may be subtle or difficult to estimate based on structure, coupling interactions would have to be verified and quantified by structure-function analysis. When only one or two structures of a channel are available, as is currently the case for BK and homologous channels, then structure-function analysis is required to determine if observed interactions participate in coupling, and residues that do not interact in an observed structure may still mediate coupling by interacting in other conformations. Second, structure-function analysis involving site-directed mutagenesis and measurements of coupling energy, as in Figs. 2 and 3, should be sufficient to identify residues involved in coupling interactions. However, such experiments must be interpreted cautiously. Allosteric proteins are often sensitive to modulation at domain interfaces by heterotropic ligands that bind and introduce interactions that do not normally exist, and mutations can have similar effects. For example, introduction of a positively charged residue near the insensitive interface where conformational changes associated with voltage-sensor activation and channel opening both occur. Such false positives cannot be avoided simply by restricting analysis to mutations that reduce coupling because, based on Eq. 2, coupling can be reduced \( \Delta \Delta G_{kT}^{RA} < 0 \) by introducing interactions that destabilize the RC or AO state or stabilize the AC or RO states.

Intracellular heme, which inhibits voltage-sensor/gate coupling in BK channels, may act in this way (Horrigan et al., 2005). Consequently, whether a mutation increases or decreases coupling is less critical than the use of mutations such as Ala that are least likely to introduce interactions. Finally, to define the mechanism of voltage-sensor/gate coupling we must not only identify mutations that alter coupling but also characterize those changes in terms of the effect on individual states (i.e., RC, RO, AC, and AO) to determine when during activation the interactions occur. Although the change in free energy of any particular state cannot be determined directly, the equilibria between states can be evaluated as in Fig. 3 to define the change in free energy of individual states relative to each other. Such analysis has indicated that Mg2+ enhances voltage-sensor/gate coupling by preferentially stabilizing the AO state (Horrigan and Ma, 2008), whereas a stabilization of the RO state is consistent with the inhibitory effect of heme (Horrigan et al., 2005). It is worth noting that, depending on their state dependence, coupling interactions may influence open probability when sensors are in a resting conformation. Thus, the basal activity of BK channels in the absence of sensor activation defined by the equilibrium constant L in the HA model cannot be interpreted simply as the intrinsic stability of the gate because it also reflects any state-dependent interactions between the gate and resting sensors.
Mechanisms of voltage-sensor/gate coupling

Kv channel structures reveal two interfaces between VSD and PGD: intrasubunit contacts between the S4–S5 linker and S6 and intersubunit contacts between S4 and S5 (Long et al., 2005a, 2007). In BK channels, additional intersubunit interactions occur between the VSD and CTD (Yang et al., 2008). All of these interfaces potentially play a role in voltage-sensor/gate coupling in BK channels, but their relative contributions and mechanisms remain unknown. The S4/S5 interface is implicated because a mutation near the top of S4 (R210E) reduces coupling energy by half (Ma et al., 2006). However, we cannot rule out that this is a false positive produced by introducing rather than disrupting an interaction because other mutations at this site (R210C and R210N) appear to constitutively activate the channel preventing measurement of voltage-sensor/gate coupling (Ma et al., 2006). Similarly, the VSD/CTD interface is implicated indirectly based on the ability of Mg⁶⁺, Q397R, and heme to modulate coupling by introducing interactions at or near this interface.

Interactions between the S4–S5 linker and S6 are widely considered to underlie voltage-sensor/gate coupling, also known as electromechanical coupling, in Kv channels (Lu et al., 2002; Tristani-Firouzi et al., 2002; Long et al., 2005b; Chowdhury and Chanda, 2012) and are also likely to be important in BK channels (Sun et al., 2012). However, even in Kv channels many of the questions raised above remain to be answered, such as what are the individual residues and nature of interactions that contribute to coupling and when do they occur during gating? The importance of these questions can be illustrated by comparing three hypothetical mechanisms of voltage-sensor/gate coupling that include S4–S5/S6 interactions and are consistent with the allosteric nature of voltage gating in Slo1 (Fig. 4).

Fig. 4 (A–C) depicts the four combinations of states the gate and voltage-sensor can assume in a single subunit. The possibility that S4–S5/S6 forms a rigid connection that forces sensor and gate to move as a unit can be ruled out because voltage sensors can activate while channels remain closed. However, it is conceivable that the S4–S5 linker remains bound to S6 at all times, whereas flexibility in adjoining regions allows sensor and gate to move as if coupled by a spring (Fig. 4 A). Another possibility is the S4–S5 linker binds to the open gate only when the voltage sensor is activated, stabilizing the AO state (Fig. 4 B). Alternatively, the S4–S5 linker of the resting voltage sensor might clash with the open gate to destabilize the RO state (Fig. 4 C). These and other mechanisms could account for the ability of voltage-sensor activation to promote opening but make different predictions concerning the source of coupling and the role of S4–S5/S6 interaction. Fig. 4 A suggests that many parts of the S4–S5 linker could contribute to coupling by influencing the mechanical properties of the linkage. In this case, S4–S5/S6 interaction acts merely as a passive connection that affects coupling only to the extent that it is intact or disrupted. In contrast, Fig. 4 (B and C) predicts that the S4–S5/S6 interaction energy is the main determinant of coupling energy. However, the panels in Fig. 4 differ in the nature of the proposed interaction (Fig. 4 B, binding; Fig. 4 C, steric hindrance) and the state dependence of the interaction. The analysis of coupling energy and equilibria for such gating cycles, as outlined above, should allow such mechanisms and predictions to be distinguished in BK channels.
Despite substantial homology between BK and Kv channels, important differences also exist that could be relevant to voltage-sensor/gate coupling. First, BK channels are weakly voltage dependent compared with Kv channels and exhibit a different pattern and contribution of voltage-sensing residues in the VSD, suggesting that conformational changes associated with voltage-sensor activation may differ (Ma et al., 2006). Second, the ability of intracellular blockers and Cys-modifying reagents to access the inner pore of closed BK channels (Wilkens and Aldrich, 2006; Zhou et al., 2011) suggests that the BK channel gate may be formed by the selectivity filter (Cox and Hoshi, 2011; Thompson and Begenisich, 2012), as in cyclic-nucleotide–gated channels (Contreras et al., 2008), rather than by crossing of S6 segments at the inner mouth of the pore, as in Kv channels (del Camino and Yellen, 2001). These differences do not require that voltage-sensor/gate coupling occurs through fundamentally different mechanisms. For example, if the BK channel gate is in the selectivity filter it is still likely to be strongly coupled to S6 movement, as in CNG channels (Flynn and Zagotta, 2001), and therefore subject to control by S4–S5/S6 interaction. Indeed, there is considerable evidence for S6 movement associated with BK channel opening (Li and Aldrich, 2006; Wu et al., 2009; Chen and Aldrich, 2011). However, the coupling mechanisms for BK and Kv channels may differ in detail, and a selectivity gate in the BK channel could potentially support a larger role for S4/S5 interaction in voltage-sensor/gate coupling. It should also be noted that regulatory β and γ subunits have been reported to modulate voltage-sensor/gate coupling (Bao et al., 2004; Zhang et al., 2010). By using mutations to eliminate each site individually and carefully measuring the effects of Ca²⁺ on Pₒ at −80 mV (similar to Fig. 2 B), Sweet and Cox (2008) determined that the contribution to Ca²⁺-sensor/gate coupling of the RCK1 site (3.74 kcal mol⁻¹) was slightly greater than that of the RCK2 Ca²⁺-bowl site (3.04 kcal mol⁻¹), but the RCK2 site has a higher affinity for Ca²⁺. In addition, the summed contribution of the individual sites exceeded their combined effect in the WT channel (∆∆Gₒ = 5.0 kcal mol⁻¹; Fig. 2 B), consistent with negative cooperativity between sites in the same subunit (Sweet and Cox, 2008). In contrast, another group performing similar experiments at +50 mV concluded that positive cooperativity exists between the two binding sites (Qian et al., 2006). In the latter case, positive cooperativity could potentially be accounted for if both Ca²⁺ sites were coupled to the voltage sensor because the voltage sensor is not held in a resting state at +50 mV. However Sweet and Cox (2008) concluded that the RCK1 site is solely responsible for Ca²⁺-sensor/voltage-sensor coupling. A recent study combining Ca²⁺ site mutations and voltage clamp fluorometry to monitor the effects of Ca²⁺ on steady-state voltage-sensor activation and Pₒ reached conclusions similar to that of Sweet and Cox (2008) regarding intrasubunit cooperativity and Ca²⁺-sensor/voltage-sensor coupling (Savalli et al., 2012). However, this study also suggested that Ca²⁺ site mutations may have effects other than elimination of Ca²⁺ binding. This caveat, together with the fact that none of the studies mentioned measured Ca²⁺-sensor/voltage-sensor coupling directly, suggests that the extent to which the individual Ca²⁺-binding sites are coupled to the
Many questions remain about the molecular basis of domain–domain coupling, but this channel represents a favorable system for studying such processes owing to its unique functional properties and methods that have allowed the energetics of coupling to be studied in detail. Combining these methods with emerging structural information about domain/domain interfaces and conformational changes in the channel should provide further insight into coupling mechanisms that are important in BK channels and in other voltage-gated or ligand-gated channels. BK channels also constitute a powerful system for understanding the interplay between ligand- and voltage-dependent gating. Defining the interactions that mediate coupling between voltage and Ca²⁺ sensors in this channel should provide unique insight into processes that may be relevant to other multi-modal channels such as HCN or TRP.

This Perspectives series includes articles by Andersen, Colquhoun and Lape, and Chowdury and Chanda.

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