How Highly Charged Anionic Lipids Bind and Regulate Ion Channels

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The modulation of channel activity by direct interaction with membrane lipids is now an emerging theme in ion channel biology. In particular, phosphoinositides such as phosphatidylinositol 4,5-bisphosphate (PIP_2) are known to regulate the activity of most major classes of ion channel, as well as a number of other membrane transport proteins. The regulation of inwardly rectifying (Kir) potassium channels by PIP_2 is one of the most intensively studied and best-defined model systems for studying channel–lipid interactions. In this review we explore the mechanisms that underlie the complex regulation of Kir channels by phosphoinositides and other highly charged anionic lipids such as long chain CoA esters. Intriguingly, these different lipids result in either activation or inhibition depending on the Kir channel subtype. We describe how recent studies have provided structural insight into these lipid-induced gating movements, and discuss how this gating mechanism is central to Kir channel physiology.

Introduction

As pointed out in the preceding perspective by Lundbæk (see p. 421), many lipids and lipophilic compounds alter ion channel function by affecting the collective physical properties of the membrane, i.e., the regulation does not depend on specific interactions with the channel. However, the regulation of potassium channels by highly negatively charged lipids such as phosphoinositides and long chain acyl-CoA esters is mechanistically distinct because these lipids bind directly to the channel and any effects mediated by changes in the physical properties of the bilayer itself are considered to be minimal.

The direct interaction of highly charged anionic lipids with ion channels is now emerging as a fundamental mechanism of channel regulation. A considerable body of work over the past decade has shown that members of almost every class of ion channel can be regulated by phosphoinositides, in particular phosphatidylinositol-4,5 bisphosphate (hereafter referred to as PIP_2) (Hilgemann et al., 2001; Suh and Hille, 2005; Gamper and Shapiro, 2007a). However, the molecular mechanisms underlying this form of direct lipid regulation are best understood in the family of inwardly rectifying potassium (Kir) channels and so will form the focus of this perspective.

Regulation of Kir Channels by Highly Charged Anionic Lipids

In 1996/1997 three papers were published that provided the first evidence that highly negatively charged anionic lipids can modulate the activity of Kir channels. Hilgemann and Ball (1996) demonstrated that phosphoinositides such as PIP_2 activate native cardiac K_{ATP} channels. In addition, Fan and Makielski (1997) showed that several cloned Kir channels, (e.g., Kir1.1, Kir2.1, and K_{ATP} [Kir6.2/SUR1] channels) are activated by PIP_2. Furthermore, Larsson et al. (1996) demonstrated activation of native K_{ATP} channels by long chain acyl-CoA esters (LC-CoA), which are metabolites of fatty acid metabolism.

It is now clear that all Kir channels are regulated by phosphoinositides (Logothetis et al., 2007a) and long chain CoA esters (Rapedius et al., 2005), and that the structure of the highly negatively charged head group present in these lipids is central to their ability to affect Kir channel activity. The anionic head group is thought to interact directly with a distinct positively charged binding site on the channel (Logothetis et al., 2007a) and can induce quite rapid gating motions (Rapedius et al., 2007a). Thus, the anionic head group appears to gate Kir channels very much like a classical ligand, with the only distinction that the ligand is tethered to the membrane. Interestingly, the functional consequences of these head group interactions are markedly different between members of the Kir channel family. For example, whereas PIP_2 activates all members of the Kir channels, LC-CoA esters inhibit their activity, except for K_{ATP} channels, which are activated by LC-CoA (Rapedius et al., 2005).

The main issues that will be discussed in this perspective center around the following questions. (a) Where and how do anionic lipids interact with Kir channels? (b) What is the mechanistic basis for the different effects of PIP_2 and LC-CoA on Kir channels? (c) What are the conformational changes induced by the binding of these lipids? (d) What is the physiological relevance of this regulation?

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Abbreviation used in this paper: PIP_2, phosphatidylinositol 4,5-bisphosphate.

A Variety of Highly Charged Anionic Lipids Activate K_{ATP} Channels

The effects of various lipids on cloned Kir6.2/SUR1 (K_{ATP}) channels have been evaluated by their application to the cytoplasmic membrane side in excised patches. From these studies it became clear that neutral lipids (e.g., phosphatidylethanolamine, phosphatidylcholine) or weakly negatively charged lipids (e.g., phosphatidylinositol) have little effect on channel activity (Fan and Makielski, 1997; Krauter et al., 2001), whereas lipids with highly negatively charged headgroups strongly activated K_{ATP} channels. These were the different phosphoinositides including PI(4)P, PI(4,5)P_2, PI(3,4)P2, and PI(3,4,5)P_3, which all restored channel activity when applied after rundown, a process that typically occurs in excised patches due to the breakdown of endogenous phosphoinositides (Hilgemann and Ball, 1996; Fan and Makielski, 1997; Baukrowitz et al., 1998; Shyng and Nichols, 1998; Rohacs et al., 2003). However, it is PIP$_2$ that is most important as it represents the major phosphoinositide in eukaryotic membranes comprising ~1% of the total phospholipids and is >100-fold more abundant than the other phosphoinositides such as PI(3,4)P_2 and PIP(3,4,5)P_3 (Gamper and Shapiro, 2007a).

LC-CoA esters (e.g., oleoyl-CoA, palmityl-CoA) also potently activate K_{ATP} channels at low concentration (<1 µM) (Larsson et al., 1996; Gribble et al., 1998; Liu et al., 2001; Schulze et al., 2003b; Branstrom et al., 2004) (Fig. 1 C). Here the negative charge is contained in the CoA headgroup (structure see Fig. 1) and the 3'-ribose phosphate is particularly important as its removal abolishes any stimulatory effect on K_{ATP} channels (Rapedius et al., 2005). Furthermore, a negatively charged artificial lipid (DOGS-NTA) also strongly activates K_{ATP} channels (Krauter et al., 2001), indicating that the specific structure of the charged head group is not critical. However, other Kir channels exhibit much greater specificity (see below).

Screening of the negative charge in these lipids by divalent cations (e.g., Mg^{2+}) or their complexation by polycations such as polylysine or neomycin abolishes their stimulatory effect, suggesting that electrostatic interactions between the negatively charged headgroup and the channel are critical (Fan and Makielski, 1997; Schulze et al., 2003a,b). However, application of the head group itself (i.e., IP$_3$ or CoA) does not activate K_{ATP} channels (Shyng and Nichols, 1998; Schulze et al., 2003b), demonstrating that lipid tethering of the charged head group to the membrane surface is required.

A Conserved Binding Site for Highly Charged Anionic Lipids in Kir Channels

Systematic mutagenesis of basic residues in the cytoplasmic domains of Kir channels has identified several potential PIP$_2$-interacting residues that are highly conserved among the different Kir channels (Logothetis et al., 2007a). Neutralization of these residues results in channels with a low open probability that increases upon application of exogenous PIP$_2$. Furthermore, these mutant channels show increased sensitivity to inhibition by polylysine and neomycin, as well as faster inhibition by PIP$_2$-specific antibodies, suggesting that these mutations reduce the apparent PIP$_2$ affinity (Huang et al., 1998; Lopes et al., 2002; Schulze et al., 2003a). When mapped onto structural models of Kir channels these basic residues cluster in a region close to the membrane interface suggestive of a binding site (for details see Haider et al., 2007; Logothetis et al., 2007a). Each of the four subunits of these tetrameric channels likely contains one binding site. A recent study on Kir2.1 channels suggest that binding of PIP$_2$ to one of the four sites is sufficient to promote channel opening, and PIP$_2$ interaction with the remaining sites further increases the open probability in a cooperative fashion (Xie et al., 2008).

The structure of the PIP$_2$ binding site is therefore beginning to emerge. However, extensive mutagenesis studies have shown that a number of other residues located at positions quite distant from this site can affect the apparent PIP$_2$ affinity (Logothetis et al., 2007a). Some of these residues are uncharged and either alter the structure of the PIP$_2$ binding site allosterically, or interfere with the transduction mechanism that couples PIP$_2$ binding and channel opening. The latter effect would also change the apparent PIP$_2$ affinity as measured with macroscopic currents that are unable to distinguish between changes in ligand affinity versus changes in ligand efficacy.

Interestingly, mutation of the conserved PIP$_2$-interacting residues within the PIP$_2$ binding site also reduce the apparent affinity for LC-CoA in K_{ATP} channels (Fox et al., 2003; Schulze et al., 2003b). In agreement, biochemical experiments on the C-terminal domains of Kir channels show that LC-CoA can competitively antagonize the binding of PIP$_2$ (Rapedius et al., 2005). In addition, the functional effects of PIP$_2$ and LC-CoA on K_{ATP} channels are similar since both lipids strongly antagonize ATP inhibition, as well as inhibition by sulphonylureas (e.g., glibenclamide) and activation by channel openers (e.g., diazoxide) (Schulze et al., 2003b). These pharmacological compounds affect K_{ATP} (Kir6.2/SUR) channels via interaction with the SUR subunit. These results suggest that PIP$_2$ and LC-CoA probably regulate K_{ATP} activation via the same mechanism and the same interaction site.

Bidirectional Regulation of Kir Channels by Phosphoinositides and LC-CoA Esters

As stated above, all tested highly charged anionic lipids activate K_{ATP} channels with similar potency. However, the K_{ATP} channel is the exception, as all other Kir channels show a bidirectional regulation by these different lipids, i.e., while PIP$_2$ activates all Kir channel subtypes, LC-CoA
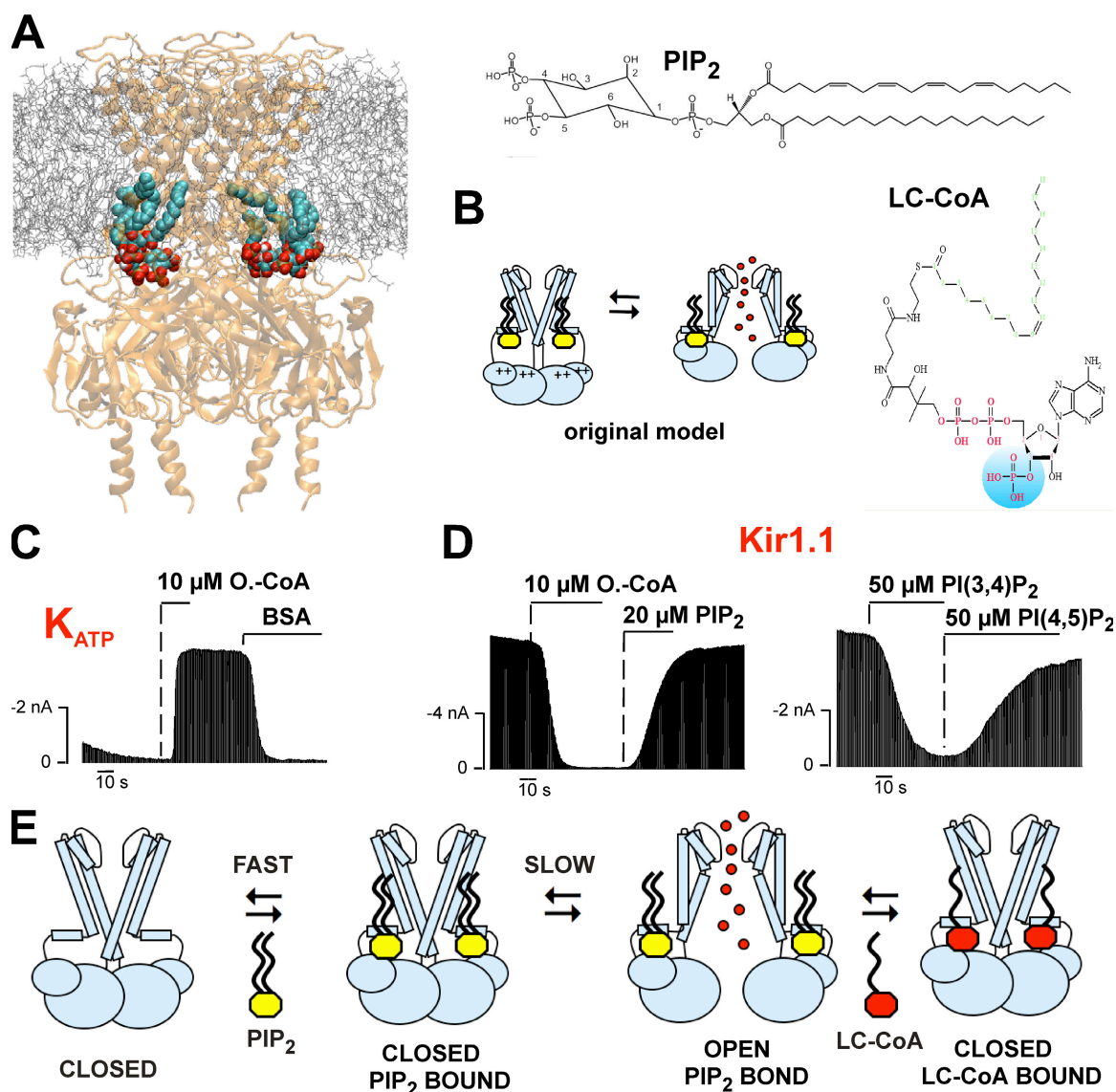
Figure 1. Proposed mechanism of phosphoinositide and LC-CoA gating in Kir channels. (A) A homology model of Kir6.2 in the closed state showing the location of the four bound PIP_2 molecules at the membrane/cytoplasm interface (position of PIP_2 was determined by a computational docking procedure (Haider et al., 2007). The negative charges on the headgroups (oxygen atoms in red) interact with a positively charged cluster in the cytoplasmic domains, for clarity the multiple residues that comprise the binding site are not shown, for details see Haider et al. (2007). (B) Previous models suggested that opening of the Kir channel is produced by electrostatic attraction between PIP_2 and its binding site that induces a major movement of the cytoplasmic domain toward the membrane. (C) In addition to being activated by PIP_2, $PI(3,4)P_2$, and $PI(3,4,5)P_3$ (not depicted), K_{ATP} channels are activated by oleoyl-CoA, a long-chain acyl-CoA ester as measured in inside-out patches from *Xenopus* oocytes. BSA is used to rapidly remove oleoyl-CoA. (D) Kir1.1 is activated by $PI(4,5)P_2$ but inhibited by oleoyl-CoA and $PI(3,4)P_2$ and inhibition could be reversed by PIP_2. (E) In contrast to the original model (B) we propose that all phosphoinositides and LC-CoAs can bind to the PIP_2 binding site on the closed Kir subunit. However, only certain bound lipids (e.g., PIP_2) are subsequently able to initiate the allosteric changes required for channel opening. Those that cannot induce channel opening (LC-CoA and $PI(3,4)P_2$) inhibit channel activity by competitive displacement of PIP_2. The chemical structures of PIP_2 and LC-CoA are shown at the top of the figure. The critical phosphate on LC-CoA required for its ability to induce opening in K_{ATP} channels and inhibition in, e.g., Kir1.1 channels is highlighted in blue. Panel A is adapted from the results of Haider et al. (2007). C and D are adapted from Rapedius et al. (2005).

as well as some phosphoinositides have the opposite effect and inhibit Kir channel activity (Rohacs et al., 1999, 2003; Rapedius et al., 2005; Shumilina et al., 2006). To determine the apparent affinity (i.e., potency to activate) of a particular phosphoinositide Logothetis and coworkers established an assay using short chain fatty acids

phosphoinositides such diC8(octanoly)-PIP_2 (Rohacs et al., 1999, 2003). These short chain phosphoinositides are soluble in aqueous solution as monomers and rapidly establish a water–membrane partitioning equilibrium allowing different diC8-phosphoionositides to be compared at a similar membrane concentration.

This assay revealed that PIP_2, $PI(3,4)P_2$ and $PI(3,4,5)P_3$ activate K_{ATP} channels with a similar potency, whereas all other Kir channels exhibit varying degrees of phosphoinositide specificity. For example, $PI(3,4,5)P_3$ produces little activation, and $PI(3,4)P_2$ no activation, of Kir1.1 and Kir2.1 channels when applied to closed channels (i.e., after rundown) (Rohacs et al., 1999, 2003). Intriguingly, $PI(3,4)P_2$ when applied to active channels (i.e., before rundown) produced marked inhibition of Kir1.1 and Kir2.1 that could be reversed by $PI(4,5)P_2$ (Rapedius et al., 2005) (Fig. 1 D). Even more strikingly, LC-CoA esters such as oleoyl-CoA potently inhibit all Kir channels (except K_{ATP} channels) in a way that can be reversed by PIP_2 (Rapedius et al., 2005) (Fig. 1 D). Furthermore, removal of the 3′-ribose phosphate in LC-CoA that prevented activation in K_{ATP} channels also abolished inhibition in Kir1.1 and Kir2.1 (Rapedius et al., 2005), indicating that this phosphate group is critical for Kir channel interaction.

How Can the Same Lipids Act as Both Activators and Inhibitors of Different Kir Channels?

As described above, LC-CoA appears to bind to the same conserved phosphoinositide binding site that is found in all Kir channels. In a previous study we proposed a mechanism whereby LC-CoA competes with PIP_2 for the same binding site, but that LC-CoA binding does not activate the channel, thereby inhibiting channel activity by displacement of PIP_2 (Rapedius et al., 2005). This hypothesis has important structural implications for the mechanism of PIP_2 activation in Kir channels as it suggests that phosphoinositides and LC-CoA bind to the closed state of the channel. This idea is different to some previously held views about PIP_2 activation (as depicted in Fig. 1 B), which suggested that opening of the channel is achieved by a movement of the positively charged cytoplasmic domains toward the membrane that is driven by electrostatic attractions between the phosphoinositide binding site and membrane bound PIP_2 (Fan and Makielski, 1997; Enkvetchakul and Nichols, 2003). If this were the case then the simple electrostatic interaction between the binding site and $PI(3,4)P_2$ or LC-CoA should also be able to stabilize the open state in all Kir channels.

These findings argue for a relatively nonspecific electrostatic interaction between all phosphoinositides (or LC-CoA) and the binding site on the channel and suggest that specificity is achieved (at least in part) in more subtle structural changes subsequent to binding. In this model the binding of PIP_2 is capable of inducing pore opening, but the binding of either $PI(3,4)P_2$ or LC-CoA is not (as depicted in Fig. 1 E). Indeed, point mutations in Kir2.1 have been found that allow LC-CoA to activate the channel probably by permitting those specific interactions in the transduction mechanism required to induce channel opening (Rohacs et al., 2003).

To understand this in structural terms will ultimately require a high resolution structure of a eukaryotic Kir channel with different phosphoinositides (or LC-CoA) bound, a goal that may not be such a dream given the recent high-resolution structures of KirBac/Kir3.1 and Kv2.1/Kv2.1 chimeras produced by the MacKinnon laboratory that resolve some bound lipids and detergents, although not yet PIP_2 (Long et al., 2007; Nishida et al., 2007). However, recently, computational ligand docking studies have been used to define the location of PIP_2 and the PIP_2 binding site in a homology model of Kir6.2 (Haider et al., 2007). This site appears to satisfy most of the available functional data and also allows the fatty acids to reside in the membrane (Fig. 1 A). This latter point is important because the Kir channel homology models are all in the closed state and therefore suggest that it is not necessary for the phosphoinositide binding site to translocate significantly toward the membrane before binding can occur. This is therefore consistent with the proposed hypothesis in which $PI(3,4)P_2$ and LC-CoA can bind to the closed state of the channel. Furthermore, even though some of the highly conserved positive charges found within the PIP_2 binding site are missing in bacterial Kir channels, these channels exhibit inhibition by PIP_2, demonstrating that the KirBac closed state can bind PIP_2 (Enkvetchakul et al., 2005).

Kir channels also differ markedly in their apparent PIP_2 affinity as determined by their sensitivity to inhibition by various PIP_2 complexing agents (e.g., neomycin, polylysine, PIP_2 antibodies) (Huang et al., 1998; Rohacs et al., 1999, 2003). For example, Kir4.1 and Kir2.1 show very low sensitivity to neomycin (i.e., they have a high PIP_2 affinity), Kir1.1, Kir2.2, and K_{ATP} (Kir6.2/SUR) show an intermediate sensitivity (i.e., intermediate PIP_2 affinity), whereas the G protein–regulated Kir3.x channels and heteromeric Kir4.1/Kir5.1 channels display a high sensitivity (i.e., they have a lower PIP_2 affinity) (Rapedius et al., 2007a,b). The molecular basis of these differences is currently unknown and might not be determined solely by differences in PIP_2 binding affinity, but also by the equilibrium between the open and closed state that is shifted toward the open state by PIP_2 binding (as implied by the term apparent PIP_2 affinity).

From the Kinetics of PIP_2 Gating to the Structural Mechanism of PIP_2 Activation

To gain insight into the mechanism of PIP_2 gating we recently established an assay that allowed measurement of PIP_2 gating kinetics using fast application of either diC8-PIP_2 or neomycin to inside-out membrane patches (Rapedius et al., 2007a). These measurements revealed that PIP_2 rapidly binds to closed Kir channels ($\tau < 300$ ms) and then induces a much slower conformational change leading to the open state of the channel (Fig. 1 E). We found that the speed of this conformational change
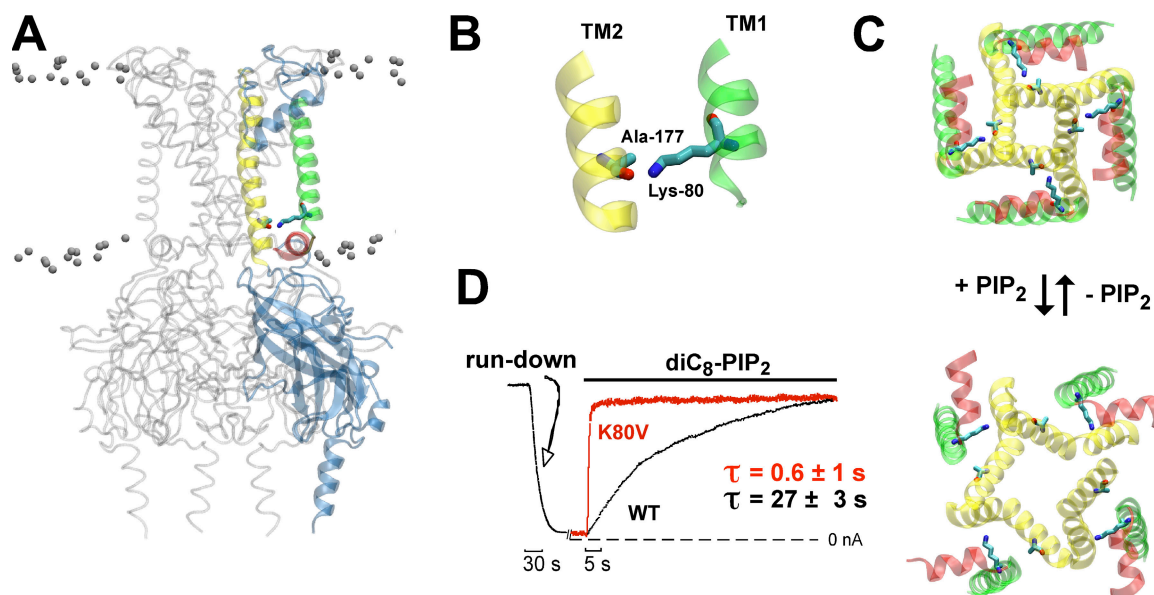
Figure 2. Gating model of Kir1.1. (A) Side view of a closed state homology model of Kir1.1 with one of the four subunits highlighted. The highlighted residues at the helix bundle crossing (K80 and A177) are proposed to form an H bond, which stabilizes the closed state. In this and all other panels TM1 is shown in green and TM2 in yellow with the slide helix in red. (B) An expanded view shows the proposed H bonding interaction between residues in the $-NH_3^+$ group of K80 and the backbone carbonyl group of A177. (C) A bottom up view through the pore of a closed state (top) and open state (bottom) model of Kir1.1 (for details see Rapedius et al., 2007a) illustrating a major movement of TM1 and TM1 induced by PIP$_2$ binding that would rupture the TM1–TM2 H bond. The highlighted residues are K80 and A177. (D) Rapid application of 3 μM diC8-PIP$_2$ on Kir1.1-WT and Kir1.1-K80V channels subsequent to rundown measured in inside-out patches. When H bonding at the helix bundle crossing is disrupted in Kir1.1-K80V channels, PIP$_2$ activation is much faster than in wild-type channels. A–D are modified from Rapedius et al. (2007a).

differs dramatically between Kir channels and that this depends on the presence (or absence) of a single lysine residue at the base of the first transmembrane domain (TM1). Kir channels possessing a lysine at this TM1 position (e.g., Kir1.1, Kir4.1) display slow PIP$_2$ activation, and mutation of this residue (e.g., Kir1.1[K80M], Kir4.1[K67M]) dramatically accelerates PIP$_2$ activation (∼50-fold) (Fig. 2 D). In agreement with the role of this lysine residue, Kir channels lacking a lysine at this position (e.g., Kir2.1) display fast PIP$_2$ activation kinetics that are dramatically slowed upon mutation of this site to a lysine (e.g., Kir2.1[M84K]). However, this positively charged residue does not interact directly with PIP$_2$. Instead, homology modeling and molecular dynamics (MD) simulations of a Kir1.1 closed state structure suggest that the $-NH_3^+$ group of this TM1 lysine forms a hydrogen bond with the backbone carbonyl group of A177 in TM2 at the helix bundle crossing (Rapedius et al., 2007a) (Fig. 2, A and B).

A recent model of the open state KirBac3.1 suggests a large rotation and tilt of the TM1 and TM2 helices during channel opening (Domene et al., 2005; Kuo et al., 2005) that would rupture this TM1–TM2 H-bond (as depicted in Fig. 2 C), thereby explaining why this H bond determines the time course of channel opening induced by PIP$_2$ as its rupture would contribute to the activation energy of the closed to open state transition. In support of this model, a study on cysteine accessibil-

ity in Kir2.1 channels also indicates conformational changes of the pore at the helix bundle crossing during PIP$_2$ gating (Xiao et al., 2003). Taken together these results suggest that PIP$_2$ gating in Kir channels involves a major conformational change at the helix bundle crossing. However, the mechanism by which PIP$_2$ triggers this conformational change remains unknown.

There is an intriguing parallel between PIP$_2$ gating and the mechanism of pH inhibition seen in Kir channels. Kir channels with H bonding at the helix bundle crossing (e.g Kir1.1 and Kir4.1) display high sensitivity to inhibition by low intracellular pH whereas Kir channels lacking this H bonding are markedly less sensitive (Rapedius et al., 2007a). Moreover, the time course of recovery from pH inhibition corresponds strikingly well to their pH sensitivity and H bonding ability as it is fast in channels lacking H bonding and slow in channels with H bonding. This suggests that although the initial events in these gating processes are different (i.e., PIP$_2$ binding versus protonation of a currently unknown H^+ sensor), the structural changes at the helix bundle crossing underlying both pH gating and PIP$_2$ gating appear to be conserved. However, it is unlikely that pH inhibition simply results from promoting PIP$_2$ to unbind because the rate of PIP$_2$ activation is much slower than the recovery rate from H^+ inhibition. Therefore, if H^+ inhibition were to cause the dissociation of PIP$_2$, then the rebinding of PIP$_2$ (i.e., the PIP$_2$ activation rate)

should govern the time course of recovery from pH inhibition, which is clearly not the case (Rapedius et al., 2007a). Nevertheless, there is a general trend that Kir channels with a lower PIP_2 affinity show a higher pH sensitivity, indicating a possible relationship between the PIP_2–channel interaction and pH sensitivity (Leung et al., 2000; Schulze et al., 2003a; Du et al., 2004), but the mechanistic basis of this remains elusive.

Physiological Implications of PIP_2 and LC-CoA Regulation

PIP_2 can be regarded as an indispensable cofactor for all eukaryotic Kir channels because no channel activity is seen in its absence. Not surprisingly therefore, inherited mutations that reduce PIP_2 affinity result in a variety of disease states such as Type II Bartter's Syndrome (Kir1.1), Andersen's Syndrome (Kir2.1) (Lopes et al., 2002), and congenital hyperinsulinaemia (Kir6.2) (Lin et al., 2006). This therefore raises the question as to the biological benefit of having PIP_2 as a cofactor. One hypothesis put forward by Hilgemann suggested that this PIP_2 dependence might be a mechanism to keep Kir channels inactive in intracellular membrane compartments (where PIP_2 levels are thought to be low) because active Kir channels might be harmful to the ion homeostasis of these compartments (Hilgemann, 2007b). Furthermore, the PIP_2 dependence may have allowed the evolution of mechanisms that control Kir channel activity by modulation of the interaction with PIP_2 (for reviews see Logothetis et al., 2007b; Xie et al., 2007) For example, G protein activation of Kir3.x channels requires PIP_2 and is thought to result from increasing the channel PIP_2 affinity from a level that is otherwise too low for the endogenous PIP_2 levels to support activity (Huang et al., 1998; Zhang et al., 1999). By contrast, PIP_2 strongly antagonizes ATP inhibition of K_{ATP} channels, and vice versa (Baukrowitz et al., 1998; Shyng and Nichols, 1998). Thus, ATP inhibition can be regarded as a reduction in the apparent PIP_2 affinity. The molecular mechanisms behind this are still controversial and could result either (or both) from the direct displacement of PIP_2 by ATP (MacGregor et al., 2002; Haider et al., 2007) (the binding sites show some overlap), or an allosteric mechanism by which ATP stabilizes a conformation that prevents PIP_2 binding (Enkvetchakul and Nichols, 2003). Furthermore, the regulation of Kir1.1 and Kir3.x by PKA and PKC also probably involves changes in PIP_2 affinity (Liou et al., 1999; Zeng et al., 2003; Logothetis et al., 2007b; Xie et al., 2007). Therefore, understanding the molecular mechanisms that underlie PIP_2 gating may well represent the key to understanding Kir channel gating in general.

The issue of whether Kir channels are regulated by cellular phosphoinositide metabolism in vivo, and the physiological relevance of such regulation, is still controversial (Gamper and Shapiro, 2007a) due to the high PIP_2 affinity of many Kir channels (e.g., Kir1.1, Kir2.1,

Kir4.1). For example, stimulation of the principal enzyme involved in PIP_2 hydrolysis (PLC), can be used as a mechanism to deplete cellular PIP_2 levels. However, PLC-mediated inhibition of Kir2.1 channels (which have high PIP_2 affinity) can only be obtained when their PIP_2 affinity is reduced by site-directed mutagenesis (Hardie et al., 2004). By contrast, PLC-mediated inhibition of Kir3.x channels (low intrinsic PIP_2 affinity) has been reported in native tissues (Cho et al., 2005) and possibly contributes to channel desensitization upon cardiac vagus stimulation by muscarinic receptors (Kobrinsky et al., 2000).

It is also still unclear as to whether such regulation occurs by a global depletion of plasma membrane PIP_2, or whether this occurs in microdomains (Gamper and Shapiro, 2007b; Hilgemann, 2007a; Xie et al., 2007). The latter mechanism seems more appealing because global PIP_2 depletion should have many potential side effects given that PIP_2 is involved in so many other cellular mechanisms including calcium signaling, endo-/exocytosis, organization of the cytoskeleton, and the regulation of many other ion channels and transporters. A physiological role for Kir channel regulation by other phosphoinositides such as $PI(3,4)P_2$ or $PI(3,4,5)P_3$ is rather unlikely because even when their production is stimulated (e.g., by growth hormones via PI-3 kinases) their global concentration is still very low compared with PIP_2 (Gamper and Shapiro, 2007a). Nevertheless, these different phosphoinositides have been mechanistically insightful in dissecting the structural basis of phosphoinositide specificity and the mechanism of PIP_2 activation.

LC-CoA esters are obligate intermediates of fatty acid metabolism that are formed in the cytoplasm and then shuttled into the mitochondria to fuel β-oxidation. In excised membrane patches, Kir channels can be markedly activated (or inhibited) by oleoyl-CoA at concentration in range of 100 to 1000 nM (Liu et al., 2001; Branstrom et al., 2004; Rapedius et al., 2005). However, the concentration of LC-CoA in the cytoplasm is strongly buffered by specific acyl-CoA binding proteins (Knudsen et al., 2002) and calculations suggest that the concentration of free LC-CoA is <10 nM under physiological conditions and should not exceed 200 nM even in pathophysiological conditions (Knudsen et al., 2002). This raises the question as to whether cytoplasmic levels of LC-CoA can rise sufficiently to affect Kir channels in vivo. However, studies have shown that extracellular application of oleic acids to cells can produce K_{ATP} channel activation and Kir2.1 inhibition via the cytoplasmic formation of LC-CoA under conditions (e.g., high glucose) that promote LC-CoA accumulation (Branstrom et al., 2004; Shumilina et al., 2006). Such activation of K_{ATP} channels in pancreatic β cells could contribute to a reduction in insulin secretion in type II diabetes patients (Riedel et al., 2003; Branstrom et al.,

2004), and the activation of cardiac K_{ATP} during ischemia (which is known to promote LC-CoA accumulation) could represent a potential cardio-protective mechanism (Liu et al., 2001). Furthermore, LC-CoA activation of K_{ATP} channels has been suggested to be involved in the sensing of circulating fatty acids by hypothalamic neurons (Lam et al., 2005).

A physiological relevance for the inhibitory effect of LC-CoA seen in most other Kir channels has so far yet to be established. However, a direct link between Kir channel activity and fatty acid metabolism could be of potential relevance to many tissues given the widespread expression of different Kir channels throughout the body and the general occurrence of LC-CoA in cells. Interestingly, a recent study demonstrated that the sodium–calcium exchanger, which is also regulated by PIP_2, displays similar regulation by LC-CoA (Riedel et al., 2006). It will therefore be interesting to see whether other PIP_2-regulated channels or transporters also exhibit regulation by LC-CoA.

In conclusion, it is now clear that PIP_2 serves as an obligate cofactor for Kir channel activity and it is difficult to examine any form of Kir channel regulation without considering the role of PIP_2. Work over the past decade has provided significant insight into the physiological aspects of phosphoinositide-mediated regulation and its structural mechanisms. It will also be interesting to see whether the lessons we have learned from Kir channels about, e.g., the regulation of PIP_2 affinity, phosphoinositide (or LC-CoA) specificity and gating efficacy, as well as the kinetics of PIP_2 gating can provide an insight into the molecular mechanisms by which so many diverse classes of other ion channels and transporters are regulated by phosphoinositides.

REFERENCES

Baukrowitz, T., U. Schulte, D. Oliver, S. Herlitze, T. Krauter, S.J. Tucker, J.P. Ruppersberg, and B. Fakler. 1998. PIP_2 and PIP as determinants for ATP inhibition of K_{ATP} channels. *Science.* 282:1141–1144.

Branstrom, R., C.A. Aspinwall, S. Valimaki, C.G. Ostensson, A. Tibell, M. Eckhard, H. Brandhorst, B.E. Corkey, P.O. Berggren, and O. Larsson. 2004. Long-chain CoA esters activate human pancreatic β-cell K_{ATP} channels: potential role in type 2 diabetes. *Diabetologia.* 47:277–283.

Cho, H., D. Lee, S.H. Lee, and W.K. Ho. 2005. Receptor-induced depletion of phosphatidylinositol 4,5-bisphosphate inhibits inwardly rectifying K^+ channels in a receptor-specific manner. *Proc. Natl. Acad. Sci. USA.* 102:4643–4648.

Domene, C., D.A. Doyle, and C. Venien-Bryan. 2005. Modeling of an ion channel in its open conformation. *Biophys J.* 89:L01–L03.

Du, X., H. Zhang, C. Lopes, T. Mirshahi, T. Rohacs, and D.E. Logothetis. 2004. Characteristic interactions with phosphatidylinositol 4,5-bisphosphate determine regulation of Kir channels by diverse modulators. *J. Biol. Chem.* 279:37271–37281.

Enkvetchakul, D., and C.G. Nichols. 2003. Gating mechanism of K_{ATP} channels: function fits form. *J. Gen. Physiol.* 122:471–480.

Enkvetchakul, D., I. Jeliazkova, and C.G. Nichols. 2005. Direct modulation of Kir channel gating by membrane phosphatidylinositol 4,5-bisphosphate. *J. Biol. Chem.* 280:35785–35788.

Fan, Z., and J.C. Makielski. 1997. Anionic phospholipids activate ATP-sensitive potassium channels. *J. Biol. Chem.* 272:5388–5395.

Fox, J.E., J. Magga, W.R. Giles, and P.E. Light. 2003. Acyl coenzyme A esters differentially activate cardiac and β-cell adenosine triphosphate-sensitive potassium channels in a side-chain length-specific manner. *Metabolism.* 52:1313–1319.

Gamper, N., and M.S. Shapiro. 2007a. Regulation of ion transport proteins by membrane phosphoinositides. *Nat. Rev. Neurosci.* 8:921–934.

Gamper, N., and M.S. Shapiro. 2007b. Target-specific PIP(2) signalling: how might it work? *J. Physiol.* 582:967–975.

Gribble, F.M., P. Proks, B.E. Corkey, and F.M. Ashcroft. 1998. Mechanism of cloned ATP-sensitive potassium channel activation by oleoyl-CoA. *J. Biol. Chem.* 273:26383–26387.

Haider, S., A.I. Tarasov, T.J. Craig, M.S. Sansom, and F.M. Ashcroft. 2007. Identification of the PIP_2-binding site on Kir6.2 by molecular modelling and functional analysis. *EMBO J.* 26:3749–3759.

Hardie, R.C., Y. Gu, F. Martin, S.T. Sweeney, and P. Raghu. 2004. In vivo light-induced and basal phospholipase C activity in *Drosophila* photoreceptors measured with genetically targeted phosphatidylinositol 4,5-bisphosphate-sensitive ion channels (Kir2.1). *J. Biol. Chem.* 279:47773–47782.

Hilgemann, D.W. 2007a. Local PIP(2) signals: when, where, and how? *Pflugers Arch.* 455:55–67.

Hilgemann, D.W. 2007b. On the physiological roles of PIP(2) at cardiac Na^+ Ca^{2+} exchangers and K(ATP) channels: a long journey from membrane biophysics into cell biology. *J. Physiol.* 582:903–909.

Hilgemann, D.W., and R. Ball. 1996. Regulation of cardiac Na^+,Ca^{2+} exchange and K_{ATP} potassium channels by PIP2. *Science.* 273:956–959.

Hilgemann, D.W., S. Feng, and C. Nasuhoglu. 2001. The complex and intriguing lives of PIP_2 with ion channels and transporters. *Sci. STKE.* 111:re19.

Huang, C.L., S. Feng, and D.W. Hilgemann. 1998. Direct activation of inward rectifier potassium channels by PIP_2 and its stabilization by Gβγ. *Nature.* 391:803–806.

Knudsen, J., T.B. Neergaard, B. Gaigg, M.V. Jensen, and J.K. Hansen. 2002. Role of acyl-CoA binding protein in acyl-CoA metabolism and acyl-CoA-mediated cell signaling. *J. Nutr.* 130:294S–298S.

Kobrinsky, E., T. Mirshahi, H. Zhang, T. Jin, and D.E. Logothetis. 2000. Receptor-mediated hydrolysis of plasma membrane messenger PIP_2 leads to K^+-current desensitization. *Nat. Cell Biol.* 2:507–514.

Krauter, T., J.P. Ruppersberg, and T. Baukrowitz. 2001. Phospholipids as modulators of KATP channels: distinct mechanisms for control of sensitivity to sulphonylureas, K^+ channel openers, and ATP. *Mol. Pharmacol.* 59:1086–1093.

Kuo, A., C. Domene, L.N. Johnson, D.A. Doyle, and C. Vénien-Bryan. 2005. Two different conformational states of the KirBac3.1 potassium channel revealed by electron crystallography. *Structure.* 13:1463–1472.

Lam, T.K., A. Pocai, R. Gutierrez-Juarez, S. Obici, J. Bryan, L. Aguilar-Bryan, G.J. Schwartz, and L. Rossetti. 2005. Hypothalamic sensing of circulating fatty acids is required for glucose homeostasis. *Nat. Med.* 11:320–327.

Larsson, O., J.T. Deeney, R. Branstrom, P.O. Berggren, and B.E. Corkey. 1996. Activation of the ATP-sensitive K+ channel by long chain acyl-CoA. A role in modulation of pancreatic β-cell glucose sensitivity. *J. Biol. Chem.* 271:10623–10626.

Leung, Y.M., W.Z. Zeng, H.H. Liou, C.R. Solaro, and C.H. Huang. 2000. Phosphatidylinositol 4,5-bisphosphate and intracellular pH regulate the ROMK1 potassium channel via separate but inter-related mechanisms. *J. Biol. Chem.* 275:10182–10189.

Lin, Y.W., C. MacMullen, A. Ganguly, C.A. Stanley, and S.L. Shyng. 2006. A novel KCNJ11 mutation associated with congenital hyper-insulinism reduces the intrinsic open probability of β-cell ATP-sensitive potassium channels. *J. Biol. Chem.* 281:3006–3012.

Liou, H.H., S.S. Zhou, and C.L. Huang. 1999. Regulation of ROMK1 channel by protein kinase A via a phosphatidylinositol 4,5-bisphosphate-dependent mechanism. *Proc. Natl. Acad. Sci. USA.* 96:5820–5825.

Liu, G.X., P.J. Hanley, J. Ray, and J. Daut. 2001. Long-chain acyl-coenzyme A esters and fatty acids directly link metabolism to K(ATP) channels in the heart. *Circ. Res.* 88:918–924.

Logothetis, D.E., T. Jin, D. Lupyan, and A. Rosenhouse-Dantsker. 2007a. Phosphoinositide-mediated gating of inwardly rectifying K+ channels. *Pflugers Arch.* 455:83–95.

Logothetis, D.E., D. Lupyan, and A. Rosenhouse-Dantsker. 2007b. Diverse Kir modulators act in close proximity to residues implicated in phosphoinositide binding. *J. Physiol.* 582:953–965.

Long, S.B., X. Tao, E.B. Campbell, and R. MacKinnon. 2007. Atomic structure of a voltage-dependent K+ channel in a lipid membrane-like environment. *Nature.* 450:376–382.

Lopes, C.M., H. Zhang, T. Rohacs, T. Jin, J. Yang, and D.E. Logothetis. 2002. Alterations in conserved Kir channel-PIP$_2$ interactions underlie channelopathies. *Neuron.* 34:933–944.

Lundbæk, J.A. 2008. Lipid bilayer–mediated regulation of ion channel function by amphiphilic drugs. *J. Gen. Physiol.* 131:421–429.

MacGregor, G.G., K. Dong, C.G. Vanoye, L. Tang, G. Giebisch, and S.C. Hebert. 2002. Nucleotides and phospholipids compete for binding to the C terminus of K$_{ATP}$ channels. *Proc. Natl. Acad. Sci. USA.* 99:2726–2731.

Nishida, M., M. Cadene, B.T. Chait, and R. MacKinnon. 2007. Crystal structure of a Kir3.1-prokaryotic Kir channel chimera. *EMBO J.* 26:4005–4015.

Rapedius, M., M. Soom, E. Shumilina, D. Schulze, R. Schonherr, C. Kirsch, F. Lang, S.J. Tucker, and T. Baukrowitz. 2005. Long chain CoA esters as competitive antagonists of phosphatidylinositol 4,5-bisphosphate activation in Kir channels. *J. Biol. Chem.* 280:30760–30767.

Rapedius, M., P.W. Fowler, L. Shang, M.S. Sansom, S.J. Tucker, and T. Baukrowitz. 2007a. H bonding at the helix-bundle crossing controls gating in Kir potassium channels. *Neuron.* 55:602–614.

Rapedius, M., J. Paynter, P.W. Fowler, L. Shang, M.S. Sansom, S.J. Tucker, and T. Baukrowitz. 2007b. Control of pH and PIP$_2$ gating in heteromeric Kir4.1/Kir5.1 channels by H bonding at the helix bundle crossing. *Channels.* 1:327–330.

Riedel, M.J., P. Boora, D. Steckley, G. de Vries, and P.E. Light. 2003. Kir6.2 polymorphisms sensitize β-cell ATP-sensitive potassium channels to activation by acyl CoAs: a possible cellular mechanism for increased susceptibility to type 2 diabetes? *Diabetes.* 52:2630–2635.

Riedel, M.J., I. Baczko, G.J. Searle, N. Webster, M. Fercho, L. Jones, J. Lang, J. Lytton, J.R. Dyck, and P.E. Light. 2006. Metabolic regulation of sodium-calcium exchange by intracellular acyl CoAs. *EMBO J.* 25:4605–4614.

Rohacs, T., J. Chen, G.D. Prestwich, and D.E. Logothetis. 1999. Distinct specificities of inwardly rectifying K+ channels for phosphoinositides. *J. Biol. Chem.* 274:36065–36072.

Rohacs, T., C.M. Lopes, T. Jin, P.P. Ramdya, Z. Molnar, and D.E. Logothetis. 2003. Specificity of activation by phosphoinositides determines lipid regulation of Kir channels. *Proc. Natl. Acad. Sci. USA.* 100:745–750.

Schulze, D., T. Krauter, H. Fritzenschaft, M. Soom, and T. Baukrowitz. 2003a. Phosphatidylinositol 4,5-bisphosphate (PIP$_2$) modulation of ATP and pH sensitivity in Kir channels. A tale of an active and a silent PIP$_2$ site in the N terminus. *J. Biol. Chem.* 278:10500–10505.

Schulze, D., M. Rapedius, T. Krauter, and T. Baukrowitz. 2003b. Long-chain acyl-CoA esters and phosphatidylinositol phosphates modulate ATP inhibition of K$_{ATP}$ channels by the same mechanism. *J. Physiol.* 552:357–367.

Shumilina, E., N. Klocker, G. Korniychuk, M. Rapedius, F. Lang, and T. Baukrowitz. 2006. Cytoplasmic accumulation of long-chain coenzyme A esters activates K$_{ATP}$ and inhibits Kir2.1 channels. *J. Physiol.* 575:433–442.

Shyng, S.L., and C.G. Nichols. 1998. Membrane phospholipid control of nucleotide sensitivity of KATP channels. *Science.* 282:1138–1141.

Suh, B.C., and B. Hille. 2005. Regulation of ion channels by phosphatidylinositol 4,5-bisphosphate. *Curr. Opin. Neurobiol.* 15:370–378.

Xiao, J., X.G. Zhen, and J. Yang. 2003. Localization of PIP$_2$ activation gate in inward rectifier K+ channels. *Nat. Neurosci.* 6:811–818.

Xie, L.H., S.A. John, B. Ribalet, and J.N. Weiss. 2007. Activation of inwardly rectifying potassium (Kir) channels by phosphatidylinosital-4,5-bisphosphate (PIP$_2$): interaction with other regulatory ligands. *Prog. Biophys. Mol. Biol.* 94:320–335.

Xie, L.H., S.A. John, B. Ribalet, and J.N. Weiss. 2008. Phosphatidylinositol-4,5-bisphosphate (PIP$_2$) regulation of strong inward rectifier Kir2.1 channels: multilevel positive cooperativity. *J. Physiol.* DOI:10.1113/jphysiol.2007.147868.

Zeng, W.Z., X.J. Li, D.W. Hilgemann, and C.L. Huang. 2003. Protein kinase C inhibits ROMK1 channel activity via a phosphatidylinositol 4,5-bisphosphate-dependent mechanism. *J. Biol. Chem.* 278:16852–16856.

Zhang, H., C. He, X. Yan, T. Mirshahi, and D.E. Logothetis. 1999. Activation of inwardly rectifying K+ channels by distinct PtdIns(4,5)P$_2$ interactions. *Nat. Cell Biol.* 1:183–188.