Ligand-insensitive State of Cardiac ATP-sensitive K\(^+\) Channels

Basis for Channel Opening

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ABSTRACT The mechanism by which ATP-sensitive K\(^+\) (K\(_{\text{ATP}}\)) channels open in the presence of inhibitory concentrations of ATP remains unknown. Herein, using a four-state kinetic model, we found that the nucleotide diphosphate UDP directed cardiac K\(_{\text{ATP}}\) channels to operate within intraburst transitions. These transitions are not targeted by ATP, nor the structurally unrelated sulfonylurea glyburide, which inhibit channel opening by acting on interburst transitions. Therefore, the channel remained insensitive to ATP and glyburide in the presence of UDP. "Rundown" of channel activity decreased the efficacy with which UDP could direct and maintain the channel to operate within intraburst transitions. Under this condition, the channel was sensitive to inhibition by ATP and glyburide despite the presence of UDP. This behavior of the K\(_{\text{ATP}}\) channel could be accounted for by an allosteric model of ligand-channel interaction. Thus, the response of cardiac K\(_{\text{ATP}}\) channels towards inhibitory ligands is determined by the relative lifetime the channel spends in a ligand-sensitive versus -insensitive state. Interconversion between these two conformational states represents a novel basis for K\(_{\text{ATP}}\) channel opening in the presence of inhibitory concentrations of ATP in a cardiac cell.

KEY WORDS: K\(_{\text{ATP}}\) channel • nucleotide diphosphate • kinetic model • allosteric model • sulfonylurea

INTRODUCTION

ATP-sensitive K\(^+\) (K\(_{\text{ATP}}\)) channels transduce cellular metabolic events into membrane potential changes (Ashcroft and Ashcroft, 1990; Lazdunski, 1994; Seino et al., 1996; Bryan and Aguilar-Bryan, 1997), which in heart muscle leads to shortening of action potential duration during ischemia (Nichols and Lederer, 1991; Findlay, 1994; Terzic et al., 1995). The defining property of K\(_{\text{ATP}}\) channels is their inhibition by intracellular ATP (Noma, 1983). In cardiomyocytes, however, the ATP concentration (~5–10 mM) exceeds by >100-fold the IC\(_{50}\) value for K\(_{\text{ATP}}\) channel closure. Thus, a change of two orders of magnitude in the ATP concentration would be required for channels to open, which does not occur even under extreme cellular hypoxia (Weiss and Hiltbrand, 1985; Decking et al., 1995, 1997), suggesting that additional modulators of K\(_{\text{ATP}}\) channel opening are important.

In this regard, intracellular nucleotide diphosphates are of particular importance since they favor opening of K\(_{\text{ATP}}\) channels even within a cytosolic environment of high ATP concentration (Ashcroft and Ashcroft, 1990; Nichols and Lederer, 1991; Weiss and Venkatesh, 1993; Findlay, 1994; Terzic et al., 1994d, Elvir-Mairena et al., 1996). However, the mechanism of this action of nucleotide diphosphates remains controversial. A conventional assumption has been that nucleotide diphosphates competitively antagonize ATP at an inhibitory binding site on the channel protein (Dunne and Petersen, 1986; Kakei et al., 1986; Misler et al., 1986; Findlay, 1987; Bokvist et al., 1991; Nichols and Lederer, 1991; Ueda et al., 1997). However, this mechanism cannot fully explain K\(_{\text{ATP}}\) channel opening since altered concentrations of cytosolic ATP and/or nucleotide diphosphates are not readily detectable, nor do they correlate with changes in K\(_{\text{ATP}}\) channel function. Moreover, nucleotide diphosphates, such as ADP or UDP, induce channel opening in the absence of ATP (Findlay, 1988; Lederer and Nichols, 1989; Tung and Kurachi, 1991; Allard and Lazdunski, 1992; Forestier and Vivaudou, 1993; Terzic et al., 1994a) and can lose their ability to antagonize ATP-dependent channel inhibition under certain operative conditions of the channel (Deutsch and Weiss, 1993; Terzic et al., 1994a). Such nonuniform regulation of K\(_{\text{ATP}}\) channel opening may be caused by other inhibitory ligands including sulfonylurea drugs (Venkatesh et al., 1991; Brady et al., 1996b, 1998) and diadenosine polyphosphates (Jovanovic et al., 1996, 1997). These findings suggest that an operative condi-
tion-dependent response of $K_{\text{ATP}}$ channels is a fundamental property of the channel, which may be the basis for channel opening in the presence of inhibitory ligands.

To determine whether nucleotide diphosphates induce an alteration in channel behavior that could account for the observed response of $K_{\text{ATP}}$ channels towards inhibitory ligands, we investigated the action of UDP on transitional states of the cardiac $K_{\text{ATP}}$ channel. Based on a kinetic model of channel behavior, we demonstrate that UDP drives the channel into a state that is insensitive towards inhibitory ligands. Interconversion between ligand-sensitive and -insensitive states could be interpreted using an allosteric model that predicted the outcome of the interaction between an inhibitory ligand and the $K_{\text{ATP}}$ channel in the presence of a nucleotide diphosphate. Transition of the channel into a ligand-insensitive channel state provides a means for $K_{\text{ATP}}$ channel opening even in the presence of high concentrations of inhibitory ligands within a cardiomyocyte.

MATERIALS AND METHODS

Isolated Cardiomyocytes

Ventricular myocytes were isolated by enzymatic dissociation (Alekseev et al., 1996a). Solutions were prepared based on a “low Ca$^{2+}$ medium” containing (mM): 100 NaCl, 10 KCl, 1.2 KH$_2$PO$_4$, 5 MgSO$_4$, 20 glucose, 50 taurocholate, 10 HEPES, pH 7.2–7.3. Guinea pigs were anesthetized with pentobarbital (1 ml/100 g body weight i.p.). After cardiotomy, the heart was retrogradely perfused (at 37°C) with: medium 199 (Sigma Chemical Co., St. Louis, MO) for 2–3 min, followed by Ca$^{2+}$-buffered low Ca$^{2+}$ medium (pCa 7) for 80 s, and finally low Ca$^{2+}$ medium containing propranolol HCl (8 mg/100 ml; Serva Biochemicals, Heidelberg, Germany), proteinase K (1.7 mg/100 ml; Boehringer Mannheim Biochemicals, Indianapolis, IN), bovine serum albumin (0.1 g/100 ml, fraction V; Sigma Chemical Co.), and 200 μM CaCl$_2$. Ventricles were separated from atria and cut into small fragments (6–10 mm$^3$) in the low Ca$^{2+}$ medium enriched with 200 μM CaCl$_2$. Single cells were then isolated by stirring the tissue (at 37°C) in a solution containing propranolol HCl and proteinase K supplemented with collagenase (5 mg/10 ml; Worthington Biochemical Corp., Freehold, NJ). After 10 min, the first aliquot was removed, filtered through a nylon sieve, centrifuged (at 300–400 rpm, 1 min), and washed twice. Remaining tissue fragments were reexposed to collagenase, and isolation continued for two to three such cycles. Isolated cardiomyocytes were stored in low Ca$^{2+}$ medium with 200 μM CaCl$_2$. Rod-shaped cardiomyocytes with clear striations and a smooth surface were used for electrophysiological recordings. Experiments were performed with the approval of the Institutional Animal Care and Use Committee (Mayo Clinic).

Single-Channel Recording

Fire-polished pipettes, coated with Sylgard (resistance ~5 MΩ), were filled with “pipette solution” containing (mM): 140 KCl, 1 CaCl$_2$, 1 MgCl$_2$, 5 HEPES-KOH, pH 7.3. Cardiac cells were superfused with “internal solution” containing (mM): 140 KCl, 1 MgCl$_2$, 5 EGTA, 5 HEPES-KOH, pH 7.3, in the absence or presence of nucleotides (UDP or ATP) and/or glyburide (Sigma Chemical Co.), and recordings made at room temperature (20–22°C) as described (Terzic et al., 1994c; Terzic and Kurachi, 1996). Glyburide was dissolved in dimethylsulfoxide as concentrated stock solution, and the final concentration of dimethylsulfoxide was <0.1%, which did not affect $K_{\text{ATP}}$ channels. UDP (Boehringer Mannheim Biochemicals) and ATP (potassium salt; Sigma Chemical Co.) were dissolved in internal solution before use. Single-channel recordings in the inside-out configuration were monitored online on a high-gain digital storage oscilloscope (VG-6025; Hitachi Ltd., Tokyo, Japan) and stored on tape using a PCM converter system (VR-10; Instrutech Corp., Great Neck, NY). Data were reproduced, low-pass filtered at 4 kHz (~3 dB) by a Bessel filter (902; Frequency Devices Inc., Haverhill, MA), sampled at 80-μs rate, and further analyzed using “BioQuest” software (Alekseev et al., 1997a, 1997b).

Analysis of Channel Activity

The threshold for judging the open state of $K_{\text{ATP}}$ channels was set at half single channel amplitude. The degree of channel activity was assessed by digitizing segments of current records, expressed as $nP_o$, where $n$ represents the number of channels in the patch and $P_o$ the probability of each channel to be open.

Kinetic schemes for cardiac $K_{\text{ATP}}$ channels are commonly represented by one open and two closed states (Kakei and Noma, 1984). Herein, in prolonged records of single channel activity (under symmetrical K$^+$ concentration and negative membrane potential), distribution of total dwell time could be best fit by three exponents, thus requiring consideration of an additional closed state as proposed for more detailed schemes of $K_{\text{ATP}}$ channel behavior (Gillis et al., 1989; Furutaka et al., 1993). Accordingly, channel kinetic analysis was performed based upon a four-state kinetic scheme with three forward and three backward rate constants:

$$C_4 \xrightarrow{k_{41}} C_3 \xrightarrow{k_{32}} C_2 \xrightarrow{k_{23}} C_1 \xrightarrow{k_{14}} C_o.$$

(1)

where transitions between the open (O) and the first closed ($C_1$) state represent transitions within a burst (intraburst kinetics), whereas transitions between the open (O) and the second ($C_2$) and third ($C_3$) closed states define interburst kinetics.

Rate constants (see Scheme 1) were calculated based on parameters obtained from the fit of separated distributions of intraburst and interburst closed times, since relative areas under exponents that correspond to interburst transitions were negligible compared with intraburst events. A critical time ($t_{\text{closed}}$) was used to define the maximal duration of an event that could still be interpreted as closure within a burst of channel activity and was used to construct distributions of open and closed events within and between bursts. The value for $t_{\text{closed}} \geq 3.5$ ms was determined based upon the relationship (Gillis et al., 1989):

$$a_1 \exp(-t_{\text{closed}}/\tau_1) + a_2 (\exp(-t_2/\tau_2) - \exp(-t_{\text{closed}}/\tau_2)) = 0.5,$$

where $\tau_1$ is the time constant of closed intervals within a burst; $\tau_2$ is the time constant of closed intervals between bursts; $a_1$ and $a_2$ are areas of exponential fits corresponding to $\tau_1$ and $\tau_2$, respectively, and $t_2$ is the “dead time;” i.e., time of underestimated events that equals the double sampling rate (~100 μs). Fitting closed and open time distributions by the sum of exponent was carried out using minimization of the $\chi^2$ criterion with the Nelder-Mead method of deformed polyhedron (Alekseev et al., 1996b).
Characteristic open time ($\tau_o$) was interpreted as:

$$\tau_o = 1 / (k_{01} + k_{02}). \quad (2)$$

Characteristic intraburst closed time ($\tau_{c,1}$), corresponding to gaps within burst, was interpreted as the lifetime in the $C_1$ state:

$$\tau_{c,1} = 1 / k_{10}. \quad (3)$$

Similarly, the first characteristic interburst closed time ($\tau_{c,2}$) was interpreted as the lifetime in the $C_2$ state:

$$\tau_{c,2} = 1 / (k_{20} + k_{23}). \quad (4)$$

Finally, the second characteristic interburst closed time ($\tau_{c,3}$) can be approximated as (see Sakmann and Trube, 1984; Gillis et al., 1989):

$$\tau_{c,3} = \frac{1}{k_{23}} \left( 1 + \frac{k_{23}}{k_{20}} \right) + \frac{1}{k_{20}}. \quad (5)$$

In addition, the number of intraburst closures per burst was expressed as:

$$\frac{N_{IB}}{N_B} = \frac{k_{01}}{k_{02}} \quad (6)$$

where $N_{IB}$ is the number of events within a burst, and $N_B$ is the number of bursts or of gaps between bursts, distribution of which was defined by $\tau_{c,2}$ and $\tau_{c,3}$ with representative relative areas under each exponent, $a_2$ and $a_3$ ($a_2 + a_3 = 1$), respectively. Therefore:

$$a_2 = \frac{k_{20}}{k_{23}} \quad \text{and} \quad a_3 = \frac{k_{20}}{k_{23}}. \quad (7)$$

Eqs. 2–7 were then solved for each of the three forward and three backward rates of transition (see Scheme 1):

$$k_{10} = 1 / \tau_{c,1}$$

$$k_{01} = N_{IB} / (\tau_{c,1} [N_{IB} + N_B])$$

$$k_{02} = 1 / (\tau_{c,2} [N_{IB} / N_B + 1])$$

$$k_{20} = a_2 / \tau_{c,2}$$

$$k_{23} = 1 / (\tau_{c,3} [a_2 / a_3 + 1])$$

$$k_{32} = 1 / (a_3 \tau_{c,3} - \tau_{c,2}). \quad (8)$$

Calculated rates of transition were used as a quantitative tool to describe the effect of nucleotides and sulfonylurea drugs on K$_{ATP}$ channel kinetics.

Results are expressed as mean ± SEM; $n$ refers to the number of myocytes used in each analysis.

**RESULTS**

**UDP Directs Cardiac K$_{ATP}$ Channel Activity Towards Intraburst Transitions**

The single channel behavior of cardiac K$_{ATP}$ channels is characterized by clustering of channel openings in groups (bursts) separated by prolonged closures (gaps between bursts; Fig. 1 A). Within a burst, distributions of closed and open times were fitted by corresponding single exponents (characteristic times $\tau_{c,1} = 0.48 \pm 0.03$ ms and $\tau_o = 2.21 \pm 0.18$ ms, respectively; $n = 5$; Fig. 1 B, left). Between bursts, distribution of gaps required at least two exponents (Fig. 1 C, left). Thus, in addition to the open and closed channel states that define intraburst ($C_1 \leftrightarrow O$) transitions, two closed states were required to describe interburst ($\leftrightarrow C_2 \leftrightarrow C_3$) K$_{ATP}$ channel behavior (Fig. 1 D, left).

The nucleotide diphosphate UDP (1 mM) eliminated gaps between bursts, promoting the channel to operate within a sustained burst (Fig. 1 A; Table I). UDP did not change the distribution of open times (Table I) that could be fitted by a single exponent (characteristic time $\tau_o = 2.36 \pm 0.22$ ms; $n = 4$; Fig. 1 B, right), not statistically different from the value obtained in the absence of UDP ($P < 0.05$; see above). However, since UDP eliminated gaps between bursts, the total distribution of closed times became a single exponent (Fig. 1 C, right) with a characteristic time $\tau_{c,1} = 0.48 \pm 0.04$ ms ($n = 4$). This value was identical to the parameter defining closures within bursts of channel activity in the absence of UDP ($P < 0.05$; see above). In terms of the four-state linear scheme of K$_{ATP}$ channel activity, UDP reduced channel operation to one closed and one open state with a rate of transition (Fig. 1 D, right), identical to the rate of intraburst transition measured in the absence of UDP (Fig. 1 D, left). Thus, UDP directed the K$_{ATP}$ channel to operate exclusively within intraburst transitions (Fig. 1 D, right).

**ATP and Glyburide Affect K$_{ATP}$ Channel Behavior Outside Intraburst Transitions**

In the absence of ligands, K$_{ATP}$ channel activity displayed intraburst and interburst transitions (Fig. 2, $a_1$ and $b_1$). ATP (100 µM; Fig. 2 A, $a_2$) or glyburide (1 µM; Fig. 2 B, $b_2$) blocked K$_{ATP}$ channel activity without affecting single channel amplitude ($n = 48$). Neither ATP ($n = 5$) nor glyburide ($n = 4$) significantly changed mean closed ($\tau_{c,1}$) and mean open ($\tau_o$) times that define intraburst kinetics (Table I). However, both inhibitory ligands did prolong the fast ($\tau_{c,2}$) and slow ($\tau_{c,3}$) characteristic times that define the distribution of gaps between bursts (Table I) and increased the number of prolonged channel closures (Table I; relative areas $a_1$ and $a_2$). This was associated with a significant change in transition rates defining interburst, without a change in rates ($k_{10}$ and $k_{01}$) defining intraburst ($C_1 \leftrightarrow O$; Fig. 2) transitions. Specifically, ATP (100 µM) promoted escape of the channel from intraburst transitions to the $C_2$ closed state by increasing the $k_{02}$ rate from 0.55 to 28 s$^{-1}$, and delayed initiation of a burst by decreasing the backward $k_{20}$ rate from 70 to 22 s$^{-1}$ (Fig. 2 A). Similarly, but to a lesser extent than ATP, glyburide (1 µM) increased by threefold the $k_{02}$ rate, and decreased by over twofold the backward $k_{20}$ rate (Fig. 2 B). Consequently, the mean duration of a burst (2,210 ms, $n_{burst} = 23$) and 2,380 ms, $n_{burst} = 14$ in the absence of ATP and glyburide, respectively) was reduced by
each of the inhibitory ligands (56 ms, \( n_{\text{burst}} = 255 \) and 850 ms, \( n_{\text{burst}} = 31 \) in the presence of ATP and glyburide, respectively).

In agreement with experimental data, calculated mean burst duration, using rates defining intraburst transitions and the rate leading away from these transitions (Sakmann and Trube, 1984):

\[
\sigma_{\text{burst}} = \frac{k_{10} + k_{01}}{k_{10}k_{02}} \tag{8}
\]

was 2,200 vs. 44 ms in the absence and presence of ATP, and 2,500 vs. 960 ms in the absence and presence of glyburide.

Since the lifetime the channel spends in a specific state is defined by the reciprocal of the sum of transition rates that lead away from this state:

\[
\sigma_{C_2} = \frac{1}{k_{20} + k_{21}}; \quad \sigma_{C_3} = \frac{1}{k_{12}} \tag{9}
\]

the lifetime the \( K_{ATP} \) channel spent in \( C_2 \) or \( C_3 \), in the presence of ATP (100 \( \mu \)M), was 12.2 and 175 ms, respectively. Although these values were within the range of values obtained in the absence of ATP (\( \sigma_{C_2} = 9.1 \pm 1.4 \) ms, and \( \sigma_{C_3} = 207 \pm 84 \) ms; \( n = 4 \)), ATP by accelerating \( k_{20} \) and by reducing \( k_{21} \) rates (Fig. 2 A) promoted the channel to operate within \( C_2 < C_3 \) closed states, away from intraburst transitions. Thereby, ATP significantly increased the combined lifetime the \( K_{ATP} \) channel spent within interburst transitions (Sakmann and Trube, 1984):

\[
\sigma_{C_2,3} = \frac{k_{11} + k_{12}}{k_{12}k_{20}} \tag{10}
\]

from 87.8 ms in the absence to 524 ms in the presence of ATP (Fig. 2 A).

Glyburide (1 \( \mu \)M) reduced the lifetime in either the \( C_2 \) (from 9.7 to 20 ms) or the \( C_3 \) (from 417 to 833 ms) closed states (Fig. 2 B). The mean lifetime (\( \sigma_{C_2,3} \)) the channel spent within \( C_2 < C_3 \) closed states increased from 132 ms in the absence to 589 ms in the presence of glyburide (Fig. 2 B). Thus, ATP and glyburide, despite apparent differences in the mechanism of chan-
channel inhibition, act outside the intraburst \( C_1 \leftrightarrow O \) transition, shorten burst duration, and prolong the time the \( K_{\text{ATP}} \) channel remains within \( C_2 \) and \( C_3 \) closed states.

**UDP Prevents Ligand Inhibition of \( K_{\text{ATP}} \) Channels by Favoring Intraburst Activity**

In the absence of UDP, \( K_{\text{ATP}} \) channel activity exhibited intraburst and interburst transitions (Fig. 3, A and B, Table I) and was sensitive to the inhibitory action of ATP (200 \( \mu \)M). Washout of ATP restored channel activity, which was directed towards intraburst transition by 1 mM UDP (Fig. 3, A and C). Intraburst forward and backward rates of transition were similar before (2,000 and 434 s\(^{-1}\)), and after (2,000 and 420 s\(^{-1}\)) addition of UDP and ATP. However, UDP eliminated gaps between bursts in all patches so tested \((n = 4)\), which induced an apparent insensitivity of the \( K_{\text{ATP}} \) channel towards ATP (Fig. 3 A).

The effect of UDP was also tested in the presence of glyburide, a nonnucleotide inhibitory ligand of the channel. As in the case of ATP (Fig. 3 A), maintenance of channel activity within intraburst transitions by UDP also prevented glyburide (3 \( \mu \)M) to block \( K_{\text{ATP}} \) channel activity (Fig. 3 D; \( n = 6 \)). Thus, regardless of the structure of the inhibitory ligand, UDP could apparently shield the \( K_{\text{ATP}} \) channel from ATP or glyburide by “trapping” the channel within ligand-insensitive transitions.

**UDP Is Not the Sole Determinant of Sensitivity to Inhibitory Ligands**

The efficacy with which UDP antagonizes ATP- and glyburide-inhibitory gating has been reported to vary with the operative condition of the \( K_{\text{ATP}} \) channel (Terzic et al., 1994; Brady et al., 1998). As shown in Fig. 4 A, sustained spontaneous \( K_{\text{ATP}} \) channel activity was only partially sensitive to ATP (300 \( \mu \)M) in the presence of UDP (2 mM), yet fully sensitive in the absence of UDP \((n = 10)\). With channel “rundown,” UDP restored channel activity but could no longer antagonize ATP (Fig. 4 A, see also Terzic et al., 1994). Similarly, after rundown, UDP induced channel opening that was inhibited by glyburide (1 \( \mu \)M; Fig. 4 B; \( n = 5 \)). However, restoration of spontaneous channel activity, by pretreatment with MgATP (5 mM), was associated with return of UDP-induced antagonism of glyburide inhibition (Fig. 4 B, see also Brady et al., 1998). Thus, channel rundown ap-

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**Table I**

Parameters of Open and Closed Time Distributions of \( K_{\text{ATP}} \) Channel Activity Obtained under Different Experimental Conditions

<table>
<thead>
<tr>
<th>Condition</th>
<th>Sustained channel activity</th>
<th>Partial rundown</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of events within burst (( N_\text{IB} ))</td>
<td>27115 + UDP</td>
<td>23094 - ATP</td>
</tr>
<tr>
<td>Number of events between burst (( N_\text{IB} ))</td>
<td>27 2</td>
<td>+ UDP 23</td>
</tr>
<tr>
<td>Gaps within a burst (( t_{\text{c1}} ), ms)</td>
<td>0.44 0.44</td>
<td>- UDP 0.49</td>
</tr>
<tr>
<td>Gaps between bursts, fast (( t_{\text{c2}} ), ms)</td>
<td>5.34 9.4</td>
<td>- UDP 12.1</td>
</tr>
<tr>
<td>Gaps between bursts, slow (( t_{\text{c3}} ), ms)</td>
<td>39.3 230</td>
<td>- UDP 700</td>
</tr>
<tr>
<td>Relative area of ( t_{\text{c2}} ) (( a_2 ))</td>
<td>0.6 -</td>
<td>- UDP 0.66</td>
</tr>
<tr>
<td>Relative area of ( t_{\text{c3}} ) (( a_3 ))</td>
<td>0.4 -</td>
<td>- UDP 0.34</td>
</tr>
<tr>
<td>Open time (( \tau_\text{o} ), ms)</td>
<td>2.83 2.9</td>
<td>- UDP 2.3</td>
</tr>
</tbody>
</table>

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**Figure 2.** Inhibitory ligands act on \( K_{\text{ATP}} \) channels outside intraburst transition. Portions of original single channel records in the absence \((a_1 \) and \( b_1 \)) and presence \((a_2 \) and \( b_2 \)) of 100 \( \mu \)M ATP or 1 \( \mu \)M glyburide \((b_2)\). Corresponding kinetic schemes with calculated rates of transitions (in s\(^{-1}\), Eq. 8) are provided for each record in the absence and presence of ATP \((A)\) and in the absence and presence of glyburide \((B)\). Holding potential was —60 mV throughout.
pears to decrease the efficacy with which UDP antagonizes the action of inhibitory ligands.

**Rundown Prevents UDP from Holding K<sub>ATP</sub> Channels within Intraburst Transitions**

Progression of rundown of K<sub>ATP</sub> channel activity was associated with an increased number of prolonged closures (Fig. 5A, top). Intraburst channel properties (τ<sub>c,1</sub> and τ<sub>c,2</sub>, Fig. 5B, Table 1) were unchanged with rundown, but both fast and slow time components defining gaps between burst (τ<sub>c,2</sub> and τ<sub>c,3</sub>) were prolonged (Fig. 5C, Table 1). As the process of rundown accelerated, the k<sub>02</sub> rate responsible for exit of the channel from a burst (from 0.52 ± 0.07 s<sup>-1</sup>, n = 4, under sustained activity to 3.1 s<sup>-1</sup> during rundown; Fig. 5), mean burst duration of partial rundown channels was shorter when compared with sustained channel activity (τ<sub>burst</sub> = 440 ms; n<sub>burst</sub> = 224 vs. τ<sub>burst</sub> = 2,456 ± 315 ms; n = 4). Furthermore, K<sub>ATP</sub> channels under partial rundown spent a significantly longer time in the C₅ state (Eq. 10) when compared with channels under sustained channel activity (670 ms vs. 207 ± 84 ms; n = 4), although the apparent lifetime in the C₅ state (12 ms vs. 9.1 ± 1.4 ms, n = 4; Eq. 10) was similar under both conditions. Thus, channel rundown directed K<sub>ATP</sub> channels away from intraburst and towards interburst transitions.

To determine the efficacy with which UDP acts on K<sub>ATP</sub> channels driven towards the C₅ state as rundown progresses, UDP (1 mM) was applied to partially run-
K\textsubscript{ATP} channel activity by Mg-ATP switches on the UDP-induced antagonism of glyburide-dependent channel block. A 10-min pretreatment of rundown K\textsubscript{ATP} channels with 5 mM Mg-ATP restored spontaneous channel activity and with it the UDP-induced antagonism of glyburide-dependent channel block lost in rundown channels. In the absence of UDP, channel activity was readily inhibited by glyburide. The dotted line with original trace corresponds to the zero-current level. The dotted line corresponds to the zero-current level. The dotted line is parallel to the zero-current level.

**Figure 4.** Dual responsive behavior of K\textsubscript{ATP} channels, in the presence of UDP, towards ATP and glyburide. (A) After patch excision, K\textsubscript{ATP} channel activity was vigorous and sustained at maximal level by UDP (2 mM), under which condition ATP (300 \( \mu \)M) produced only partial channel inhibition. Removal of UDP was associated with channel inhibition by ATP. Such effect was reproducible. With time after patch excision, K\textsubscript{ATP} channel activity was observed to rundown. Under partial rundown, UDP enhanced channel activity, but only partially antagonized ATP-induced channel inhibition. The dotted line corresponds to the zero-current level. (B) Conversion of rundown to spontaneous rundown channels (Fig. 5 A, bottom). UDP increased channel activity and reduced the number of channel closures (Fig. 5 A, bottom). Similar to its effect on sustained K\textsubscript{ATP} channel activity, UDP did not affect intraburst kinetics; i.e., UDP did not significantly change rates defining the C\textsubscript{1} \( \leftrightarrow \) O transition (\( k_{o1} \) and \( k_{i1} \)) of partially rundown channels (Fig. 5 A and B). However, in contrast to sustained K\textsubscript{ATP} channel activity (Fig. 1), UDP did not eliminate interburst events in rundown channels, the distribution of which remained biexponential (Fig. 5 C). Also, in contrast to its effect on sustained channel activity where UDP eliminated the O \( \leftrightarrow \) C\textsubscript{2} transition (from 0.35 to \( \sim \)0 s\textsuperscript{-1}; Fig. 1, Table I), UDP only decreased the transition rate (\( k_{o2} \)) associated with burst closure of partially rundown channels (i.e., the O \( \leftrightarrow \) C\textsubscript{2} transition changed from 3.1 to 2.0 s\textsuperscript{-1}; Fig. 5 D). Under this condition, the K\textsubscript{ATP} channel could still transit between intraburst and interburst states despite the presence of UDP (Fig. 5 A and C). Mean burst duration (Eq. 9) of partially rundown channels increased in the presence of UDP from \( \tau_{\text{burst}} = 440 \) ms (\( \eta_{\text{burst}} = 224 \)) to \( \tau_{\text{burst}} = 684 \) ms (\( \eta_{\text{burst}} = 125 \)), similar to calculated values of \( \tau_{\text{burst}} \) (412 and 631 ms in the absence and presence of UDP, respectively; Eq. 9). Acting on partially rundown channels, UDP apparently reduced the lifetime the channel spent within interburst transitions (3 and 15 ms for C\textsubscript{2} and C\textsubscript{5}, respectively; Fig. 5 A; Eq. 10). Thus, under such conditions, although UDP still directed partially rundown channels towards intraburst ligand-insensitive transitions, the nucleotide diphosphate could not maintain the channel within a ligand-insensitive state.

**Allosteric Model of Ligand/Channel Interaction**

It has been reported that UDP shifts to the right the concentration–response curve to ATP (Terzic et al., 1994a), whereas it completely eliminates the sensitivity of the K\textsubscript{ATP} channel to glyburide (Brady et al., 1998). Based on the kinetic model, it was not possible to quantitatively predict the different response of K\textsubscript{ATP} channels to inhibitory ligands. Therefore, an allosteric model of ligand/protein interaction (Monod et al., 1965), previously applied to analyze ligand regulation of ion channels (Karlin, 1967; Hosoya et al., 1997; Tibbs et al., 1997), was used. The features of such allosteric models are that (a) the allosteric protein (i.e., the channel complex) interconverts within two distinct conformational states: ligand-sensitive (S) and -insensitive (I); (b) the channel complex possesses two sets of binding sites (\( n \) and \( m \)), one for the inhibitor (A), and the second for the activator (B); (c) each set of binding sites is equivalent within a state, but exhibits different microscopic dissociation constants (\( K_{A,S} \) or \( K_{B,S} \) in S and \( K_{A,I} \) or \( K_{B,I} \) in I) between states; and (d) binding of an inhibitor or an activator shifts, in opposite directions, the equilibrium between the two conformational states and thus increases the fraction of total protein (chan-
Allosteric Regulation of K\textsubscript{ATP} Channels

Channel complex) in the state with higher affinity for a particular ligand and decreases the apparent (macroscopic) affinity towards the other ligand.

The equilibrium constant (\(L\)) in the absence of a ligand was expressed by the ratio between the channel lifetime in ligand-insensitive (i.e., mean burst duration; Eq. 9) and -sensitive (i.e., lifetime spent in \(C_2\) plus \(C_3\); Eq. 11) states:

\[
L = \frac{\sigma_{\text{burst}}}{\sigma_{C_{2,3}}} = \frac{(k_{30} + k_{10})k_{20}}{(k_{32} + k_{12})k_{02}}. \tag{11}
\]

From our experimental data (i.e., Figs. 1 and 2), calculation of \(L\) revealed a value in the range of 150–200 under spontaneous channel activity. This indicates that under sustained spontaneous channel activity the equilibrium between ligand-sensitive and -insensitive states is significantly shifted towards ligand-insensitive states, which corresponds to a prolonged burst of channel activity.

Channel inhibition is a function of the fraction of the protein in the \(S\) state:

\[
S = \frac{1}{1 + L \left[ \frac{1 + d\beta}{1 + \beta} \right]^{n} \left[ 1 + c\alpha \right]^{n} + \alpha}. \tag{12}
\]

where \(d = K_{B,S}/K_{B,F}\), \(\beta = [B]/K_{B,S}\), \(c = K_{A,S}/K_{A,F}\), and \(\alpha = [A]/K_{A,S}\). For \(A\), the allosteric inhibitor (e.g., glyburide or ATP), \(c < 1\). For \(B\), the allosteric activator (i.e., UDP), \(d > 1\).

In the absence of UDP, the concentration dependence of \(K_{\text{ATP}}\) channel inhibition by glyburide (\(A\); Fig. 6...
Alekseev et al. was well fitted by the 1-S function (Eq. 13) using the following parameters: $L = 200; K_{AS} = 1$ nM, $K_{AI} = 1$ mM, $n = 1$ (Fig. 6 A, solid line). In the presence of 1 mM UDP, the observed loss of sensitivity of the $K_{ATP}$ channel towards the sulfonylurea (Fig. 6 A, ○) was well described by the allosteric model ($L = 200; K_{AS} = 1$ nM, $K_{AI} = 1$ mM, $n = 1; K_{BS} = 3.5$ mM, $K_{BI} = 0.1$ mM, $m = 4$). The model predicts that at millimolar concentrations of the activator (UDP) the effect of glyburide on $K_{ATP}$ channel activity will be fully antagonized even at tens of micromoles of the inhibitor (Fig. 6 A, solid line).

In the absence of UDP, the concentration dependence of $K_{ATP}$ channel inhibition by ATP (A; Fig. 6 B, ■) was also well fitted by the 1-S function (Eq. 13) using the following parameters: $L = 200; K_{AS} = 8.5 \mu$M, $K_{AI} = 70$ nM, $n = 3.6$ (Fig. 6 B, curve 1). However, in the presence of UDP (5 mM; $K_{BS} = 3.5$ mM, $K_{BI} = 0.1$ mM, $m = 4$), the allosteric model predicted a rightward shift but failed to precisely fit (Fig. 6 B, curve 2) the experimentally obtained data defining the concentration response of ATP-induced $K_{ATP}$ channel inhibition under this condition (Fig. 6 B, ▽). Since varying the number of binding sites, cooperativity, and/or dissociation constants for ATP did not improve the fit, we further developed the model taking into account the existence of an additional presumed binding site for ATP not affected by nucleotide diphosphate regulation (Tucker et al., 1997; Ueda et al., 1997). Therefore, we added to the 1-S function (Eq. 13) an additional allosteric regulation-independent inhibitory process to account for both mechanisms of ATP inhibitory action:

**Figure 6.** Use of an allosteric model to predict the effect of glyburide or ATP on $K_{ATP}$ channel opening in the absence and presence of UDP. (A) Concentration dependence of glyburide-induced $K_{ATP}$ channel inhibition in the absence (●) and presence (○) of 1 mM UDP. Data points are from five to nine patches. Relative effect of glyburide was calculated in each patch as a ratio between slopes of cumulative $n_P$, measured in the presence over the value obtained in the absence of glyburide (see Brady et al., 1998). Solid curves were constructed using Eq. 13 at various concentrations of UDP (see text for values of parameters). (B) Concentration dependence of ATP-induced $K_{ATP}$ channel inhibition in the absence (■) and presence (◇) of 5 mM UDP. Data points are from 4 to 10 patches. Relative effect of ATP was calculated in each patch as a ratio between $n_P$ values measured in the presence over the value obtained in the absence of ATP (see Terzic et al., 1994a). Curves 1 and 1′ (at 0 mM UDP), 2 and 2′ (at 5 mM UDP) were constructed using Eqs. 13 and 14, respectively. See text for values of parameters.
where $K_d$ is the dissociation constant to this additional ATP binding site. In this adjusted model, $K_d = 610 \, \mu M$ could fully account for the ATP-induced channel inhibition in the absence (Fig. 6 B, curve 1') and presence (Fig. 6 B, curve 2') of UDP. The prediction based on the developed model can be interpreted to mean that UDP antagonized ATP-induced $K_{ATP}$ channel inhibition through one set of ATP-binding sites, thus reducing channel inhibition to the other set of ATP-binding sites.

Despite the lack of reliable means to quantify the rundown process, the allosteric model could, in principle, also be used to describe the effects of ligands under rundown of $K_{ATP}$ channel activity. Based on our experimental data (Fig. 5), rundown shifted the equilibrium constant ($L$) from 150–200 under spontaneous channel activity to 10–20 under partial rundown, and to even lower values with further progression of rundown. This was associated with a prolongation of the lifetime the channel spent in C$_d$ and C$_3$ closed states. In contrast to spontaneous channel activity, where UDP increased $L \rightarrow \infty$(by $k_{a0} \rightarrow 0$), under partial rundown UDP elevated $L$ only up to 70–90 (i.e., Fig. 5). However, such a change in $L$ was not sufficient to restore the experimentally obtained channel sensitivity towards ATP and glyburide (Terzic et al., 1994) and Brady et al., 1998). This could indicate that besides the effect on $L$, rundown could also alter other parameters of channel/ligand interaction. For instance, rundown could decrease the affinity of ligands for the I state, which would promote the effect of inhibitors (Thuringer and Escande, 1988; Deutsch and Weiss, 1993). Thus, the use of the allosteric model could explain the nonuniform responsive behavior of $K_{ATP}$ channels to inhibitory ligands in the presence of UDP depending on the operative condition of the channel.

**Discussion**

The present study demonstrates that cardiac $K_{ATP}$ channels can be directed to operate within ligand-insensitive conformational states. The switch into ligand-insensitive behavior was induced by the nucleotide diphosphate, UDP. Interconversion between ligand-sensitive and -insensitive states represents a novel mechanism of $K_{ATP}$ channel regulation. The property of a nucleotide diphosphate to direct cardiac $K_{ATP}$ channels towards a state that is insensitive towards inhibitory ligands could provide a mechanistic basis for channel opening in the presence of inhibitory concentrations of ATP within an intact cell.

**Ligand–Channel Interaction and Kinetic Model**

To distinguish between conformational transitions that define $K_{ATP}$ channel activity, we applied a linear kinetic model used previously (Sakmann and Trube, 1984; Gillis et al., 1989; Nichols et al., 1991; Furukawa et al., 1993; Takano and Noma, 1993). This entropic model does not describe all conformations through which a channel transits, but it does allow description of end points of sequential conformational transitions accessible to direct measurement. Although this simplified model was developed for inward $K_{ATP}$ channel current as recorded under present experimental conditions (with symmetrical $K^+$ solutions and at a holding potential of $-60 \, mV$), intraburst and interburst transitions can also be distinguished for outward $K_{ATP}$ channel currents despite more complex intraburst kinetics (Zilberter et al., 1988; Larsson et al., 1993; Alekseev et al., 1997b). Herein, we found that the inhibitory ligands, ATP and glyburide, inhibited $K_{ATP}$ channel activity by acting upon conformational states that define interburst behavior without affecting intraburst channel transitions. This is in agreement with previous studies that have also shown that inhibitory ligands target specific rates of channel kinetics (Gillis et al., 1989; Qin et al., 1989; Nichols et al., 1991; Takano and Noma, 1993; Benz and Kohlhardt, 1994; Smith et al., 1994). We further found that UDP could keep the channel within a burst, preventing interburst transitions. Therefore, the observed effect of UDP to antagonize channel inhibition by ATP and glyburide could be attributed to the limitation of channel behavior within ligand-insensitive intraburst conformational transitions. Such a mechanism could explain the altered responsiveness of cardiac $K_{ATP}$ channels towards ATP and sulfonylureas observed in the presence of nucleotide diphosphates (Nichols and Lederer, 1991; Venkatesh et al., 1991; Virag et al., 1993; Findlay, 1994; Terzic et al., 1994a; Brady et al., 1998). Based on the kinetic model used, the present study provides evidence that the response of the cardiac $K_{ATP}$ channel depends not only on the concentration of an inhibitor, but also on the lifetime the channel spends within ligand-sensitive states. This concept may not be limited to UDP. Indeed, it has been shown that other agents, such as potassium channel openers (Fan et al., 1990; Terzic et al., 1994b), intracellular protons (Vivaudou and Forestier, 1995; Alekseev et al., 1997), cytoskeleton disrupters (Brady et al., 1996), or channel trypsinization (Deutsch and Weiss, 1994), which also promote the $K_{ATP}$ channel to operate within a burst, decrease the sensitivity of the channel towards inhibitory ligands. Furthermore, combined application of ADP and the opener diazoxide potentiated the ability of these agents to antagonize ATP inhibition of $K_{ATP}$ channels by prolonging the lifetime the channel spends within a burst (Larsson et al., 1993). Conversely, ATP and related nucleotides that direct the $K_{ATP}$ channel to operate within interburst transitions were shown to enhance the sensitivity of $K_{ATP}$ channels towards sul-
Application of an Allosteric Model to the Regulation of $K_{\text{ATP}}$ Channels

The dual nature of $K_{\text{ATP}}$ channel behavior, in terms of ligand-sensitive and -insensitive states, drew parallelism with interconversion of an allosteric protein between two significant conformational states with different affinities to ligands (Monod et al., 1965; Karlin, 1967). This allosteric model predicted the observed change in the ATP- and glyburide-dependent inhibitory gating of the channel induced by a UDP-mediated shift in the equilibrium towards the ligand-insensitive state of the $K_{\text{ATP}}$ channel. The difference in the microscopic affinities for the two conformational states ($10^6$ for glyburide and $\sim 10^4$ for ATP) predicted by the present allosteric model is consistent with the existence of ligand-insensitive and -sensitive states of the channel. In fact, the allosteric model predicted that at millimolar concentrations of UDP the cardiac $K_{\text{ATP}}$ channel loses its sensitivity towards glyburide. This is in accord with previous studies that have established that under spontaneous $K_{\text{ATP}}$ channel activity, nucleotide diphosphates, such as UDP or ADP, antagonize sulfonylurea-induced channel inhibition (Venkatesh et al., 1991; Virag et al., 1993; Brady et al., 1998). Although it is difficult to compare microscopic with apparent dissociation constants, high and low affinities for sulfonylurea binding have been previously reported (Fosset et al., 1988; Aguilar-Bryan et al., 1992). Thus, due to the negligible affinity of glyburide towards the ligand-insensitive (I) state, UDP by shifting the equilibrium of the $K_{\text{ATP}}$ channel towards this particular state could effectively antagonize the effect of the sulfonylurea. In the case of ATP, for which the model predicts an additional, nucleotide diphosphate-independent, ATP-inhibitory channel gating, UDP could produce only a rightward shift in the concentration response curve of ATP-induced channel inhibition, as previously experimentally observed with UDP (Terzic et al., 1994a) or other nucleotide diphosphates such as ADP (Findlay, 1988; Lederer and Nichols, 1989). In contrast to UDP, channel rundown shifted the equilibrium towards the ligand-sensitive state of the $K_{\text{ATP}}$ channel. This increased sensitivity of the channel towards inhibitory ligands is in accord with experimental findings that have shown that rundown enhances the inhibitory action of ATP on cardiac $K_{\text{ATP}}$ channel activity (Thuringer and Escande, 1989; Deutsch and Weiss, 1993). Since rundown is believed to be associated with changes in the phosphorylation status of the $K_{\text{ATP}}$ channel or associated proteins (Trube and Hescheler, 1984; Findlay and Dunne, 1986; Findlay, 1987; Ohno-Shosaku et al., 1987; Takano et al., 1990; Furukawa et al., 1996; Hilgemann and Ball, 1996), the equilibrium between the S and I channel states may be dependent upon a phosphorylation process. Treatment of rundown membrane patches with Mg-ATP (but not with ATP alone or with nonhydrolyzable ATP analogs), through presumed “rephosphorylation” of channel proteins, restored spontaneous cardiac $K_{\text{ATP}}$ channel activity, and with it the efficacy of UDP to antagonize ATP- and glyburide-induced channel inhibition (see also Terzic et al., 1994a; Brady et al., 1998).

Relevance to the Molecular Structure of $K_{\text{ATP}}$ Channels

Results predicted by the allosteric model applied herein to the native cardiac $K_{\text{ATP}}$ channel are in agreement with the reported structure and stoichiometry of the recombinant $K_{\text{ATP}}$ channel complex (Inagaki et al., 1995, 1996; Isomoto et al., 1996; Clement et al., 1997; Tucker et al., 1997). This channel is a heteromultimer that combines four Kir6.2 and four SUR subunits into an octamer (Clement et al., 1997; Inagaki et al., 1997). It has been suggested that ATP binds to both the pore-forming Kir6.2 (Tucker et al., 1997) and the regulatory SUR (Bernardi et al., 1992; Ueda et al., 1997) subunits. In view of this, the requirement of two sets of binding sites for ATP could be interpreted to indicate two separate ATP-binding sites on each subunit of the channel complex. The allosteric model further predicts four binding sites for UDP on the $K_{\text{ATP}}$ channel complex. This apparently correlates with the previously observed binding of a nucleotide diphosphate to only one of the channel subunits, the SUR subunit (Bernardi et al., 1992; Nichols et al., 1996; Gribble et al., 1997; Trapp et al., 1997; Tucker et al., 1997; Ueda et al., 1997). The binding of sulfonylureas to the $K_{\text{ATP}}$ channel is also presumed to occur on the SUR subunit (Aguilar-Bryan et al., 1995; Inagaki et al., 1995, 1996; Clement et al., 1997). However, in terms of the allosteric model and in contrast to nucleotides, $K_{\text{ATP}}$ channel regulation by glyburide was characterized by lack of cooperativity (see also Venkatesh et al., 1991).

Intraburst kinetics that define ligand-insensitive transitions are apparently associated with conformational fluctuation of Kir6.2 itself (Alekseev et al., 1997b; Tucker et al., 1997), whereas interburst kinetics are modulated by association of Kir6.2 with the SUR subunit (Inagaki et al., 1996). In view of the proposed structure of the $K_{\text{ATP}}$ channel complex (Inagaki et al., 1995, 1996, 1997; Clement et al., 1997; Tucker et al., 1997), the kinetic and allosteric properties of channel behavior may provide the basis for a mechanistic model of the UDP-induced changes in the ATP- and glyburide-dependent regulation of $K_{\text{ATP}}$ channel gating (Fig. 7). Such a model implies the existence of two inhibitory gating pathways. The first, mediated through binding of inhibi-
An allosteric mechanism, which takes into account the proposed structure of the K<sub>ATP</sub> channel (Inagaki et al., 1995, 1996, 1997; Clement et al., 1997), as well as the kinetic and allosteric properties of channel behavior, suggests the existence of two inhibitory gating mechanisms of K<sub>ATP</sub> channels labeled 1 and 2. The inhibitory gating mechanism number 1 transduces inhibitory signals from glyburide (Glyb) and ATP-binding sites on the SUR channel subunit. This inhibitory gating can be intercepted after binding of a nucleotide-diphosphate (NDP) to the SUR subunit. Presumed dephosphorylation of the channel affects nucleotide diphosphate-dependent regulation of channel gating. The gating mechanism number 2 transduces inhibitory signals from the ATP-binding site on the Kir6.2 channel subunit, which appears to be insensitive to nucleotide-diphosphate regulation.

**Concluding Remarks**

Although the present study used UDP as a nucleotide diphosphate, the observed effect on K<sub>ATP</sub> channel behavior may also be attributable to other nucleotide diphosphates, such as ADP. In contrast to UDP, the presence of the adenine moiety could make the interpretation of the effect of ADP more complex due to possible competitive interaction of ADP with an ATP-binding site (Ueda et al., 1997). Despite this, similar effects of ADP (MgADP) in modulating the K<sub>ATP</sub> channel inhibitory gating and postrundown channel behavior have previously been demonstrated (Dunne and Petersen, 1986; Tung and Kurachi, 1991; Venkatesh et al., 1991; Weiss and Venkatesh, 1993; Findlay, 1988, 1994; Elvir-Mairena et al., 1996), as well as the ability of MgADP to prolong burst duration (Larsson et al., 1993).

The property of cardiac K<sub>ATP</sub> channels to interconvert between ligand-sensitive and -insensitive states, described herein, resembles other ion channels that also show differential sensitivity towards ligands depending on their operative state, including “use-dependent” blockade of Na<sup>+</sup> and Ca<sup>2+</sup> channels (Lee and Tsien, 1983; Hill et al., 1989; Ragsdale at al., 1994; Nuss et al., 1995). Entry of the K<sub>ATP</sub> channel into a ligand-insensitive state by a nucleotide diphosphate could provide a basis for cardiac K<sub>ATP</sub> channel opening during hypoxia or ischemia despite rather constant levels of ATP within the cell.

**Figure 7.** Scheme of UDP-induced change in ATP- and glyburide-dependent inhibitory channel gating. This mechanistic model, which takes into account the proposed structure of the K<sub>ATP</sub> channel (Inagaki et al., 1995, 1996, 1997; Clement et al., 1997), as well as the kinetic and allosteric properties of channel behavior, suggests the existence of two inhibitory gating mechanisms of K<sub>ATP</sub> channels labeled 1 and 2. The gating mechanism number 1 transduces inhibitory signals from glyburide (Glyb) and ATP-binding sites on the SUR channel subunit. This inhibitory gating can be intercepted after binding of a nucleotide-diphosphate (NDP) to the SUR subunit. Presumed dephosphorylation of the channel affects nucleotide diphosphate-dependent regulation of channel gating. The gating mechanism number 2 transduces inhibitory signals from the ATP-binding site on the Kir6.2 channel subunit, which appears to be insensitive to nucleotide-diphosphate regulation.

This work was supported by grants from the Bruce and Ruth Rappaport Program in Vascular Biology and Gene Delivery, the Miami Heart Research Institute, the American Heart Association, the George M. Einseberg Cardiovascular Research Fund, and the Harrington Professorship Fund (to A. Terzic). P.A. Brady is supported by a Clinician-Investigator Fellowship from General Mills.

**Original version received 18 July 1997 and accepted version received 24 November 1997.**

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