

Molecular physiology of neuronal K-ATP channels (Review)

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Summary

ATP sensitive potassium (K-ATP) channels are widely expressed in many cell types including neurons. K-ATP channels are heteromeric membrane proteins that consist of two very different subunits: the pore-forming, two-transmembrane spanning potassium channel subunit (Kir6) and the regulatory, 17 transmembrane spanning sulphonylurea receptor (SUR). This ensemble—joined together in a 4:4 stoichiometry—endows this channel with a unique combination of functional properties. The open probability of K-ATP channels directly depends on the intracellular ATP/ADP levels allowing the channels to directly couple the metabolic state of a cell to its electrical activity. Here, recent progress on the molecular composition and functional diversity of neuronal K-ATP channels is reviewed. One is particular concerned with single-cell mRNA expression studies that give insight to the coexpression patterns of Kir6 and SUR isoforms in identified neurons. In addition, the physiological roles of neuronal K-ATP channels in glucose sensing and adapting neuronal activity to metabolic demands are discussed, as well as their emerging pathophysiological functions in acute brain ischemia and chronic neurodegenerative diseases.

Keywords: K-ATP channels; single-cell RT-PCR; glucose sensing; ischemia; Parkinson's disease

Abbreviations: CXI, complex I of the respiratory chain; ER, endoplasmic reticulum; Girk2, G-protein coupled inwardly rectifying potassium channel 2; GR, glucose responsive; K-ATP, ATP sensitive potassium channel; bp, basepairs; Kir, inwardly rectifying potassium channel; NBF, nucleotide binding folds; RT-PCR, reverse-transcriptase polymerase chain reaction; MPTP, 1-methyl-4-phenyl-1,2,3,5-tetrahydropyridine; NTS, nucleus tractus solitarius; SNpc, substantia nigra pars compacta; SUR, sulphonylurea receptor; TPEA, three prime end amplification; VMH ventromedial hypothalamus.

Introduction

ATP sensitive potassium (K-ATP) channels were first discovered by Noma (1983) in cardiac myocytes and were subsequently found in many other excitable celltypes, like cardiac and smooth muscle cells, pancreatic islet cells, and various brain regions (Ashcroft 1988). K-ATP channels are unique in their molecular makeup and their cellular function: Functional channels are octameric proteins formed by two different types of subunits, members of the Kir6 inwardly rectifying potassium channel family (Reimann and Ashcroft 1999) and sulphonylurea receptor (SUR) subunits, members of the ABC transporter superfamily (Higgins 1995). As the open probability of K-ATP channels directly depends on the

intracellular ATP/ADP levels, the channels directly couple the metabolic state of a cell to its electrical activity. The physiological role of K-ATP channels is best understood in pancreatic beta cells, where they couple blood glucose levels to insulin secretion. In cardiac myocytes, their activation during ischemia leads to shortening of the action potential. In vascular smooth muscle cells, they are involved in controlling the vessel tone and in skeletal muscle they contribute to the exercise induced K⁺ efflux (Quayle *et al.* 1997, Ashcroft and Gribble 1999). This review will focus on the differential expression and functional roles of neuronal K-ATP channels in the brain.

Molecular composition of K-ATP channels

Functional K-ATP channels are octameric complexes, consisting of four Kir6 subunits joined together with four regulatory SUR subunits (Clement *et al.* 1997, Inagaki *et al.* 1997, Shyng and Nichols 1997) (Figure 1). The K-ATP channel pore is formed by the Kir6 subunits. Like other members of the inwardly rectifying potassium channel family, the Kir6 subunit consists of two transmembrane domains (TMs), linked by a pore loop, and intracellular amino- and carboxyterminal ends. An endoplasmic reticulum (ER) retention signal is located in the C-terminus of Kir6.2, preventing the delivery of functional K-ATP channels to the plasmamembrane in the absence of SUR subunits. However, a C-terminally truncated form of Kir6.2 (Kir6.2ΔC26 or Kir6.2ΔC36) gives rise to functional, ATP-sensitive potassium channels that reach the plasmamembrane without the SUR subunits (Tucker *et al.* 1997, Zerangue *et al.* 1999). The SUR is believed to contain 17 TMs, with an extracellular N- and an intracellular C-terminus. The TMs are arranged in three groups (5, 6, 6), connected by cytoplasmatic linkers, and two intracellular SUR domains contain a nucleotide-binding domain (NBD). These NBDs contain the classical Walker A and B motive for ATP binding and hydrolysis. Surprisingly, the ATP sensitivity of K-ATP channels is not located on the SUR subunits, but on the Kir6 subunit and is decreased by phosphoinositolphosphates like PIP2 (Baukrowitz *et al.* 1998, Shyng and Nichols 1998). The ATP binding site of Kir6.2 has not yet been identified, although several important C and N-terminal residues have been described (Tucker *et al.* 1997, 1998, Aguilar-Bryan *et al.* 1998). The regulatory SUR subunits mask the Kir6.2 ER retention signal and transfer the sensitivity to K-ATP channel blockers (e.g. sulphonylureas like tolbutamide and glibenclamide) and activators (e.g. diazoxide, pinacidil and nicrandil). The high-affinity binding site for sulphonylureas is located on the SUR1 subunit; a low affinity site is located on the Kir6.2 subunit (Gribble *et al.* 1997). In addition, SUR is critically involved in the metabolic sensitivity of K-ATP channels as the binding of magnesium nucleosides and nucleotides leads to an increase of channel activity. The pharmacological diversity of native and recombinant K-ATP channels has

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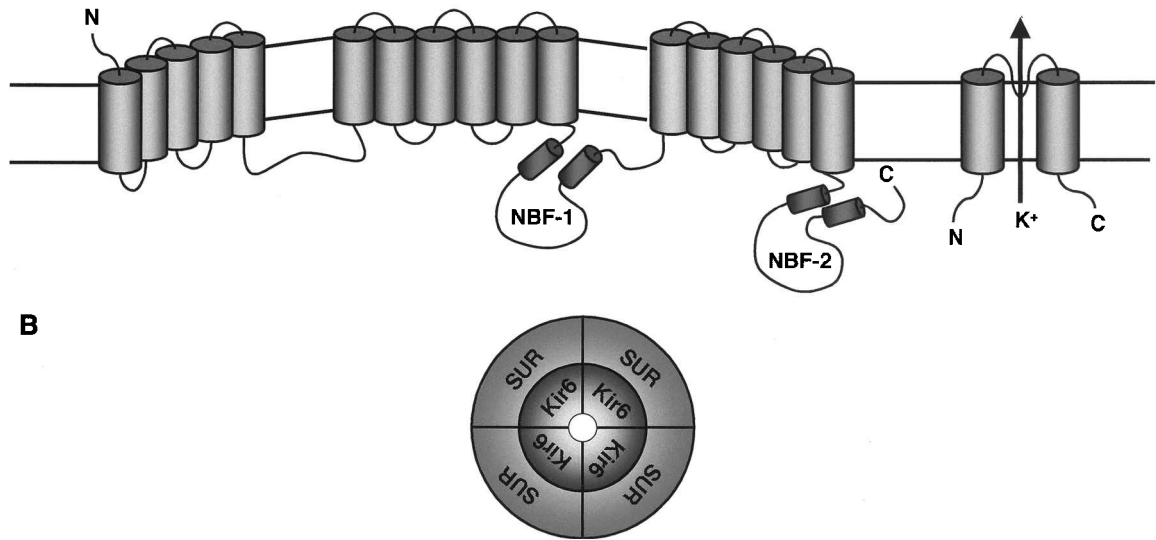


Figure 1. Subunit composition and stoichiometry of K-ATP channels. (a) K-ATP channels are made up by inwardly rectifying potassium channel subunits (Kir6.1 or Kir6.2) and sulphonylurea receptor subunits (SUR1, SUR2A or SUR2B). Two intracellular nucleotide-binding folds (NBF-1 and NBF-2) are located intracellularly on the SUR subunit. (b) In functional K-ATP channels, four pore forming Kir6 subunits are joined together with four regulatory SUR subunits.

recently been reviewed (Bryan and Aguilar-Bryan 1999, Seino 1999, Ashcroft and Gribble 2000).

Up until now, two members of the Kir6 family have been cloned, Kir6.2 and Kir6.1 (Inagaki *et al.* 1995a, c, Sakura *et al.* 1995), and two SUR isoforms have been identified, SUR1 and SUR2 (Aguilar-Bryan *et al.* 1995). Furthermore, a variety of SUR1 and SUR2 splice variants have been described, with SUR2A and SUR2B being the most important (Sakura *et al.* 1995, Chutkow *et al.* 1996, 1999, Inagaki *et al.* 1996, Isomoto *et al.* 1996). The clustered localization of Kir6.2 and SUR1 on the human chromosome 11p15.1 (Inagaki *et al.* 1995a) and of Kir6.1 and SUR2 at 12p11 (Inagaki *et al.* 1995b, Chutkow *et al.* 1996) indicate that they might have been separated from a single ancestral gene earlier in evolution. In this context, it is noteworthy that a recently cloned *Drosophila* SUR could form functional sulphonylurea sensitive potassium channels in the absence of Kir6 subunits (Nasonkin *et al.* 1999). Recently, an additional player has been cloned. Alpha-endosulphine is a peptide highly expressed in the brain that acts like an endogenous sulphonylurea on the SUR and might be involved in the control of K-ATP channel activity. However, its precise functional role remains unclear at present (Heron *et al.* 1998).

Diversity of K-ATP channels

In heterologous expression systems, different combinations of the possible K-ATP channel subunits give rise to functional K-ATP channels with different biophysical, pharmacological and metabolic properties (Yokoshiki *et al.* 1998). Kir6.2, in combination with SUR1, forms highly diazoxide-sensitive K-

ATP channels with single-channel conductances of 60–80 pS and properties very similar to those present in pancreatic beta cells (Inagaki *et al.* 1995a, Sakura *et al.* 1995). Kir6.2 and SUR2A resemble the K-ATP channels of cardiac and skeletal muscle, relatively insensitive to diazoxide with similar single-channel conductances (Inagaki *et al.* 1996, Okuyama *et al.* 1998). SUR2B, in combination with Kir6.1 or Kir6.2 subunits, generates diazoxide-sensitive K-ATP channels that possess properties reminiscent of those studied in smooth muscle. K-ATP channels, with Kir6.1 as pore forming subunit, display a significantly smaller single-channel conductance of ~30 pS (Isomoto *et al.* 1996, Yamada *et al.* 1997). The molecular composition of the mitochondrial K-ATP channels remain unclear; however, its single channel conductance of 10–30 pS would be consistent with Kir6.1 subunits forming the channel pore of mitochondrial K-ATP channels (Inoue *et al.* 1991, Mironova *et al.* 1999). In addition, Kir6.1 protein has been immunocytochemically localized at mitochondria (Suzuki *et al.* 1997, Zhou *et al.* 1999).

Neuronal K-ATP channels

K-ATP channel subunits are also widely expressed throughout different brain regions, as indicated by sulphonylurea binding studies (Mourre *et al.* 1990, Treherne and Ashford 1991, Zini *et al.* 1991, Hicks *et al.* 1994, Dunn-Meynell *et al.* 1997), *in situ* hybridization and immunohistochemistry data (Karschin *et al.* 1997, Dunn-Meynell *et al.* 1998, Zhou *et al.* 1999). Moreover, a variety of different neuronal populations possess somatodendritic K-ATP currents with diverging

biophysical and pharmacological properties, indicating that the K-ATP channels in the brain do not belong to a homogeneous group. K-ATP channels have been described in cortical and hippocampal pyramidal- and interneurons (Ohno-Shosaku and Yamamoto 1992, Hyllienmark and Brismar 1996, Fujimura *et al.* 1997, Zawar *et al.* 1999, Pelletier *et al.* 2000), striatal neurons (Schwanstecher and Panten 1994, Schwanstecher and Bassen 1997, Lee *et al.* 1998), various nuclei of the hypothalamus (Ashford *et al.* 1990, Spanswick *et al.* 1997, 2000, Lee *et al.* 1999), GABAergic and dopaminergic substantia nigra neurons (Schwanstecher and Panten 1993, Roper *et al.* 1995, Stanford and Lacey 1995, 1996, Watts *et al.* 1995, Guatteo *et al.* 1998, Liss *et al.* 1999a), locus coeruleus neurons (Finta *et al.* 1993, Illes *et al.* 1994, Koyama *et al.* 1999), dorsal vagal (Trapp and Ballanyi 1995, Karschin *et al.* 1998), and other brainstem neurons (Dallaporta *et al.* 2000). Also, there is evidence for functional presynaptic K-ATP channels (Amoroso *et al.* 1990, Watts *et al.* 1995, Ye *et al.* 1997).

In accordance with the described high and low sulphonylurea binding sites and the functional and pharmacological diversity of K-ATP currents, the molecular makeup of neuronal K-ATP channels appears to be not homogeneous. However, it seems that Kir6.2 is the pore forming subunit in most neuronal populations and Kir6.1 may form the pore of glial and mitochondrial K-ATP channels in the brain (Karschin *et al.* 1997, Suzuki *et al.* 1997, Dunn-Meynell *et al.* 1998, Zawar *et al.* 1999, Zhou *et al.* 1999).

A combined approach of electrophysiological patch-clamp and single-cell mRNA expression profiling techniques (RT-PCR) (Monyer and Lambolez 1995) was used to study the coexpression patterns of K-ATP channel subunits in individual neurons. As illustrated in Figure 2, in this method, the cytoplasm of an electrophysiologically characterized neuron is harvested and the cellular mRNA is subsequently reverse transcribed into cDNA. After an optional amplification step of the single-cell cDNA pool, the expression of K-ATP channel subunits is detected by PCR amplification. So far, three variants of the single-cell method have been described: multiplex nested RT-PCR (Lambolez *et al.* 1992), antisense RNA (aRNA) amplification (Eberwine *et al.* 1992) and three prime and amplification (TPEA) PCR (Dixon *et al.* 1998).

Single-cell RT-PCR studies detected heterogeneous expression profiles of K-ATP channel subunits between and also within different neuronal populations. Table 1 summarizes the results of these studies. All known K-ATP channel subunits (except SUR2A) have been detected in different combinations in individual neurons. This suggests the presence of molecularly distinct neuronal K-ATP channels that might reflect different functional roles in the brain. However, very little is known about the plasticity and regulation of gene expression of neuronal K-ATP channels in the brain and, thus, any firm conclusions might be premature.

Function of neuronal K-ATP channels

Similar to peripheral tissues, two functional roles for neuronal K-ATP channels have been proposed. Inspired by the key role of K-ATP channels in beta cells, it is assumed that in

certain specialized neurons, e.g. in the hypothalamus, K-ATP channels might serve a similar role in glucose sensing and control of glucose homeostasis (Levin *et al.* 1999). As K-ATP channels are very widely expressed in the CNS, they are likely to serve a different functional role in most neuronal populations that are not involved in glucose-sensing; presumably in adapting electrical activity of neurons and synapses to their intrinsic energy metabolism.

Essential role of hypothalamic K-ATP channels in central glucose sensing

The functional role of K-ATP channels is best understood for the pancreatic beta cells, where these channels couple blood glucose levels to insulin secretion. In beta cells, K-ATP channels close in response to increased extracellular glucose concentrations that arise after food intake. To induce K-ATP channel closure, glucose has to be taken up and metabolized by the beta cells. Therefore, proteins like the low affinity glucose carrier GLUT2 and the glucose phosphorylating enzyme glucokinase are also essential components of glucose sensing. Furthermore, the NADH shuttle links cytosolic glycolysis with the activation of mitochondrial energy metabolism that increases the ATP/ADP ratio of the cell (Eto *et al.* 1999). This increased ATP/ADP ratio induces closure of K-ATP channels and subsequent membrane depolarization, which in turn initiates electrical activity and calcium-mediated exocytosis of insulin (Ashcroft and Gribble 1999). Recent dominant-negative transgenic and K-ATP knockout models have given explicit genetic evidence for the key role of Kir6.2/SUR1 containing K-ATP channels in glucose-induced insulin secretion (Miki *et al.* 1997, 1998, Seghers *et al.* 2000, Seino *et al.* 2000). Furthermore, targeting mutated K-ATP channels with reduced ATP-sensitivity to beta cells severely disrupts glucose-induced insulin secretion directly, demonstrating that accurate tuning of the ATP/ADP sensing function of the K-ATP channel is an essential molecular mechanism of peripheral glucose sensing *in vivo* (Koster *et al.* 2000).

Do some neuronal K-ATP channels serve an analogous function in central glucose sensing? In the hypothalamus, especially in the ventromedial hypothalamus (VMH) and the arcuate nucleus, a subset of neurons, called glucose-responsive (GR) neurons, are known to enhance their rate of action potential firing in response to physiological increases in glucose levels. These neurons are known to be involved in the neuroendocrine control of glucose homeostasis (Minami *et al.* 1986, Silver and Erecinska 1998, Yang *et al.* 1999). In this context, it is important to note that hypothalamic neurons also express glucokinase and GLUT2, other essential proteins for glucose sensing (Rayner *et al.* 1994, Nualart *et al.* 1999, Lynch *et al.* 2000). Further interesting parallels between beta cell and hypothalamic glucose sensors have been described (Yang *et al.* 1999, Schuit *et al.* 2001). GR neurons not only sense glucose concentrations like beta cells, but their electrical activities are also modulated by important hormones like leptin and insulin (Spanswick *et al.* 1997, 2000, Shiraishi *et al.* 2000). Although the existence of K-ATP channels has been demonstrated in GR neurons, the direct evidence for their involvement in the physiological

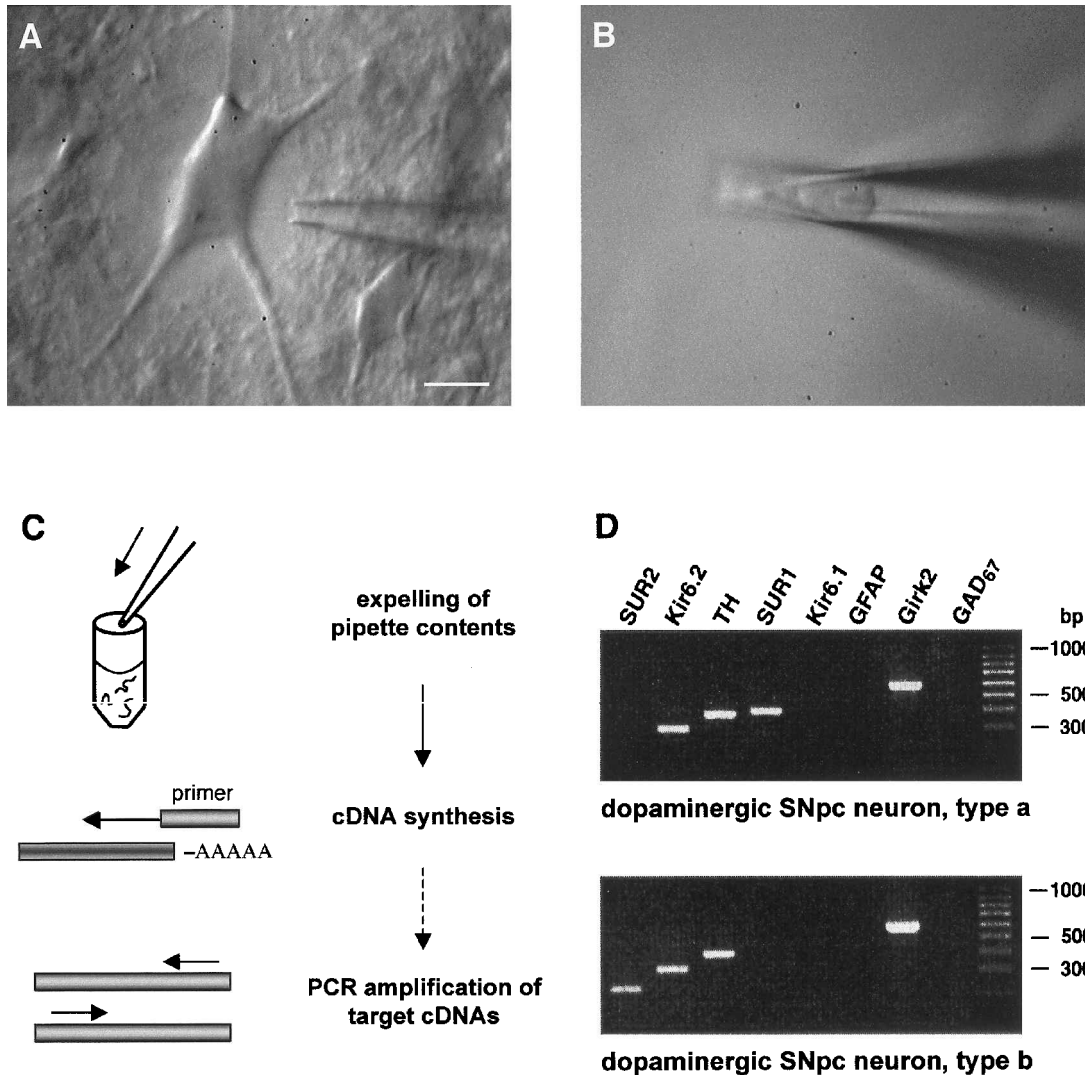


Figure 2. Principle of the single-cell RT-PCR technique to study K-ATP channel subunit expression in individual neurons. (a) A dopaminergic neuron in an acute mouse brain slice preparation before patch clamp recording visualized by IR-DIC videomicroscopy (scale bar: 15 μ m). (b) After electrophysiological characterization, the cytoplasmic contents of the neuron, containing the mRNA and the nucleus, are harvested with the patch pipette without losing the gigaseal. Picture shows the pipette after aspiration with the nucleus visible inside. (c) The contents of the patch pipette are subsequently expelled into a PCR reaction tube containing the contents for reverse transcription of the mRNA. After cDNA synthesis with random hexamer- or oligo-dT-primers, the cDNA is directly used for PCR amplification of target genes. Alternatively, the cDNA pool could be amplified prior to PCR. (d) After PCR amplification with gene-specific primers, the single-cell expression profiles are analysed via gelelectrophoresis. Picture shows the multiplex nested PCR results for two dopaminergic SNpc neurons. In addition to the four K-ATP channel subunits, it is probed in parallel for the expression of four marker genes (TH-tyrosine hydroxylase, GFAP-gial fibrillaric acidic protein, Girk2-G-protein coupled inwardly rectifying potassium channel, GAD67-glutamic acidic decarboxylase). A band indicates single-cell expression of the respective gene.

glucose-dependent regulation of excitability of GR neurons was missing. We could, recently, show the complete absence of both, functional K-ATP channels and glucose sensing in VMH neurons in a Kir6.2 knockout mouse (Liss *et al.* 2000). These findings demonstrate that the Kir6.2 subunit of K-ATP channels is not only a necessary molecular component for native VMH plasmamembrane K-ATP channels, it is also essential for glucose sensing in GR neurons. Furthermore, single-cell mRNA expression profiling and quantitative pharmacological data indicate that SUR1, in

combination with Kir6.2, builds the native beta cell-like K-ATP channel in GR neurons in the VMH (Miki *et al.* 2001). In contrast to the beta cell, glucose-induced activity in GR neurons does not induce direct secretion of neuronal hormones. It controls, via brainstem nuclei, the release of peripheral hormones, e.g. glucagons, that are mediators of glucose homeostasis (Steffens *et al.* 1990, Levin *et al.* 1999, Miki *et al.* 2001). How many other types of neurons, e.g. in the nucleus tractus solitarius (NTS), are involved in central glucose sensing is unclear, as well as the molecular identities

Table 1. Single-cell RT-PCR expression profiling of K-ATP channel subunits in different neuronal populations.

Brain region	Neuronal type	Single channel conductance	Reference electrophysiology	K-ATP subunit expression	Reference single-cell RT-PCR
Hippocampus (rat)	CA1 pyramidal cells	?	Hyllenmark and Brismar (1996) Fujimura et al. (1997)	SUR1/Kir6.1 SUR2/Kir6.2 SUR1/Kir6.2 SUR2/Kir6.1	Zawar et al. (1997)*
Hippocampus (rat)	Stratum radiatum interneurons	?	Zawar et al. (1997)	SUR1/Kir6.1 SUR2/Kir6.2 SUR1/Kir6.2 SUR2/Kir6.1	Zawar et al. (1997)*
Striatum (rat)	Cholinergic interneurons	44 pS	Lee et al. (1998)	SUR1/Kir6.1	Lee et al. (1998)
Hypothalamus (rat)	Ventromedial hypothalamic neurons	65 and 140 pS	Ashford et al. (1990) Spanswick et al. (1997) Liss et al. (2000)	SUR1/Kir6.1 SUR1/Kir6.2	Lee et al. (1999) Miki et al. (2001)
Substantia nigra pars compacta (mouse, guinea-pig)	Dopaminergic neurons	64 pS	Roeper et al. (1990) Stanford and Lacey (1996)	SUR1/Kir6.2 SUR2B/Kir6.2	Liss et al. (1999a)
Substantia nigra pars reticulata (mouse)	GABAergic neurons	71 pS	Schwanstecher and Panten (1993) Stanford and Lacey (1996)	SUR1/Kir6.2	Liss et al. (1999a)
Brainstem (rat)	Dorsal vagal neurons	73 pS	Trapp and Ballanyi (1995)	SUR1/Kir6.2	Karschin et al. (1998)

Note that three different variants of the single-cell RT-PCR method are used. Liss and Zawar: multiplex nested RT-PCR, Lee: three prime end amplification (TPEA) PCR, Karschin: antisense RNA amplification. *Primers did not discriminate between SUR2A and SUR2B splice variants.

and functional roles of K-ATP channels in these neurons (Dallaporta *et al.* 2000). A different aspect of the important role of K-ATP channels for glucose sensing was illustrated by the recent finding that the Kir6.2 and SUR1 transcription rates are decreased with increasing glucose levels in isolated beta cells (Moritz *et al.* 2001). The glucose-dependent regulation of K-ATP subunit expression might also be operative in the brain, as neurons and beta cells possess the same K-ATP subunit promoter (Hernandez-Sanchez *et al.* 1999). In addition to central neurons, peripheral enteric neurons have also been shown to be glucose sensing and to express the K-ATP channel subunits SUR1 and Kir6.2 (Liu *et al.* 1999).

Neuronal K-ATP channels as metabolic gatekeepers?

As mentioned above, most neuronal populations are not directly involved in beta cell-like glucose sensing. Nevertheless, many of them express functional K-ATP channels. It is likely that these neuronal K-ATP channels act as general energy control elements that adapt the electrical activity and consequently neuronal ATP consumption to the delicate metabolic state of neurons. Increased electrical activity will lead to internal sodium accumulation that stimulates Na⁺/K⁺ ATPase activity, which is by far the most dominant consumer (40–70%) of neuronal ATP (Erecinska and Dagoni 1990). K-ATP channels that have been found on axonal, terminal and somatodendritic membranes, are ideal sensors to detect locally-enhanced activity-dependent changes in ATP/ADP ratio and translate them into an altered channel activity. The activity-dependent activation of K-ATP channels will tend to hyperpolarize the membrane and dampen excitability. Thus,

K-ATP channel activation will act as negative feedback in order to match electrical signalling and energy consumption. Supportive of this notion is the evidence that some K-ATP channels are active *in vivo* in the brain under physiological conditions (Fellows *et al.* 1993). In accordance, intracellular sodium loading and increased Na⁺/K⁺ ATPase activity have been shown to enhance neuronal K-ATP channel activity (Seutin *et al.* 1996). These mechanisms might also be operative at presynaptic membranes that are compartments of high metabolic demands. Here, K-ATP channel activation will reduce neurotransmitter release, which has been demonstrated in particular for GABAergic neurotransmission (Amaroso *et al.* 1990, Mourre *et al.* 1990, Luhmann and Heinemann 1992, Watts *et al.* 1995). Recent evidence suggests that this metabolic tuning of neuronal activity is not simply a homeostatic 'safety' device, but might control higher functions like memory, learning or voluntary movement (Lamensdorf *et al.* 1999, Stefani *et al.* 1999). There is also another possible mechanism to be taken into account. Activity-dependent K-ATP channel activation not only increases membrane conductance, but also leads to enhanced activity-dependent K⁺ efflux that rapidly accumulates in the small extracellular space of the CNS (Laming 2000). These activity-dependent changes in external K⁺ concentration might serve as coupling between local metabolic demands and cerebrovascular perfusion, as mild increases in external K⁺ are potent inducers of local vasodilatation (Quayle *et al.* 1997, Nguyen *et al.* 2000). In this way, K-ATP channel activity might provide two feedback loops: a cellular one that controls the excitability of individual neurons or synapses and a regional one that uses K⁺ fluxes as readout to match regional electrical activity with local blood flow. There are

conflicting results in the literature, whether neuronal K-ATP channels are involved in this type of signalling or not (Schaeffer and Lazdunski 1991, Jiang *et al.* 1992, Fellows *et al.* 1993, Zetterstrom *et al.* 1995). In this context, K-ATP channels in dopaminergic neurons might have an additional role, as it has been shown that dopaminergic terminals directly innervate brain arterioles. Thus, dopaminergic neurons might not only control neuronal activity, but also the perfusion of their axonal target areas (Krimer *et al.* 1998). There is increasing evidence that neuronal K-ATP channels are not just pure metabolic sensors, but that they can also serve as effectors for other biochemical pathways and second messenger systems, like G-proteins, PIP cascades, and protein kinase-mediated phosphorylations. This has already been appreciated for native peripheral and also recombinant heterologously expressed K-ATP channels (Sanchez *et al.* 1998, Baukowitz and Fakler 2000, Lin *et al.* 2000, Wada *et al.* 2000). Neuronal K-ATP channels can be modulated by coupling to metabotropic receptors, cytoskeletal changes and other mechanisms (Tanaka *et al.* 1996, Hosseinzadeh and Stone 1998, Mironov and Richter 2000). Thus, K-ATP channels act as integrators of multiple signalling pathways that converge on these channels.

Neuronal K-ATP channels and disease

Role of neuronal K-ATP channels in acute ischemia/hypoxia

With respect to acute or chronic perturbations of energy metabolism, the brain is by far the most vulnerable organ. A few minutes of hypoxia or ischemia can lead to irreparable structural and functional loss. Conceptionally, K-ATP channels are attractive targets in the pathophysiological scenario of hypoxia/ischemia, not only in the heart but also in the brain. The initiation and execution of hypoxic/ischemic neuronal death is believed to critically depend on excessive glutamate release and subsequent excitotoxicity (Dirnagl *et al.* 1999). It has been argued that in these acute scenarios, K-ATP channel activation might reduce terminal depolarization and, thus, decrease ischemic glutamate release. In addition, somatodendritic K-ATP channel activation might diminish the glutamate-induced calcium overload and initiation of necrotic or apoptotic cell death (Haddad and Jiang 1994). On the other hand, opening of K-ATP channels by ischemia will accelerate the external K^+ accumulation, which will shift the equilibrium potential of potassium to more positive values, resulting in membrane depolarization and, finally, collapse of ionic gradients. In this context, it is noteworthy that organisms with a high brain-hypoxia tolerance, like deep-diving turtles or new-borns, have a very low density of neuronal K-ATP channels compared to highly vulnerable adult mammalian brains (Jiang *et al.* 1992). Apparently, there is an inevitable trade-off between protecting the integrity of the membrane potential and at the same time accelerating external K^+ accumulation by active K-ATP channels during metabolic challenges (Cameron and Baghdady 1994). However, in rats, K-ATP channel activating drugs have been shown to reduce the infarct volume in a middle cerebral artery occlusion paradigm (Takaba *et al.* 1997). This indicates that activation or

overexpression of K-ATP channels can not only be neuroprotective in *in vitro* model systems (Wind *et al.* 1997, Reshef *et al.* 1998, Jovanovic *et al.* 1999), but also appears to be beneficial in *in vivo* focal cerebral ischemia. As K^+ channel openers might also act on vascular K-ATP channels, the specific role of neuronal K-ATP channels in the pathophysiology of acute ischemia needs to be further clarified. It is likely that the best evidence will come from cell-type specific transgenic mouse models. Recent interest focused on the possible contribution of K-ATP channels to a phenomenon called ischemic preconditioning that is studied predominantly in the heart (Cohen *et al.* 2000), but is also present in the brain (Cheung 2000). Here, a short and fully reversible hypoxic or ischemic insult precedes the genuine hypoxia/ischemia test period and induces a set of protective adaptive changes that increases the hypoxic tolerance and speed of recovery for the second challenge. There is increasing evidence that the opening of K-ATP channels could play a central role either as trigger or effector of this protective preconditioning in the brain (Perez-Pinzon and Born 1999, Blondeau *et al.* 2000). Protein kinase C-mediated phosphorylation of K-ATP channels and a subsequent increase in open probability is one of the suggested molecular mechanisms (Wang and Ashraf 1999, Light *et al.* 2000). More work is needed to understand the mechanisms of preconditioning. Deeper insight in the respective roles of plasmamembrane and mitochondrial K-ATP channels in preconditioning could have important clinical implications for neuroprotective therapies.

K-ATP channels in neurodegenerative disease

It has been demonstrated for a variety of brain regions that metabolic inhibition of glycolysis or the mitochondrial respiratory chain act as potent activators of neuronal K-ATP channels (Riepe *et al.* 1992, Roeper and Ashcroft 1995, Hyllienmark and Brismar 1996, Ballanyi and Kulik 1998, Koyama *et al.* 1999, Sun *et al.* 2000, Zawar and Neumcke 2000). This is not only relevant for acute metabolic challenges, as discussed above, but also in the more chronic settings of neurodegenerative disorders like Alzheimer's or Parkinson's disease (PD). Chronic impairment of mitochondrial function has been identified in these diseases and is believed to play a crucial role in their pathogenesis (Beal 2000). PD is a common neurodegenerative movement disorder that affects more than 1% of the elderly population. The pathological hallmark of PD is the selective degeneration of a subpopulation of dopaminergic midbrain neurons, mainly in the substantia nigra pars compacta (SNpc). Recent work suggests a potential role for K-ATP channel subtypes expressed in dopaminergic neurons of the SNpc for their selective vulnerability in PD. Dopaminergic midbrain neurons play a crucial role in a variety of brain functions like reward, working memory and voluntary movement. The latter is severely affected in PD. However, whilst some subpopulations of dopaminergic neurons are highly vulnerable to the disease process, others remain largely unaffected (Damier *et al.* 1999). This suggests the presence of relevant differences in gene expression that determine the differential vulnerability of single dopaminergic neurons. Metabolic

stress has been identified as an important trigger factor for the neurodegenerative process of PD. In particular, reduced activity of the mitochondrial respiratory chain complex I (CXI–NADH ubiquinone reductase) of ~40% has been consistently found in PD patients (Beal 2000). However, the pathophysiological downstream events that are induced by CXI inhibition and lead to the selective dopaminergic degeneration are still unclear. In this context, K-ATP channels in DA neurons might act as candidate targets of the chronic metabolic disturbance present in PD. Under physiological conditions, dopaminergic midbrain neurons show spontaneous action potential firing and—at least in *in vitro* brain slices—most K-ATP channels are closed (Roper and Ashcroft 1995, Liss *et al.* 1999a). The activation of K-ATP channels in response to metabolic inhibition leads to an hyperpolarization of the dopaminergic neurons, accompanied by a complete loss of their normal pacemaker activity. However, the K-ATP channel response to metabolic stress is not uniform within the population of dopaminergic SNpc neurons. In acute mouse brain slices, a partial inhibition of the mitochondrial CXI by rotenone activates K-ATP channels only in a subpopulation of ~40% of dopaminergic neurons with a half maximal effective concentration (EC_{50}) of 15 nM. This corresponds to a degree of CXI inhibition similar to that found in brains of PD patients (Beal 1999) and suggests the possibility of K-ATP channel activation in PD. Combined single-cell RT-PCR experiments demonstrated that these highly responsive dopaminergic neurons express the K-ATP channel subunits SUR1 and Kir6.2 (see Figure 2D, upper panel). In contrast, the other population of dopaminergic SNpc neurons possess a more than 100 fold higher EC_{50} (2 μ M) for rotenone-induced K-ATP channel activation—indicative of a significantly lower sensitivity to CXI inhibition. These neurons, which maintain their pacemaker activity during partial CXI inhibition, express the other SUR isoform, SUR2B, in combination with Kir6.2 mRNA (see Figure 2D) (Liss *et al.* 1999a). By analogy, the activity of SUR2B-expressing dopaminergic neurons might not be perturbed in PD. It is important to note that the molecular mechanisms defining metabolic sensitivity of K-ATP channels are still not clear. However, recombinant SUR1/Kir6.2 containing K-ATP channels also show a higher sensitivity to metabolic stress compared to SUR2A/Kir6.2 mediated channels (Ashcroft and Gribble 1998). This demonstrates that the alternative expression of SUR subunits is a major determinant of metabolic sensitivity of K-ATP channels.

K-ATP channels in the weaver mouse—a genetic model of dopaminergic degeneration

Studies of dopaminergic mid-brain neurons in the *weaver* mouse, a genetic mouse model of dopaminergic degeneration similar to that in PD (Patil *et al.* 1995), support the idea of K-ATP channel activation as a neuroprotective strategy. The *weaver* mouse is characterized by a point mutation in the pore region of a G-protein coupled inwardly rectifying potassium channel (GIRK2). As homomers, the mutated GIRK2 channel lost its potassium selectivity and can be constitutively active, resulting in a chronic, depolarizing sodium influx into dopaminergic SNpc neurons (Kofuji *et al.*

1996, Navarro *et al.* 1996, Slesinger *et al.* 1996, Liss *et al.* 1999b, Guatteo *et al.* 2000). The chronic sodium overload is expected to further enhance ATP consumption of the Na^+/K^+ ATPase, which is already a major single consumer of neuronal ATP. It was demonstrated, for dopaminergic neurons in homozygous *weaver*, that SUR1/Kir6.2 containing K-ATP channels are tonically activated in direct consequence to the activity of *weaver* GIRK2 channels. This partially compensates the chronic depolarization of the dopaminergic *weaver* neurons. Single-cell RT-PCR experiments revealed the complete absence of SUR2B expressing dopaminergic neurons in *weaver* (Liss *et al.* 1999a, b). These results give the first evidence that alternative SUR1 expression and activation of K-ATP channels can affect the process of dopaminergic neurodegeneration. Furthermore, preconditioning might also be a relevant mechanism reducing the vulnerability of dopaminergic neurons towards neurotoxins like MPTP (Duan and Mattson 1999). In summary, there is growing evidence that the differential expression of K-ATP channel subunits in DA neurons not only determines the acute response to metabolic stress, but might also be an important molecular mechanism for their differential vulnerability in chronic neurodegenerative disorders.

To explicitly test the potential roles of molecularly defined K-ATP channels in the brain, as reviewed in this article, one need to combine existing electrophysiological and molecular methods with a new generation of cell-type specific transgenic mouse models of K-ATP channel function.

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