



# Potassium channels in behavioral brain disorders. Molecular mechanisms and therapeutic potential: A narrative review

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## ABSTRACT

Potassium channels (K<sup>+</sup>-channels) selectively control the passive flow of potassium ions across biological membranes and thereby also regulate membrane excitability. Genetic variants affecting many of the human K<sup>+</sup>-channels are well known causes of Mendelian disorders within cardiology, neurology, and endocrinology. K<sup>+</sup>-channels are also primary targets of many natural toxins from poisonous organisms and drugs used within cardiology and metabolism. As genetic tools are improving and larger clinical samples are being investigated, the spectrum of clinical phenotypes implicated in K<sup>+</sup>-channels dysfunction is rapidly expanding, notably within immunology, neurosciences, and metabolism. K<sup>+</sup>-channels that previously were considered to be expressed in only a few organs and to have discrete physiological functions, have recently been found in multiple tissues and with new, unexpected functions. The pleiotropic functions and patterns of expression of K<sup>+</sup>-channels may provide additional therapeutic opportunities, along with new emerging challenges from off-target effects. Here we review the functions and therapeutic potential of K<sup>+</sup>-channels, with an emphasis on the nervous system, roles in neuropsychiatric disorders and their involvement in other organ systems and diseases.

## 1. Introduction

Ion channels are found in all living organisms, from bacteria to advanced multicellular organisms, including humans. Such channels serve a remarkable diversity of physiological functions, yet their fundamental structure and functional properties are conserved across phyla and millions of years of evolution. Potassium channels (K<sup>+</sup>-channels) are involved in various physiological processes by controlling selectively the flow of potassium ions across the membrane and controlling cellular membrane excitability (Choe, 2002; Miller, 2000). It is well established that K<sup>+</sup>-channels regulate the contractility of the cardiac muscle cells, and thereby heart function, by modulating the coordinated cardiac repolarization (Snyders, 1999; Coetzee et al., 1999; Nerbonne, 2000; Grandi et al., 2017). Similarly, in neuronal cells, K<sup>+</sup>-channels maintain homeostasis and regulate neuronal firing

properties and membrane potential (Bean, 2007; Jan and Jan, 2012; Trimmer, 2015). Moreover, it has been shown that these channels have roles in other cellular processes such as glucose homeostasis through insulin secretion, regulation of neurotransmitter release in muscle and brain cells, regulation of heart contractility, and immune functions (Abbott and Goldstein, 2001; Chen et al., 2023; Choi and Kim, 2022). Since the discovery of the electrochemical nature of nerve signal conduction in the early 1900s, introduction of patch-clamp recordings in late 1970s (Neher, Sakmann, and Steinbach, 1978), and determination of the first molecular structures of K<sup>+</sup>-channels 30 years later (MacKinnon et al., 1998), the function of K<sup>+</sup>-channels has been intensively investigated and subject to many reviews, also focusing on their roles in health and disease.

A literature search using the PubMed database revealed > 77,000 articles mentioning K<sup>+</sup>-channels, with > 20,000 articles being published

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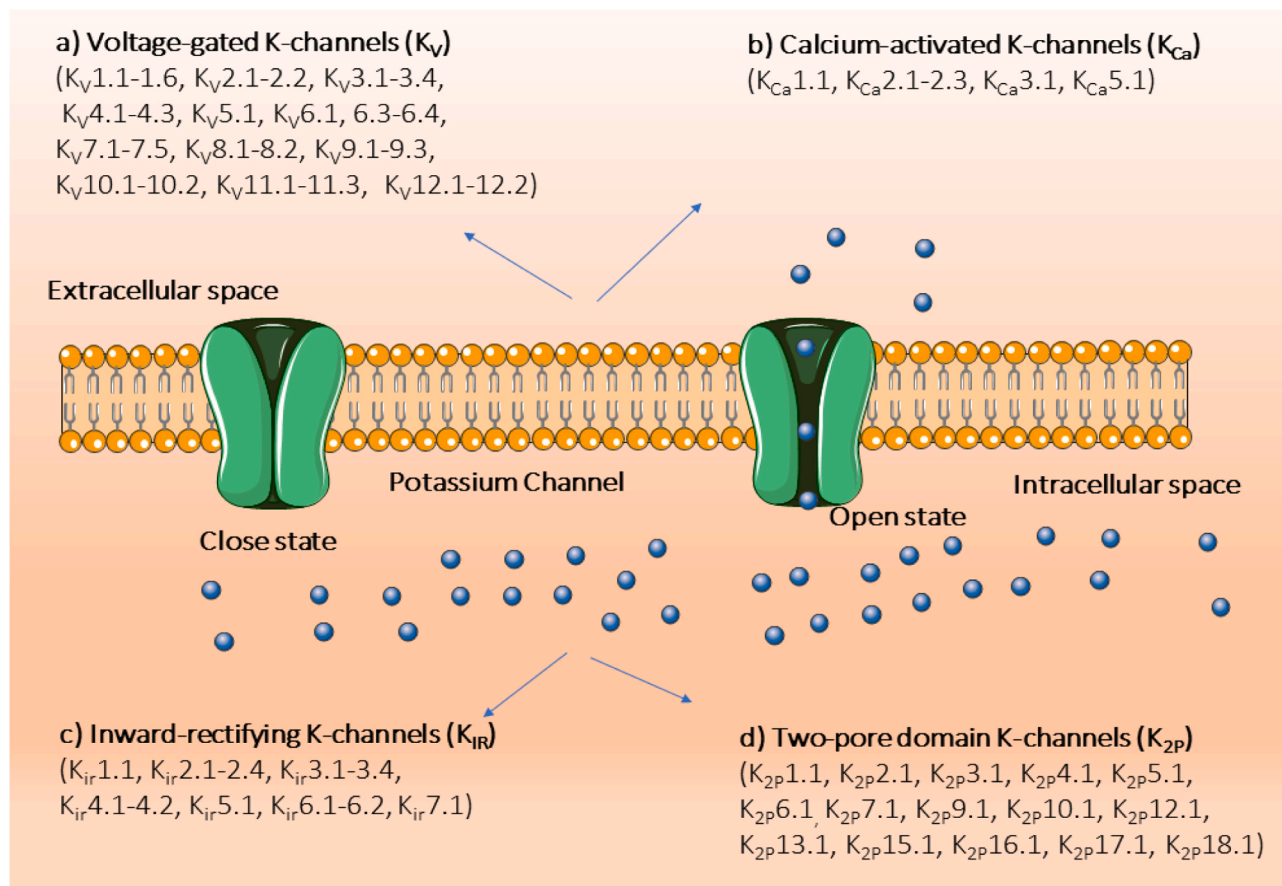
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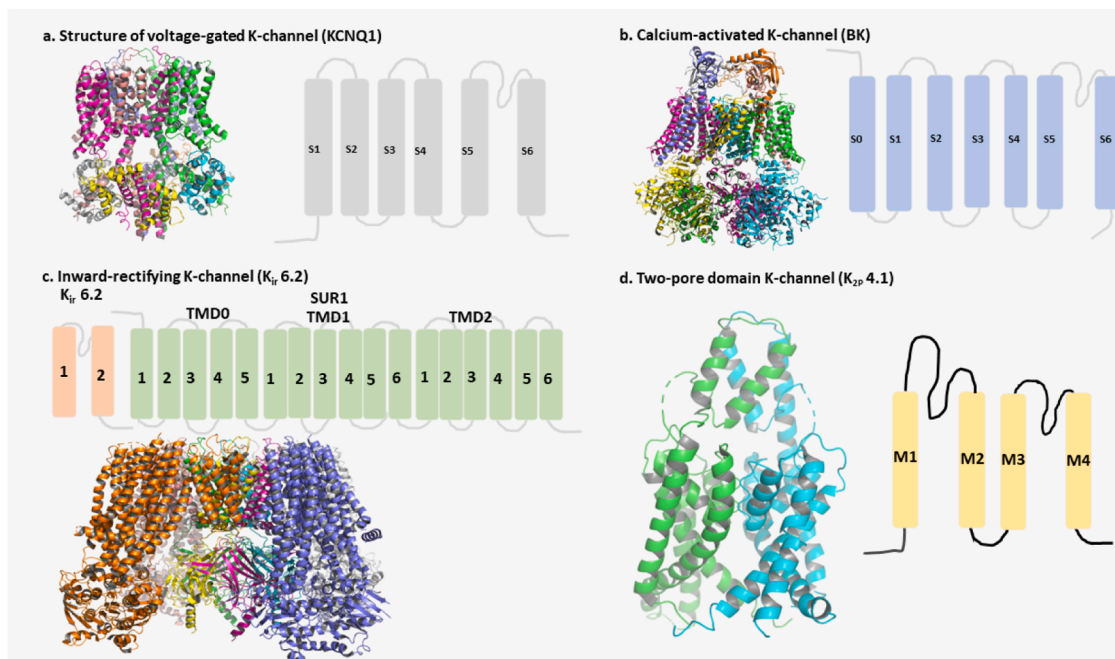
between 2013 and 2023. As it obviously is an impossible task to satisfactorily cover all relevant aspects of the > 100 reported human  $K^+$ -channel genes and proteins in a single review article, we have limited our scope to  $K^+$ -channels that we consider most relevant for understanding and treating neuropsychiatric disorders and recently emerging functions of  $K^+$ -channels in the interplay between the endocrine and nervous system. For the purpose of this review, we have mainly focused on the following  $K^+$ -channels: KCNQ1–5, KCNT1, KCNA2, KCNB1, KCNC1, KCND3, KCNA1,  $K_{ATP}$ , and KCNH2. Furthermore, considering the diversity of results, methods and study designs cited, this is presented as a narrative review and not a systematic one. Firstly, we briefly introduce some fundamental structural properties of the major classes of  $K^+$ -channels. Next, we present an overview of their tissue distribution and biological functions, with an emphasis on the central nervous system (CNS). Finally, we discuss recent emerging associations of  $K^+$ -channels, endocrine and neuropsychiatric disorders and future prospects of pharmacological modification of  $K^+$ -channel functions. The literature covering these subjects comes from many disciplines, including physiology, genetics, structural biology, clinical medicine and pharmacology. In this narrative review we aim to integrate and discuss these findings, with an emphasis on discoveries reported during the past decade, until March 2023. We conclude that  $K^+$ -channels are important drug targets in several therapeutic areas, but that many obstacles remain in terms of achieving the necessary selectivity and potency in clinical context.

## 2. Organization and structural properties

Traditionally,  $K^+$ -channels have been subcategorized into three to five major classes based on their structural and functional properties (Fig. 1). This nomenclature is based on gene families and whether the channels have 2, 4 or 6/7 transmembrane domains. Fig. 1 lists members of the four major groups of K-channels. Alternative classifications have also been suggested, such as a separate family of sodium-activated channels ( $K_{Na}$  channels), see section 4.22. For historical reasons, the corresponding genes have a different nomenclature. Here we mainly use protein-based terminology but also refer to the  $K^+$ -channel encoding genes when appropriate. The largest family is the voltage gated ( $K_V$ )  $K^+$ -channels, with over 40 distinct members identified in the human genome and usually grouped into 12 subfamilies (Wulff, Castle, and Pardo, 2009; Tian et al., 2014). These channels are highly conserved, all having four identical  $\alpha$ -subunits, each formed by six transmembrane (TM) segments (S1-S6) (Fig. 2), allowing  $K^+$  to pass through the channels (Long, Campbell, and Mackinnon, 2005). The ion permeability of the voltage-gated channels depends on their ability to detect changes of the voltage with respect to the membrane potential in the cell (Swartz, 2004; del Camino, Kanevsky, and Yellen, 2005; del Camino and Yellen, 2001), making these channels well suited for maintaining physiological processes in the nervous system, heart, pancreas and other tissues (Wulff, Castle, and Pardo, 2009). Additionally, the function of  $K_V$  channels is also regulated by a smaller beta subunit (see Section 4.1.3)



**Fig. 1.** Potassium channels are grouped into four major types according to their structural and functional properties. The channels are named according to their protein sequence nomenclature and potassium ions are marked as blue spheres. a) Voltage-gated  $K^+$ -channels ( $K_V$ ) are regulated by membrane potential and sub-grouped into 12 classes which include  $K_V1-12$  (Gutman et al., 2005). b) Calcium-activated  $K^+$ -channels ( $K_{Ca}$ ) are regulated by calcium gating. The  $K_{Ca}$  are further classified as large conductance (BK), intermediate conductance (IK), and small conductance (SK) calcium-activated  $K^+$ -channel. c) Inward rectifying  $K^+$ -channels allow  $K^+$  to inward direction into the cell and are sub-divided into 7 classes,  $K_{IR}1-7$  (Kubo et al., 2005). d) Two-pore domain or tandem pore domain ( $K_{2P}$ ) K-channels consist of 15 members (Goldstein et al., 2005).  $K_{2P}$   $K^+$ -channels have two pores and exist both in excitable and non-excitable cells (Lesage and Lazdunski, 2000). The figure was created using the Servier Medical Art Commons Attribution 3.0 Unported License (<https://creativecommons.org/licenses/by/3.0/>).



**Fig. 2.** Representative structures of four major types of potassium channels families based on 3D-structures (cartoon representations) and sequence (schematic representation of TM helices). a) KCNQ1 (PDB ID: 7XNK) is a member of voltage-gated  $K^+$ -channel and consists of four identical subunits, each containing six TM segments (S1-S6). b) Calcium-activated  $K^+$ -channel,  $K_{Ca}1.1$  (PDB ID: 6V22), is a tetramer complex with seven TM segments (S0-S7). c) Inward-rectifying  $K^+$ -channel,  $K_{ir}6.2$  consists of two transmembrane domains (PDB ID: 6C30) (Lee et al., 2017).  $K_{ir}6.2$  forms the channel with SUR (Sulfonylurea receptor) in the pancreatic  $\beta$ -cells and regulate insulin secretion (Martin et al., 2017). SUR is composed of three TM domains (TMD0-TMD2) where each domain has six segments except TMD0. d)  $K_{2p}4.1$  is a member of two-pore domain  $K^+$ -channel (PDB ID: 3UM7), which has two pore forming domains (P-loop domains) and four TM segments (M1-M4) (Brohawn, del Marmol, and MacKinnon, 2012). The figures were made using PyMOL (Schrodinger).

(Abbott and Goldstein, 2001; McCrossan and Abbott, 2004).

The calcium-activated  $K^+$ -channels ( $K_{Ca}$ ) include the six/seven TM family of  $K^+$ -channels which are activated by the intracellular  $Ca^{2+}$  concentration and regulate the resting membrane potential and  $K^+$  conductance (Vergara et al., 1998; Stocker, 2004; Swarthout and Walling, 2000).  $K_{Ca}$  channels are sub-grouped into three types; large conductance (big potassium; BK), small conductance ( $SK_{Ca}$ ), and intermediate conductance ( $IK_{Ca}$ ) calcium-activated  $K^+$ -channels (Weaver, Bomben, and Sontheimer, 2006). Like  $K_V$  channels,  $K_{Ca}$  channels have six TM segments, with the exception of seven TM elements (Fig. 2) found in  $K_{Ca}1$  (Tian et al., 2014).  $K_{Ca}$  channels are expressed throughout the CNS and regulate neuronal firing, the vascular tone of blood vessels, and neurotransmitter release (Sah and Davies, 2000; Sah and Faber, 2002; Bahia et al., 2005; Berkefeld, Fakler, and Schulte, 2010).

The inward-rectifying  $K^+$ -channels ( $K_{ir}$ ) have seven different subtypes, that allow  $K^+$  to move inside the cell through a homo- or hetero tetramer pore structure (Hibino et al., 2010). The channel consists of two transmembrane domains (Fig. 2) and the extracellular loop making up the channel (Hibino et al., 2010; Heginbotham et al., 1994). The  $K_{ir}$  channels are widely expressed in the cells and the channels are regulated by cellular metabolism, G protein-coupled receptors, and  $K^+$  transport channels (Hibino et al., 2010).

The two-pore domain  $K^+$ -channel family ( $K_{2p}$ ) includes 15 different members, each consisting of four TM segments (Fig. 2) forming two pore domains (Alexander et al., 2021). The expression of these channel is widespread in the CNS and peripheral tissues (Medhurst et al., 2001). They have distinct structural properties and can be constitutively open or show inward (TASK-1) or outward (TREK1) rectification, presenting leaky channel properties (Innamaa et al., 2013; Niemeyer et al., 2010; Lesage and Lazdunski, 2000).

### 3. Potassium channel expression

Some members of the  $K^+$ -channels family appear to be expressed in

nearly every cell type in all organisms that have been studied (Littleton and Ganetzky, 2000). It is therefore not surprising to find that  $K^+$ -channels in general are also widely expressed in various human tissues. Among 97 different  $K^+$ -channel genes listed in the human protein atlas (Accessed February 2023), at least some tissue expression information is available for all members (www.proteinatlas.org). In particular, the voltage-gated, and inward rectifying  $K^+$ -channels are highly expressed in brain, endocrine, kidney, skeletal muscle, and heart tissues (https://gtexportal.org/home/)(Tian et al., 2014). Calcium-activated, and two-pore domain  $K^+$ -channels are also expressed in the heart, lung, intestine, reproductive system, and other organs. Possibly reflecting their diverse physiological roles,  $KCNJ1$  ( $K_{ir}1.1$ ) is highly expressed in kidney, while the structurally related channels  $KCNJ6$  is mainly expressed in brain,  $KCNJ10$  in brain and digestive tract,  $KCNJ11$  in heart and skeletal muscle and  $KCNJ15$  is expressed in kidney and multiple endocrine tissues.  $KCNMA1$  ( $K_{Ca}1.1$ ) and  $KCNMB1$  appear to be highly expressed in arteries, colon, uterus, fallopian tube, and bladder, and higher expression of  $KCNK3$  is observed in lungs and heart (www.proteinatlas.org). This highly distributed pattern of expression is consistent with diverse functions of  $K^+$ -channels in many different organs. As this review is particularly focused on the role of  $K^+$ -channels in behavioral and endocrine disorders, their pattern of expression in brain and pancreatic tissue is briefly reviewed below.

#### 3.1. $K^+$ -channels in the central nervous system (CNS)

Inward-rectifying, and voltage-gated K-channels are expressed in multiple regions of the CNS, including the cerebellar hemispheres, frontal cortex, and basal ganglia (https://gtexportal.org/home/multi-GeneQueryPage/KCNJ11). Disease related variants within several classes of K-channels have been described, including variants of  $KCNJ16$  ( $K_{ir}5.1$ ),  $KCNJ11$  ( $K_{ir}6.2$ ),  $KCNJ8$  ( $K_{ir}6.1$ ),  $KCND3$  ( $K_V4.3$ ),  $KCNJ5$  ( $K_{ir}3.4$ ) and  $KCNQ1$  ( $K_V7.1$ ) (Goldman et al., 2009; Karschin et al., 1997; Noh et al., 2019). Among the voltage gated  $K^+$ -channels;  $KCNQ2-5$  are

highly expressed in the CNS. In comparison, only a moderate expression of *KCNQ1* has been reported in brain tissues. Still, variants in all of these  $K^+$ -channels have been linked to behavioral phenotypes (see 4.2.1) (<https://gtexportal.org/home/multiGeneQueryPage/KCNQ1>).

### 3.2. Pancreas

Many of the inward-rectifying channels, *KCNJ5* ( $K_{ir3.4}$ ), *KCNJ8* ( $K_{ir6.1}$ ), *KCNJ11* ( $K_{ir6.2}$ ), *KCNJ15* ( $K_{ir4.2}$ ), and *KCNJ16* ( $K_{ir5.1}$ ), are highly expressed in the pancreas (see 4.1.1) (Ferrer et al., 1995). Among the voltage-gated  $K^+$ -channels, *KCNQ1* is highly expressed in pancreas, apparently different from the other members of the  $K_v7$  family. *KCNQ4* has moderate expression and *KCNQ2*, *KCNQ3*, and *KCNQ5* have low expression levels in the pancreas (<https://gtexportal.org>).

## 4. $K^+$ -channels in human disease

Because of their wide range of functions and patterns of expression, altered functions of  $K^+$ -channels have been implicated in a range of human conditions, including common cardiovascular, brain, and metabolic diseases (Tian et al., 2014). Rare Mendelian inherited channel defects can also cause syndromic disease with various symptoms from different organs in the same patients, as illustrated in the DEND syndrome (development delay with epilepsy in addition to neonatal diabetes) in patients with *KCNJ11/ABCC8* ( $K_{ir6.2}/SUR1$ ) mutations and neonatal diabetes (Hattersley and Ashcroft, 2005). It is highly likely that other constellations of symptoms might not yet have been recognized as having common pathophysiologic pathways related to  $K^+$ -channel dysfunction.

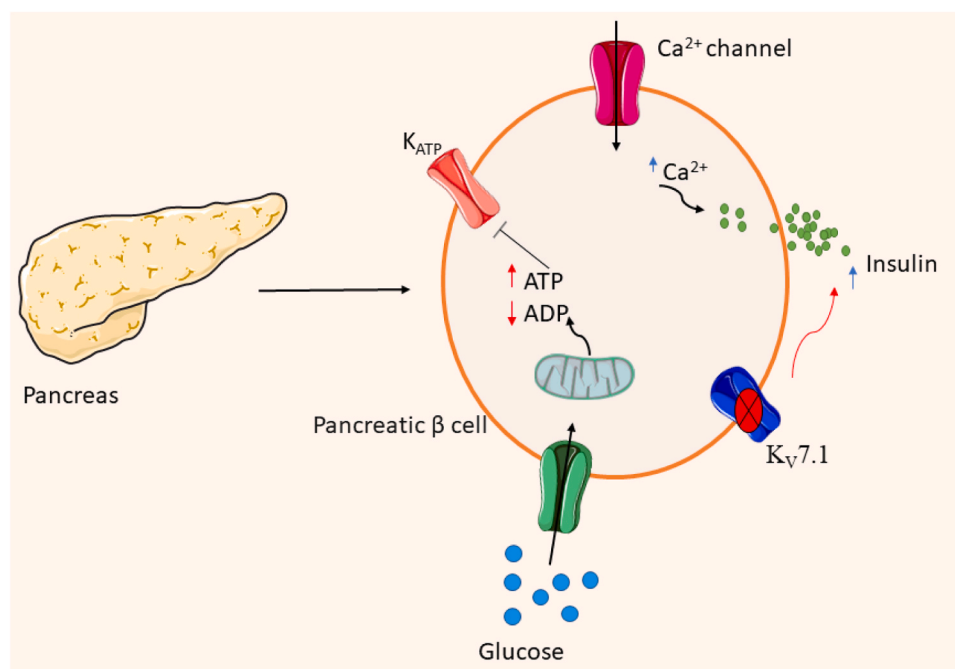
### 4.1. Diabetes

#### 4.1.1. Type 2 diabetes mellitus (T2DM)

Several studies have established that *KCNQ1* plays a role in insulin secretion in pancreatic  $\beta$ -cells and that channel dysregulation is associated with T2DM (Asahara et al., 2015). A similar voltage-gated channel, *KCNE2* has also been implicated in diabetes, with knockout mice (*Kcne2*<sup>-/-</sup>) developing diabetes mellitus at five weeks of age (Hu et al., 2014; Lee et al., 2017). Acute application of insulin suppressed the

*KCNQ1/KCNE1* currents, but the use of insulin for more than 6 h had opposite effects in *Xenopus oocyte* studies (Wu et al., 2017). Combined, these results point to both *KCNQ1* and *KCNE1* as important interaction partners in insulin secretion and T2DM pathophysiology (Wu et al., 2017). Genome-wide association studies (GWAS) have also implicated common *KCNQ1* gene variants in T2DM in several populations (Unoki et al., 2008; Yasuda et al., 2008; Voight et al., 2010; Li, Wang, and Lu, 2014; Qian et al., 2015). Yasuda and co-workers showed that the polymorphism rs223782 had the strongest link with the T2DM (Yasuda et al., 2008). However, the molecular mechanisms of *KCNQ1* involvement in diabetes are not fully understood. It has been suggested that impaired *KCNQ1* ( $K_v7.1$ ) activity could delay repolarization of  $\beta$ -cells, and by this mechanism increase insulin secretion. Correspondingly, knockdown of *KCNQ1* with siRNA enhances insulin secretion (Rosengren et al., 2012), while overexpression of *KCNQ1* in MIN6 cells decreases insulin secretion (Yamagata et al., 2011). Mutations leading to a loss-of-function (LOF) of the *KCNQ1* increase insulin secretion (Fig. 3). Patients may present with hyperinsulinemia and symptomatic hypoglycemia, but later in life, insulin secretion may shift to hyposecretion, and these patients therefore have an elevated risk of developing T2DM (Torekov et al., 2014). Additionally, studies in mice carrying a *KCNQ1* mutation (*KCNQ1-A340V*) demonstrated that insulin production can shift from hypo- to hyper secretion as the mice get older (Lubberding et al., 2021). The observation that patients with long QT syndrome (LQTS) have an increased risk of diabetes and that inhibition of *KCNQ1* increases insulin secretion in  $\beta$ -cells diabetes strengthen the association of variants in voltage-gated  $K^+$ -channels with diabetes (Torekov et al., 2014; Yasuda et al., 2008). Thus, LOF mutations in *KCNQ1* or *KCNH2* (HERG or  $K_v11.1$ ) in LQTS patients are accompanied by increased insulin secretion (Torekov et al., 2014; Engelbrechtsen et al., 2018; Hyltén-Cavallius et al., 2017).

In contrast, gain-of-function (GOF) variants in *KCNQ1* reduce glucose stimulated insulin secretion (Zhang et al., 2020). In studies using GWAS and single-cell epigenomics, Chiou and co-workers showed that the *KCNQ1* locus is linked to the T2DM variant and co-accessibility of the insulin (*INS*) promoter in  $\beta$ -cells. This may explain why the variant rs231361 at the *KCNQ1* locus was found to regulate insulin synthesis (Chiou et al., 2021). In addition, the C-allele of *KCNQ1* rs2237895, which is associated with an increased risk of T2DM, was found to result



**Fig. 3.** Insulin secretion in pancreatic  $\beta$ -cell. High glucose level induces uptake of glucose in  $\beta$ -cell which is mediated through GLUT2 transporters and lead to increased ATP/ADP ratio in the cell. Increased ATP initiated a cascade mechanism by closing the ATP sensitive ion channel,  $K_{ATP}$  and causes depolarization and subsequently opening of the  $Ca^{2+}$  channel and releasing of insulin (Ashcroft, 2005). Opening of *KCNQ1* ( $K_v7.1$ ) inhibits insulin secretion by an unknown mechanism, possibly by hyperpolarization. However, inhibition or LOF of *KCNQ1* increases insulin secretion in pancreatic  $\beta$ -cell (Torekov et al., 2014). The mechanism by which of  $K_v7.1$  causes higher insulin secretion is not understood yet.

in reduced glucose-stimulated insulin secretion in human islets (Jonsson et al., 2009).

#### 4.1.2. Gestational diabetes mellitus (GDM)

*KCNQ1* is a candidate gene for gestational diabetes mellitus (GDM) which is characterized by maternal glucose intolerance during pregnancy. GDM affects both mother and offspring as the neonate may be born large for gestational age and furthermore suffer from hypoglycemia after delivery due to a glucose-induced hypersecretion of insulin in the fetus (Ortega-Contreras et al., 2022). Genetic studies have shown an association between the variant rs2237892 in *KCNQ1*, increased glucose levels, reduced  $\beta$ -cell function, and decreased insulin secretion in the cells which pose a higher risk for GDM (Jonsson et al., 2009; Wang et al., 2013; Yasuda et al., 2008; Shin et al., 2010; Ao et al., 2015; Fatima et al., 2016).

#### 4.1.3. Neonatal diabetes mellitus (NDM)

Neonatal diabetes mellitus (NDM) is a rare disorder affecting 1 in 160 000–520 000 live births, with around half of patients presenting with a permanent type (PNDM) and the remainder having transient symptoms (TNDM) (Shield et al., 1997; Slingerland et al., 2009; Stanik et al., 2007; Vonmuhlenand and Herkenhoff, 1995; Wiedemann et al., 2010). The majority of cases are caused by a dysfunctional pancreatic ATP-sensitive potassium channel ( $K_{ATP}$  channel) (Vaxillaire et al., 2004) due to mutations in one of the two genes coding for the heterodimeric subunits, *KCNJ11* encoding the  $K_{ir}6.2$ -channel pore, and the ATP-binding cassette transporter sub-family (*ABCC8*) gene, encoding the regulatory subunit sulfonylurea receptor (SUR1). The  $K_{ATP}$  channel translates the signal of energy excess from glucose metabolism to membrane activity and ultimately insulin release by controlling  $K^+$  influx through the  $K_{ir}6.2$  pore (Ashcroft, Harrison, and Ashcroft, 1984), (Fig. 3). Activating mutations compromising channel closure halt insulin secretion and neonatal diabetes is usually diagnosed before the age of six months (Ashcroft, 2005; Hattersley and Ashcroft, 2005; Rubio-Cabezas et al., 2012; Proks et al., 2006). The neonate is often born small for gestational age (birth weight <10 percentile) since fetal insulin is important for normal growth *in utero* (Gloyn et al., 2004; Slingerland and Hattersley, 2006; Vaxillaire et al., 2004). The SUR1 protein regulates channel activity and contains the binding site for the sulfonylureas (Ashcroft and Gribble, 2000; Gribble and Reimann, 2003). A genotype-phenotype correlation to the severity of mutations has been observed, both within the phenotype of neonatal diabetes, but also reaching across the spectrum of monogenic diabetes. Certain genetic variants are causing later debut of diabetes with maturity onset diabetes of the young (MODY) or give increased risk of T2DM (Hattersley, Greeley, Polak, Rubio-Cabezas, Njolstad et al., 2018; Martagón et al., 2018; Najmi et al., 2017).

#### 4.1.3.1. Neurological defects associated with neonatal diabetes mellitus (NDM).

$K_{ATP}$  channels are expressed in pancreas but also in other tissues, including many brain areas, such as the hippocampus, neocortex, midbrain, brainstem nuclei and cerebellum (see Section 3). Thus, it is not unexpected that patients with  $K_{ATP}$  channelopathies also may suffer from neurological symptoms (Clark et al., 2010; Karschin et al., 1997). Hattersley and Ashcroft defined two syndromes in *KCNJ11*-carriers with the acronyms DEND (Developmental delay, Epilepsy, Neonatal Diabetes) or intermediate DEND (iDEND) for patients without epilepsy (Hattersley and Ashcroft, 2005). A genotype-phenotype correlation to this neurological phenotype has been reported in several studies (Gloyn et al., 2004; Hattersley and Ashcroft, 2005; Sagen et al., 2004) where *ABCC8* mutation carrier status also is associated with DEND (Proks et al., 2006). Since these early observations, multiple studies have revealed a high prevalence of learning disabilities, visuospatial disability, ADHD, anxiety, autism spectrum disorders or developmental coordination disorder including dyspraxia and hypotonia in  $K_{ATP}$ -associated neonatal

diabetes (Beltrand et al., 2015; Bowman et al., 2019; Bowman et al., 2017; Bowman et al., 2021; Bowman et al., 2020; Busiah, Drunat, and Vaivre-Douret, 2013; Carmody et al., 2016; Landmeier et al., 2017; Svalastoga et al., 2020). These clinical features are not found in other types of monogenic diabetes e.g., due to mutations in the insulin gene (*INS*) (Bowman et al., 2019). Formal cognitive testing of carriers of variants affecting the gating properties in *KCNJ11* (e.g., V59M) demonstrate moderate intellectual disability and high prevalence of psychiatric comorbidity (Svalastoga et al., 2020). This pathogenic effect is likely to be neuronal in origin as recombinant mice with altered nerve-*KCNJ11* isoforms displayed a similar phenotype (Clark et al., 2010). In summary, there are reports in the literature that the  $K_{ATP}$  channel in NDM is linked with developmental delay within DEND. Now, with the latest reports providing additional data from larger cohorts over ten years and also cohorts containing deeper phenotyping for carriers of specific gene variants, a clear genotype-phenotype correlation of severity has been established. We believe there is a scientific basis for this relationship, as those carrying genotypes highly affecting the open-close probability of the channel (e.g. *KCNJ11*, p.V59M) show a higher burden of psychiatric morbidity and intellectual disability. Moreover, studies in rodents also find the same genotype when the mutation occurs in neuronal  $K_{ATP}$  channels. Reports on other types of neonatal diabetes (e.g. *INS* mutations) are not associated with developmental delay. What remains to be settled is the role of sulfonylurea to prevent brain injury, and whether there is a time sensitive period of this effect. It's a question of much debate. The field currently lacks studies on children switched to sulfonylurea early in life. The characterization of the phenotypic changes following treatment change have not yet been fully assessed across sites. While some clinical centers recommend high-dose sulfonylurea, its impact in moderating effects induced by  $K_{ATP}$  channel mutations require investigation.

#### 4.1.4. Congenital hyperinsulinism (CHI)

Congenital hyperinsulinism (CHI) is a rare condition affecting between 1:25.000–1:70.000 of live births (Sandal et al., 2009; Glaser et al., 2000; Otonkoski et al., 1999), with higher prevalence (up to 1:2700) in isolated and or highly consanguineous populations (Otonkoski et al., 1999; Mathew et al., 1988; Levy-Shraga et al., 2013). In CHI, recessive inactivating mutations in *ABCC8* or more rarely *KCNJ11* cause  $K_{ATP}$  channel closure leading to membrane depolarization in the  $\beta$ -cells, and ultimately inappropriate insulin secretion with a risk of hypoglycemia (Thomas et al., 1995; De Franco et al., 2020). CHI is categorized into a transient type, spontaneously reaching remission during infancy, and a persistent type, where patients typically will require medical and surgical interventions before remitting during childhood. Based on histological examination of pancreas tissue, it is possible to distinguish between focal and diffuse subtypes that may be used to guide treatment options (Sempoux et al., 2004).

Usually, CHI present as isolated hypoketotic hypoglycemia, but facial dysmorphic features (high forehead, bulbous nose, smooth philtrum) have also been described (de Lonlay et al., 2002). In severe cases, the neonate can present within the first few days with poor feeding, floppiness, jitteriness, lethargy, cyanosis and hypothermia, seizures or coma (Cosgrove et al., 2004), but CHI can also be discovered by routine testing of blood glucose. Macrosomia is a common feature due to intrauterine hyperinsulinemia, but birth weight can also be low or normal, and some are born prematurely (Cosgrove et al., 2004). In rare cases hypertrophic cardiomyopathy and hepatomegaly are seen, also caused by the elevated insulin (Demirbilek and Hussain, 2017). CHI can also present in infancy, and more rarely in childhood or adulthood, usually with a milder phenotype. Some patients are only diagnosed when they regress into the opposite phenotype, diabetes, and a history of unexplained hypoglycemia is revealed (Descamps et al., 2021; Vieira et al., 2010). Although rare syndromic cases exist (e.g. Beckwith-Wiedemann, Sotos, Perlman, Kabuki, congenital disorders of glycosylation) CHI is, for the most part, isolated and caused by  $K_{ATP}$  channel deficiency (Arnoux

et al., 2010) in 40–70% (Thomas et al., 1995; Thomas, Ye, and Lightner, 1996; Sandal et al., 2009; Gloyn, Siddiqui, and Ellard, 2006; Fernández-Marmiesse et al., 2006; Tanizawa et al., 2000; Raicevic et al., 2021; Park et al., 2011).  $K_{ATP}$  channel CHI is more common in treatment-resistant cases (82%) (Bellanné-Chantelot et al., 2010) than in diazoxide-responsive patients (approx. 15%) (Flanagan et al., 2010). Mutations affecting the *ABCC8* gene are implicated up to tenfold more often than *KCNJ11* (Sandal et al., 2009; Bellanné-Chantelot et al., 2010). As expected, homozygosity in carriers tend to be more prevalent in consanguineous populations (Razzaghy-Azar et al., 2022; Amaratunga et al., 2022).

As the neonate brain has a high energy need, it is particularly susceptible to hypoglycemic injury (Rodrigues Vilela et al., 2014). As the elevated insulin levels in CHI suppress utilization of alternative energy sources such as ketone bodies it increases the risk of neonatal brain injury. No exact definition or critical value of hypoglycemia in neonates exists, but both the severity and the duration of hypoglycemia may have long-term neurological and developmental consequences (Stomnaroska-Damcewski et al., 2015). Hypoglycemic injury can cause intellectual disability, cerebral palsy, seizure disorder, microencephaly, spasticity, and ataxia (Steinkrauss et al., 2005). Therefore, early diagnosis and prompt management of hypoglycemia is essential to avoid long-term neurological complications (Demirbilek and Hussain, 2017; Gataullina et al., 2013; Steinkrauss et al., 2005; Helleskov et al., 2017).

**4.1.4.1. Neurological defects associated with CHI.** Similar to what is seen in neonatal diabetes, early reports indicated that up to half of children with CHI suffered from developmental delay and psychomotor disturbances, and a third was diagnosed with epilepsy (Meissner et al., 2003; Menni et al., 2001; Cresto et al., 1998; Jack et al., 2003; Rother et al., 2001; Steinkrauss et al., 2005). It has been debated whether surgical or medical interventions would improve the long-term outcome in CHI (Jack et al., 2003). There are also disagreements as to whether an early diagnosis is associated with an increased risk (Menni et al., 2001), or whether early treatment can improve the long-term prognosis, since later debut age and milder symptoms have been correlated with poor neurodevelopmental outcomes (Jack et al., 2003; Meissner et al., 2003). As these historic records lack detailed genetic data, it is unclear to what extent the intellectual disability is linked to a primary channelopathy or to hypoglycemic sequela. In more recent studies, high rates of neurological comorbidity have also been confirmed, with up to a third of patients showing neurocognitive problems and epilepsy. However, as some of these cases are found in highly consanguineous populations, careful interpretation will be needed to establish the causal effect in a genotype, as multiple genetic traits might be shared in these carriers (Laimon, Aboelenin, and El Tantawi, 2021; Razzaghy-Azar et al., 2022; Levy-Shraga et al., 2013). In non-consanguineous populations, abnormal behaviors were observed in a third of British CHI cases, showing that a late diagnosis was associated with higher rates of comorbidity (Salomon-Estebanez et al., 2017). Furthermore, 28 out of 60 German CHI patients (38% with  $K_{ATP}$  channel CHI) revealed delay in at least one developmental area. A third of these had motor problems, but only four patients were diagnosed with mild to moderate intellectual disability (Ludwig et al., 2018). Similar findings were published by a Finnish group, reporting that CHI patients did not differ in intellectual functioning compared to the general population. Even so, retrospective analyses revealed intellectual disability in up to 7% (Muukkonen et al., 2019). Since only a subset of patients was systematically assessed, 11 of which were  $K_{ATP}$  channel CHI, no conclusions as to the association between genotype and phenotype could be reached either in the German or Finnish studies. In a smaller Serbian study, where five *ABCC8* carriers were identified, two heterozygotic carriers suffered from neurodevelopmental delay and seizures (Raicevic et al., 2021), and both were reported diazoxide responsive. We appreciate that the evidence to date within the CHI field is equivocal in some respects and strong in others

and have sought to clarify within this section where the knowledge gaps are within the  $K_{ATP}$  field.

## 4.2. $K^+$ -channels implicated in epilepsy

### 4.2.1. *KCNQ* channels

Mutations in  $K^+$ -channels are found in many diseases affecting the brain and peripheral tissues (see [Supplementary Table S1](#) and [Supplementary figs. S1-S8](#) for a list of mutations and diseases). Mutations in *KCNQ1* are strongly associated with LQTS, an autosomal dominantly inherited heart condition where an unusually long repolarization causes life-threatening arrhythmias and even sudden cardiac death (Algra et al., 1993; Lamberts et al., 2015; Surges et al., 2010; Seyal et al., 2011). In addition to the well-established role of *KCNQ1* in cardiac arrhythmias, this ion channel has also been implicated in epilepsy, including sudden unexpected death in epilepsy (SUDEP), which is responsible for 20% of epilepsy-related mortality (Tiron et al., 2015; Nashef, Hindocha, and Makoff, 2007; Tomson, Nashef, and Ryvlin, 2008). The molecular mechanism for the involvement of *KCNQ1* in epilepsy is still not resolved; Tiron et al. and González et al., have presented family cases of patients linking *KCNQ1* variants (L273F, Q530X) to LQTS epilepsy (Tiron et al., 2015; González et al., 2018). The pathogenic variant L273F is conserved among  $K_v7$  mutation family members (Fig. 4).

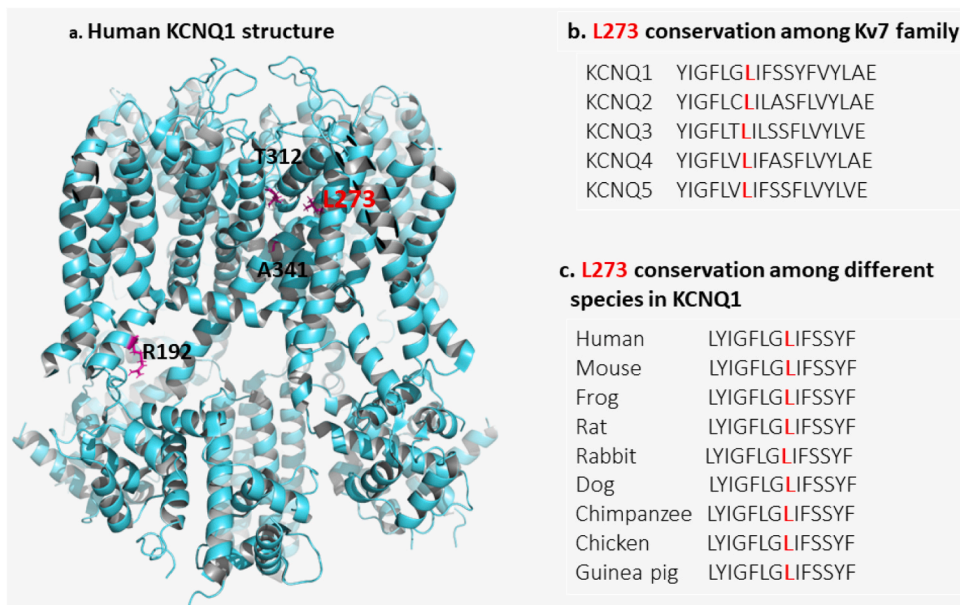
The *KCNQ2* gene encodes *KCNQ2* ( $K_v7.2$ ), which is a voltage-gated slowly activating and deactivating  $K^+$ -channel (M-channel) that regulates neuronal excitability. Mutations in *KCNQ2* result in many pathogenic protein variants that cause various neurological diseases. Examination of *KCNQ2* pathogenic and likely pathogenic variants as assembled in the ClinVar database (<https://www.ncbi.nlm.nih.gov/clinvar/>) shows that *KCNQ2* variants are implicated in early infantile epileptic encephalopathy with suppression bursts, benign familial neonatal seizures, developmental and epileptic encephalopathy, childhood epilepsy with centrotemporal spikes, and intellectual disability ([Supplementary Table S1](#)). More than 100 different pathogenic or likely pathogenic *KCNQ2* mutations have been reported. Nonsense mutations of *KCNQ2* are found in patients with the autosomal dominant epilepsy form termed Benign familial neonatal convulsions (BFNC) (Biervert et al., 1998). As *KCNQ2* and *KCNQ3* form the heteromeric M-channel, mutations in *KCNQ3* are also associated with BFNC (Hirose, 2000; Charlier et al., 1998; Allen et al., 2014). Missense variants in *KCNQ2* have also been associated with abnormalities in cortical development (Legros et al., 2022) and early onset epilepsy and encephalopathy (EOEE) (Devaux et al., 2016).

Likewise, coding variants in *KCNQ3* ( $K_v7.3$ ) have been associated with epilepsy ([Supplementary Table S1](#), Fig. S1), including Juvenile myoclonic epilepsy (a monogenic form of human epilepsy) (Vijai et al., 2003). The variant (W309R in *KCNQ3*) which changes the function of the channel has been identified in human epilepsy, explaining the CNS hyper-excitability in patients with BFNC.

In the brain, *KCNQ5* ( $K_v7.5$ ) shows high expression in the neocortex and hippocampus where it is important in regulating neuronal excitability (Tasic et al., 2018; Tzingounis et al., 2010). Several *de novo* *KCNQ5* variants have been found in children with epilepsy, intellectual disability (ID) or language delay ([Supplementary Table S1](#), Fig. S3). Functional characterization of these variants showed both GOF and LOF (nonsense) mutations, both of which are associated with neurological impairment (Wei et al., 2022).

### 4.2.2. *KCNT1* ( $K_{Na1.1}$ )

$K_{Na1.1}$  is a sodium-activated potassium channel encoded by the human gene *KCNT1*. This channel, also known as SLACK, SLO2.2, or  $K_{Ca4.1}$  (Borlot et al., 2020), is opened by increased cytoplasmic sodium concentrations. The resulting potassium outflux counteracts the membrane potential change caused by sodium influx and regulates neuronal firing patterns, e.g. in response to hypoxia (Ruffin et al., 2008; Bhattacharjee and Kaczmarek, 2005). Mutations of  $K_{Na1.1}$  are associated with



**Fig. 4.** The structure of KCNQ1 and the conservation of L273. a) Human KCNQ1 structure (PDB ID: 7XNK). Residues associated with LQTS and epileptic phenotype, as is the case for pathogenic variants L273F and R192C, are marked as stick in magenta. The variants T312I and A341F are, both found to be pathogenic and associated with LQTS in human. Mice with the corresponding mutations (T311I and A341E) developed epilepsy (Goldman et al., 2009). b) The residue L273 located in the S5 TM segment (see Fig. 2) is quite conserved among Kv7 family members. c) Sequence alignment of KCNQ1 across different species shows the conservation of L273.

epilepsy (Supplementary Table S1) such as autosomal dominant nocturnal frontal lobe epilepsy (ADNFLE) and epilepsy of infancy with migrating focal seizures (EIMFS) (Lim et al., 2016). *De novo* mutations have been observed in patients with epilepsy, with the most frequent variants being A394T, and G288S (Borlot et al., 2020; Khamdiyeva et al., 2021). Functional assays revealed that a GOF mutation in *KCNT1* affects the gating properties and activates the channel, an effect that can be reversed by quinidine, a classic antiarrhythmic pharmacological agent (Milligan et al., 2014).

#### 4.2.3. *KCNA2* ( $K_v1.2$ )

The gene *KCNA2* encodes the  $K_v1.2$  voltage-gated potassium channel which is expressed in the CNS and acts on regulating neurotransmitter release and neuronal excitability (Sheng et al., 1993; Lai and Jan, 2006). Variants of *KCNA2* (Supplementary Table S1, Fig. S7) are found in patients with epileptic encephalopathy, and both LOF and GOF are implicated with disease (Syrbe et al., 2015).

#### 4.2.4. *KCNB1* ( $K_v2.1$ )

The  $K_v2.1$  is a voltage-gated delayed rectifier potassium channel encoded by the *KCNB1* gene. Expression of *KCNB1* is prominent in various parts of the brain and regulates neuronal excitability (Bishop et al., 2015). A *KCNB1* variant was found to cause developmental and epileptic encephalopathy with intellectual disability (Torkamani et al., 2014; Saito et al., 2015; Bar et al., 2020,2020; Bar et al., 2020,2020; Kang et al., 2019) (Supplementary Table S1, Fig. S8). A *de novo* mutation in the *KCNB1* (V378A), located in the pore-helix domain of the channel, was discovered in a family with idiopathic epileptic encephalopathy. This mutation affected the normal function of the channel, including expression levels, subcellular localization, and ion selectivity (Thiffault et al., 2015). Similar results were also observed for a mutation in the equivalent position in the *Drosophila melanogaster* Shaker  $K_v$  channel (Heginbotham et al., 1994).

#### 4.2.5. *KCNC1* ( $K_v3.1$ )

$K_v3.1$  and  $K_v3.3$  channels are expressed at high levels in parvalbumin positive GABAergic, inhibitory interneurons where they are involved in action potential propagation and synaptic transmission (Goldberg et al., 2005).  $K_v3.1$  undergoes alternative splicing to generate two channel isoforms, AUT00206, a  $K^+$ -channel modulator, was recently found to modulate resting state electroencephalogram (EEG)

recordings and psychiatric symptoms in patients with schizophrenia (Kaar et al., 2023). Loss-of-function variants in *KCNC1* ( $K_v3.1$ ) have been associated with neurological disorders, including developmental delay, intellectual disability, and epilepsy (Supplementary Table S1, Fig. S5) (Cameron et al., 2019). A coding variant (R320H) in the voltage-sensing domain of  $K_v3.1$  causes the progressive myoclonus epilepsy and ataxia (Carpenter et al., 2021). The diverse clinical features for *KCNC1* variants might indicate that they have multiple disease mechanisms (Oliver et al., 2017).

#### 4.2.6. *KCND3* ( $K_v4.3$ )

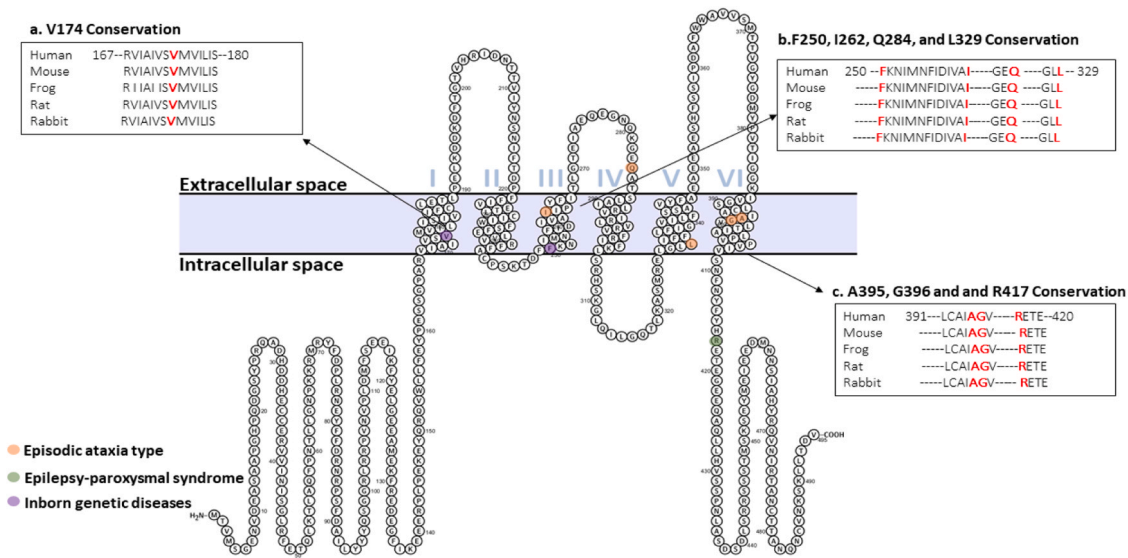
$K_v4.3$  is encoded by the *KCND3* gene and expressed in the brain, smooth muscle, and the heart (Postma et al., 2000; Gutman et al., 2005). *KCND3* ( $K_v4.3$ ) plays a role in action potential firing and neuronal excitability by mediating subthreshold-operating transient (A-type)  $K^+$  currents (Nadal et al., 2001).  $K_v4.3$  mutants are linked to spinocerebellar ataxia type 19 and 22 (SCA19/22) (Lee et al., 2012). Whole exome sequencing identified the heterozygous variant R419H that displayed a dominant increase in potassium current amplitudes and changes in voltage-dependent gating properties (Hsiao et al., 2021).

#### 4.2.7. *KCNA1* ( $K_v1.1$ )

Coding variants in *KCNA1* ( $K_v1.1$ ) are found in several human neurological diseases, including episodic ataxia type 1, episodic epilepsy, severe developmental and epileptic encephalopathy (Browne et al., 1994). Related to their role in renal magnesium reabsorption, mutations in the *KCNA1* are also associated with hypomagnesemia with myokymia and tetanic crises (Bianchi et al., 2020). For some of the mutations in *KCNA1* (Fig. 5), functional assays in human embryonic kidney cells have demonstrated loss of function (Tomlinson et al., 2013).

#### 4.2.8. *KCNH2* ( $K_v11.1$ )

The human gene *KCNH2* (Ether-à-go-go-Related Gene, hERG) encodes the pore-forming subunit protein called  $K_v11.1$  which is essential for cardiac repolarization (Sanguinetti and Tristani-Firouzi, 2006).  $K_v11.1$  also controls the electrical activity of neurons by delaying the repolarization phase. Dysregulation of the  $K_v11.1$  channel have been associated with various neurological and cardiovascular disorders such as epilepsy, schizophrenia, and arrhythmias (Huffaker et al., 2009; Lubberding et al., 2022; Sanchez-Conde et al., 2022; Partemi et al., 2013; Zamorano-León et al., 2012, Sanguinetti and Tristani-Firouzi,



**Fig. 5.** The schematic diagram of KCNA1(K<sub>v</sub>1.1) shows pathogenic variant and their location in the protein. Amino acid residues are numbered according to human Kv1.1. a) The variant V174F is situated at the S1 TM, and all the pathogenic mutations are conserved among human, mouse, frog, rat, and rabbit species. b) and c) Residue conservation at the position of the indicated variants in different species and their location in the channel. The 2D diagram was generated by Protter (Omasits et al., 2014).

2006). Mutations in Kv1.1 are linked to long QT syndrome (LQTS) which is characterized by a prolongation of the repolarization phase of the cardiac action potential with increased risk of cardiac arrhythmias and sudden death (Dekker et al., 1994; Splawski et al., 2000). LQTS patients carrying Kv1.1 mutations may also have increased insulin secretion in pancreatic islets and decreased glucagon release (Engelbrechtsen et al., 2018). In addition, it appears that disease associated mutations in Kv1.1 also can impact on the trafficking of the protein to the plasma membrane (Anderson et al., 2014).

#### 4.3. Obsessive-compulsive disorder (OCD) and other neuropsychiatric dysfunctions

Obsessive-compulsive disorder (OCD) is a psychiatric disorder characterized by uncontrollable obsessive thoughts or an insurmountable urge to perform repetitive actions (American Psychiatric Association, 2013), with a lifetime prevalence of 2.5% (Weissman et al., 1994; Ruscio et al., 2010). Although OCD is highly polygenic and published GWAS studies have not identified genome wide significantly associated genetic markers, a link between OCD and insulin signaling has been suggested based on human GWAS studies, murine models, and epidemiological data. Analysis of GWAS studies in OCD, led van de Vondervoort and colleagues to identify a genetic signature that is enriched in genes of insulin and insulin-related signaling cascades (van de Vondervoort et al., 2016), which was also confirmed in murine models (van de Vondervoort et al., 2019). At the genetic level, it was reported that the genes *INS* (encoding insulin) and *IGF2*, are located on a region on chromosome 11p15, in a region previously identified by linkage analysis in families with OCD (Wang et al., 2009). Bralten et al., noted genetic correlations between OCD and obsessive-compulsive symptoms in the general population with the gene-set for insulin signaling in the central and peripheral nervous systems (Bralten et al., 2020) which confirmed a role for insulin signaling in cognitive flexibility established in preclinical models (van de Vondervoort et al., 2019). Together with analyses of GWAS data sets, *KCNQ1* was identified as a possible treatment target in OCD (van de Vondervoort et al., 2016). Possibly, the association between *KCNQ1* and OCD traits may occur via its regulation of pancreatic insulin release which reaches the brain, or via another CNS mechanism under the control of *KCNQ1*. In this regard, *KCNQ1* imprinting may be important as Beckwith-Wiedemann syndrome, a disorder of *KCNQ1*

imprinting, is associated with an increased incidence of diabetes and autistic-like traits (including increased compulsivity, a feature common to both autism and OCD) (Valente et al., 2019).

#### 5. Pharmacology of K<sup>+</sup>-channel directed drugs and their therapeutic targets

Due to their role in the regulation of neuronal excitability and cardiac rhythm, K<sup>+</sup>-channels have long been considered promising drug targets on one side, but also risky in terms of potential side-effect profiles. For ligands targeting K<sup>+</sup>-channels, it has generally been difficult to achieve satisfactory target selectivity and specificity. Off-target effects at other channels or receptors are frequent and dose dependent. Furthermore, different K<sup>+</sup>-channels often have complex structures with multiple subunits, and lack of high-resolution channel structural data has made structure-based drug discovery difficult. Moreover, the expression of different K<sup>+</sup>-channels within the same cell, coupled to frequent expression of multiple K<sup>+</sup>-channel subtypes in the same tissue, makes drug development often challenging, but theoretically amenable to drug delivery approaches such as those offered through nanotechnology (Wulff, Castle, and Pardo, 2009). Modulation of potassium channels by activators or inhibitors could potentially influence a range of clinical conditions, including epilepsy, diabetes, atrial fibrillation, multiple sclerosis, Parkinson's disease, schizophrenia, and musculoskeletal disorders (Li, Zhang et al., 2021; Bajaj, Ong, and Chandy, 2020; Wulff, Castle, and Pardo, 2009; Grandi et al., 2017; Sturgess et al., 1988), but has so far been limited by their potential side effect profiles. As an example, activation of K<sup>+</sup>-channels relaxes smooth muscles and reduces neuropathic pain (Weston and Edwards, 1992; Tian et al., 2014). In contrast, inhibition of the K<sup>+</sup>-channel increases cell excitability and prolongs repolarization (Lenz and Hilleman, 2000) while also stimulating insulin secretion from pancreatic  $\beta$ -cells. The pharmacological potential of these compounds (Tables 1 and 2, Figs. 6–8) targeting voltage-gated potassium channel KCNQs and K<sub>ir</sub>, an inward-rectifying potassium channel are described below.

##### 5.1. KCNQ Activators

The Kv7 activators, which are in different stages of development, are summarized in Fig. 6a. ML277 is a KCNQ1 specific activator which has



**Table 1**Voltage-gated K<sup>+</sup>-channel (K<sub>v</sub>7 and K<sub>ir</sub>) activators, development status, disease, human studies, and targets.

Drug	Target channel	Disease (indication)	Human Studies (n)	Status	Reference
ML277	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Mattmann et al., 2012)
L364373(R-L3)	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Salata et al., 1998)
Zinc pyrithione (ZnPy)	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Eid and Gurney, 2018)
Phenyl boronic acid	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Mruk and Kobertz, 2009)
Compound 41	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Amato et al., 2011)
Retigabine	KCNQ2(K <sub>v</sub> 7.2)	Epilepsy	376 (NCT00310388)	FDA approved, 2011 (Discontinue, 2017)	(Epilepsy, 2016; Stafstrom, Grippon, and Kirkpatrick, 2011)
ML213	KCNQ2-5(K <sub>v</sub> 7.2-7.5)	Epilepsy	Not tested	Investigative	(Seefeld et al., 2018)
ZTZ-240	KCNQ1-3(K <sub>v</sub> 7.1-7.3)	Epilepsy	Not tested	Investigative	(Gao et al., 2010)
Compound 51	KCNQ2(K <sub>v</sub> 7.2)/KCNQ3(K <sub>v</sub> 7.3)	Epilepsy	Not tested	Preclinical	
ICA-27243	KCNQ2-5(K <sub>v</sub> 7.2-K <sub>v</sub> 7.5)	Epilepsy	Not tested	Investigative	(Padilla et al., 2009)
Flupirtine	KCNQ2-5(K <sub>v</sub> 7.2-K <sub>v</sub> 7.5)	Epilepsy	20 (NCT01450865)	Clinical Trial	(Szelenyi, 2013; Fleckenstein et al., 2013)
XEN1101	KCNQ (K <sub>v</sub> 7)	Epilepsy	360 (NCT05614063)	Clinical Trial	(Bajaj, Ong, and Chandy, 2020)
Diazoxide	KCNJ11(K <sub>ir</sub> 6.2)	Hypoglycemia, Type 1 diabetes	12 (NCT01488136)	FDA approved, 1973	(Edwards and Weston, 1993; Alexander et al., 2021; George et al., 2015)
Minoxidil	KCNJ11(K <sub>ir</sub> 6.2)	Blood pressure	558 (NCT00283686)	FDA approved, 1979	(Edwards and Weston, 1993; Alexander et al., 2021; Schrier et al., 2014)
Bimakalim	KCNJ11(K <sub>ir</sub> 6.2)	Arrhythmia, Hypertension	Not tested	Investigative	(Edwards and Weston, 1993)
Cromakalim	KCNJ11(K <sub>ir</sub> 6.2)	Arrhythmia, Hypertension	Not tested	Investigative	(Edwards and Weston, 1993)
Aprikalim	KCNJ11(K <sub>ir</sub> 6.2)	Arrhythmia, Hypertension	Not tested	Investigative	(Edwards and Weston, 1993)
BMS-180448	KCNJ11(K <sub>ir</sub> 6.2)	Ischaemic heart disorder	Not tested	Investigative	(Lawson, 2000; Lee et al., 2007)
BMS-182264	KCNJ11(K <sub>ir</sub> 6.2)	Ischaemic heart disorder	Not tested	Investigative	(Lawson, 2000)
Pinacidil	KCNJ11(K <sub>ir</sub> 6.2)	Blood pressure	NA	FDA approved, 1989 (marking: discontinued)	(Lawson, 2000; Alexander et al., 2021)
Nicorandil	KCNJ11(K <sub>ir</sub> 6.2)	Angina	402 (NCT01396395)	Approved 2009 in UK	(Lawson, 2000; Alexander et al., 2021; Jiang et al., 2016)

been identified by high-throughput screening (Mattmann et al., 2012). The binding affinity of ML277 (Fig. 7a) is 260 nM for KCNQ1, for which it has > 100-fold selectivity over KCNQ2 and KCNQ4 (Mattmann et al., 2012). ML277 enhances  $I_{KS}$  (slow delayed rectifier potassium current), reduces the action potential (Hou et al., 2019; Xu et al., 2015; Willegems et al., 2022), and temporarily suppressed QT interval prolongation (van Bavel et al., 2023).

However, the properties and pharmacological sensitivity of KCNQ1 are affected by its binding to the auxiliary subunit KCNE1 (Yu et al., 2013). Another ligand R-L3 (L364373), is also reported to enhance channel activity, which is modified by KCNE1 subunit (Salata et al., 1998). Zinc pyrithione is another activator of the KCNQ channels identified by high-throughput screening and this compound can restore channel function (Xiong, Sun, and Li, 2007). Zinc pyrithione, however, is not selective across pharmacophores and also activates KCNQ4, and KCNQ5, besides KCNQ1 (Gao et al., 2008).

The KCNQ channel activator retigabine was originally developed by GlaxoSmithKline and Valent Pharmaceuticals and approved by FDA in 2011 as an antiepileptic agent (Stafstrom, Grippon, and Kirkpatrick, 2011). Retigabine activates KCNQ2-KCNQ5, augments the current, limits the neuronal excitability, and has anticonvulsant activity in seizure models (Blackburn-Munro et al., 2005; Humphries and Dart, 2015; Tatulian et al., 2001). Retigabine binds at the pore-helix of KCNQ2 (Fig. 7b) and activates the channel by allosteric modulation (Li, Zhang et al., 2021). XEN1101 is an analogue of retigabine, selective for KCNQ2/KCNQ3 potassium channel opener in the development stage for the treatment of epilepsy and major depressive disorder (MDD). XEN1101, developed by Xenon pharmaceuticals and is now in Phase 3 clinical trials (Bialer, M., Johannessen, S. I., Koepp, M. J., Levy, R. H.,

Perucca, E., Perucca, P., Tomson, T., & White, H. S., 2020; Premoli et al., 2019).

Flupirtine is a structural analogue of retigabine that works as a KCNQ channel opener with nonopioid features and is in use for chronic pain (Szelenyi, 2013). The compound activates KCNQ2-5, reduces excitatory postsynaptic firing frequency in neurons and exhibits analgesic activity in rat models (Sun and Kapur, 2012; Blackburn-Munro and Jensen, 2003).

ICA-27243, a benzanilide compound, also activates the KCNQ2-5 channels. The activity of this compound is pronounced in the hetero-multimeric channels KCNQ2/KCNQ3 compared to KCNQ3/KCNQ5. Anticonvulsant activity of ICA-27243 has been observed in a rodent seizure model (Wickenden et al., 2008; Padilla et al., 2009; Roeloffs et al., 2008). Another activator of KCNQ channels, Ztz-240, was identified by screening 20,000 compounds in a cell-based rubidium flux assay. Ztz-240 activates all KCNQ channels except KCNQ1 in a concentration dependent manner, increases the KCNQ2 outward current amplitude and delays its deactivation (Gao et al., 2010; Li et al., 2013). A recent comparison of cryo-electron microscopy (cryo-EM) structures of KCNQ2 with retigabine and with ztz-240 revealed different patterns of binding. Ztz-240 binds at the voltage sensing domain and coordinates stabilization of the channel while retigabine binds at the pore domain (Li, Zhang et al., 2021). These two ligands have slightly different ways of modulating channel functions, which may be relevant at different membrane potentials.

## 5.2. K<sub>ir</sub> Activators

A number of activators (Table 1) of K<sub>ir</sub> channels are in different

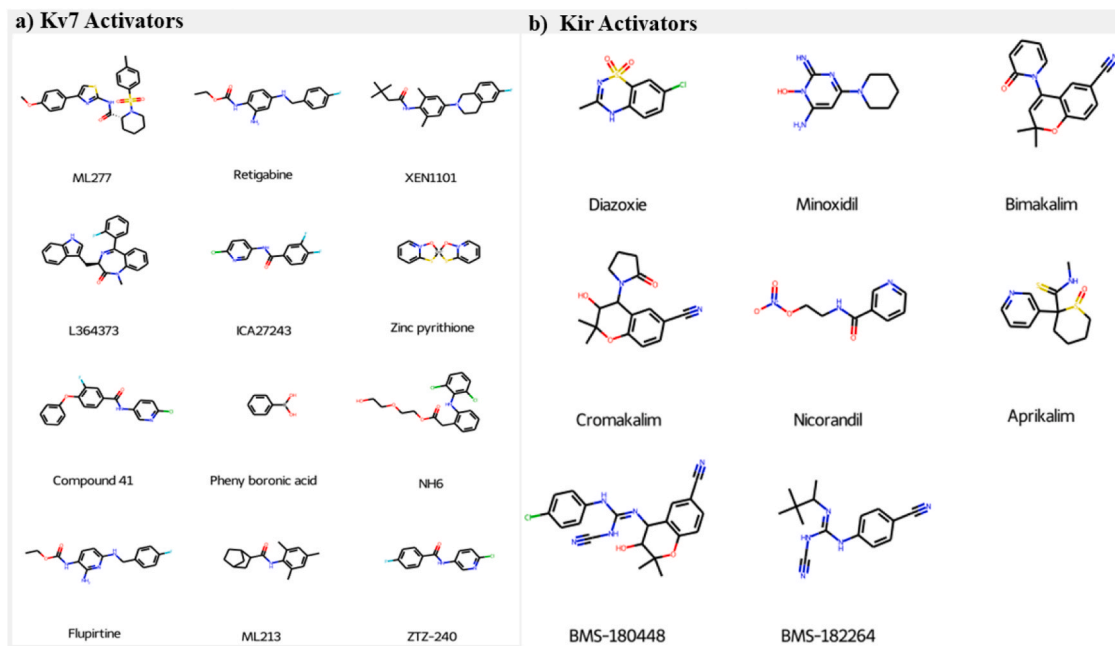
**Table 2**Voltage-gated K<sup>+</sup>-channel (K<sub>v</sub>7 and Kir) Inhibitors, development status, disease, human studies, and targets.

Drug	Target channel	Disease (indication)	Human studies (n)	Status	Reference
Chromanol 293B	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Gerlach et al., 2001)
Azimilide	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	NA	Clinical Trial (Dogs)	(Wulff, Castle, and Pardo, 2009; Nattel, Liu, and St-Georges, 1998)
Compound 19 S	KCNQ1(K <sub>v</sub> 7.1)-KCNQ1	LQTS, Arrhythmia	Not tested	Investigative	(Lloyd et al., 2001)
Compound 24 A	KCNQ1(K <sub>v</sub> 7.1)-KCNQ1	LQTS, Arrhythmia	Not tested	Investigative	(Lloyd et al., 2001)
Bepidil	KCNQ1, KCNQ4(K <sub>v</sub> 7.1, K <sub>v</sub> 7.4)	LQTS, Arrhythmia	NA	FDA approved 1990 as a calcium blocker	(Chouabe et al., 2000; Alexander et al., 2021)
MK-0448	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Wolkenberg et al., 2017)
S-5557	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Butcher et al., 2003)
L-365260	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Towart et al., 2009)
JNJ-303	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Towart et al., 2009)
BDBM50106236	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Gerlach et al., 2001)
L-735821	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Lynch et al., 1999)
ICA-15451	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Coghlan, Carroll, and Gopalakrishnan, 2001)
DMP-543	KCNQ2-5(K <sub>v</sub> 7.2-K <sub>v</sub> 7.5)	LQTS, Arrhythmia	Not tested	Investigative	(Zaczek et al., 1998)
XE-991	KCNQ1-2,4-5(K <sub>v</sub> 7.1-K <sub>v</sub> 7.2, K <sub>v</sub> 7.4-K <sub>v</sub> 7.5)	LQTS, Arrhythmia	Not tested	Investigative	(Porter et al., 2019)
L-768673	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Stump et al., 2003)
L-761710	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Stump et al., 2003)
L-763540	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Stump et al., 2003)
L-761334	KCNQ1(K <sub>v</sub> 7.1)	LQTS, Arrhythmia	Not tested	Investigative	(Stump et al., 2003)
Linopirdine	KCNQ2-5(K <sub>v</sub> 7.2-K <sub>v</sub> 7.5)	LQTS, Arrhythmia	Not tested	Investigative	
Chlorpropamide	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Type II diabetes	NA, NCT00004363	FDA approved, 1958	(Alexander et al., 2021)
Acetohexamide	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Type II diabetes	NA	FDA approved, 1964	(Alexander et al., 2021)
Mitiglinide	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Type II diabetes	367 (NCT00519142)	not yet Approved FDA, but in Japan	(Alexander et al., 2021)
Gliclazide (Diamicon)	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Type II diabetes	357 (NCT01798706)	FDA approved, 1972	(Bajaj, Ong, and Chandy, 2020)
Tolbutamide	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Type II diabetes	12 (NCT05097716)	FDA approved, 1979	(Isomoto et al., 1996; Alexander et al., 2021)
Glipizide	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Type II diabetes	1000 (NCT01762046)	FDA approved, 1984	(Alexander et al., 2021)
Glibenclamide	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Type II diabetes	58 (NCT00232583)	FDA approved, 1984	(Alexander et al., 2021)
Glisoxepide	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Type II diabetes	1499650 (NCT02456428)	Clinical Trial	(Alexander et al., 2021)
Tolazamide	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Type II diabetes	246 (NCT01068860)	FDA approved 1986 (marketing-Discontinued)	(Alexander et al., 2021)
Glimepiride	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Type II diabetes	100 (NCT00353691)	FDA approved, 1995	(Alexander et al., 2021)
Repaglinide	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Type II diabetes	560 (NCT00399711)	FDA approved, 1997	(Alexander et al., 2021)
Nateglinide	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Type II diabetes	28 (NCT00402909)	FDA approved, 2001	(Alexander et al., 2021)
Amifampridine	KCNJ11/ABCC8(K <sub>ir</sub> 6.2/SUR)	Lambert-Eaton-myasthenic syndrome	26 (NCT02970162)	FDA approved, 2019	(Alexander et al., 2021)

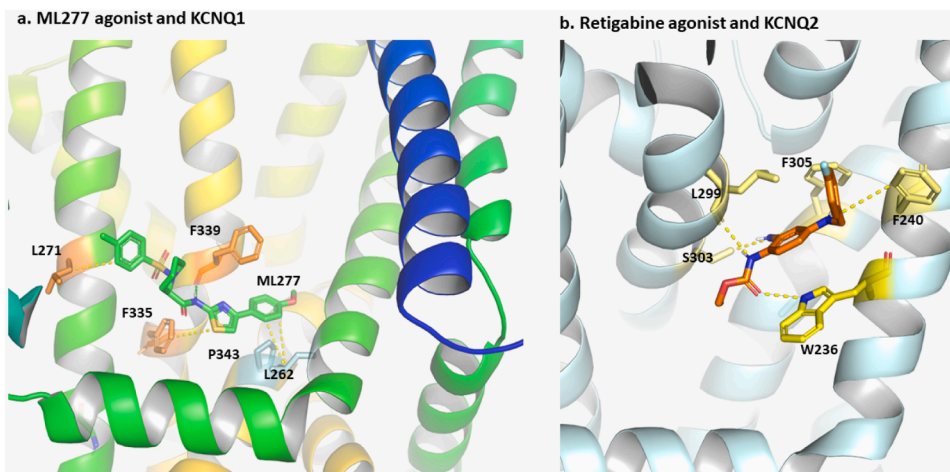
phases of clinical development and some of them are already FDA approved (Fig. 6b). Diazoxide, a K<sub>ir</sub> channel drug (FDA approved in 1973), stimulates the opening of K<sub>ATP</sub> channels, hyperpolarizes the membrane of pancreatic β-cells and inhibits insulin secretion (Dunne, Illot, and Peterson, 1987; Sturgess et al., 1988). It is used to reduce blood glucose concentrations and to treat hypertension and congenital hyperinsulinism (Hibino et al., 2010; van Hamersvelt et al., 1996). The first line of treatment for CHI is to avoid hypoglycemia with continuous enteral feeding with carbohydrate-enriched diet and glucose infusions in addition to precision medicine with the oral K<sub>ATP</sub> channel opener diazoxide (Arnoux et al., 2010). However, as diazoxide is not always effective, especially when the K<sub>ATP</sub> harbors pathogenic mutations (Bellanné-Chantelot et al., 2010), the somatostatin analog octreotide is the second option. In rare cases, the calcium-channel blocker nifedipine (Baş et al., 1999) or sirolimus (Maria et al., 2019) have been successfully tried. Like diazoxide, other K<sub>ir</sub> activators are potent, but their mechanism of action is restricted in a cell specific manner (Lawson, 2000).

### 5.3. KCNQ inhibitors

Theoretically, KCNQ inhibitors can be used to modify cardiac and neuronal action potentials and as such adjust heart rate and neuronal activity. However, there are still no KCNQ blockers on the market—some are in clinical development and others have failed due to serious side effects (Towart et al., 2009). Although the development of potent inhibitors targeting KCNQ is of great interest for the treatment of arrhythmia, their therapeutic utility in the nervous system remains unclear (Wulff, Castle, and Pardo, 2009). The compound XE991 and its structural analogue linopirdine both block KCNQ2 and KCNQ3 channels (Wang, H. S., Pan, Z., Shi, W., Brown, B. S., Wymore, R. S., Cohen, I. S., Dixon, J. E., & McKinnon, D., 1998). Chromanol-293B and HMR-1556 are I<sub>Ks</sub> inhibitors, with different stereochemistry developed from the sulfonamide scaffold of the K<sub>ATP</sub> channel activator cromakalim (Gerlach et al., 2001; Hamilton, Weir, and Weston, 1986). Chromanol-293B exhibits higher potency against KCNQ1 (IC<sub>50</sub> = 120 nM) compared to other KCNQ 2–5 members and hERG channels in *Xenopus* oocytes (Lerche et al., 2007; Gerlach et al., 2001). Chromanol-293B prolongs cardiac action potentials in anaesthetized guinea pigs (Yang et al., 2004)



**Fig. 6.** The chemical structure of  $K_v7$  and  $K_{ir}$  activators. a) Activators of  $K_v7$  that have been used in investigative and clinical studies in various stages. b) Structure of  $K_{ir}$  activators that are FDA approved and in the clinical phase. The figures were generated using “RDKit: Open source chemoinformatics. <https://www.rdkit.org>”.



**Fig. 7.** The structure of complexes of ML277 (KCNQ1) and retigabine (KCNQ2) a.) ML277 is a potent agonist for KCNQ1. ML277 binds to KCNQ1 in an elbow manner (PDB ID: 7XNK) and interacts in a hydrophobic pocket, including the residues F335, F339, and L271 (orange). L262 and P343 also interact with the ligand. The residues L271, F335 and F339 are critical for ML277 binding as their mutation reduces the agonist effect (Ma et al., 2022). b.) Retigabine, binds to KCNQ2–5, but with weaker affinity than for KCNQ1. The structure of KCNQ2 with the agonist retigabine bound (PDB ID: 7CR2) reveals the pore binding mechanism. Retigabine also interacts with a hydrophobic environment including the residues W236, F240, F305, L299, and S303 (Li, Zhang et al., 2021).

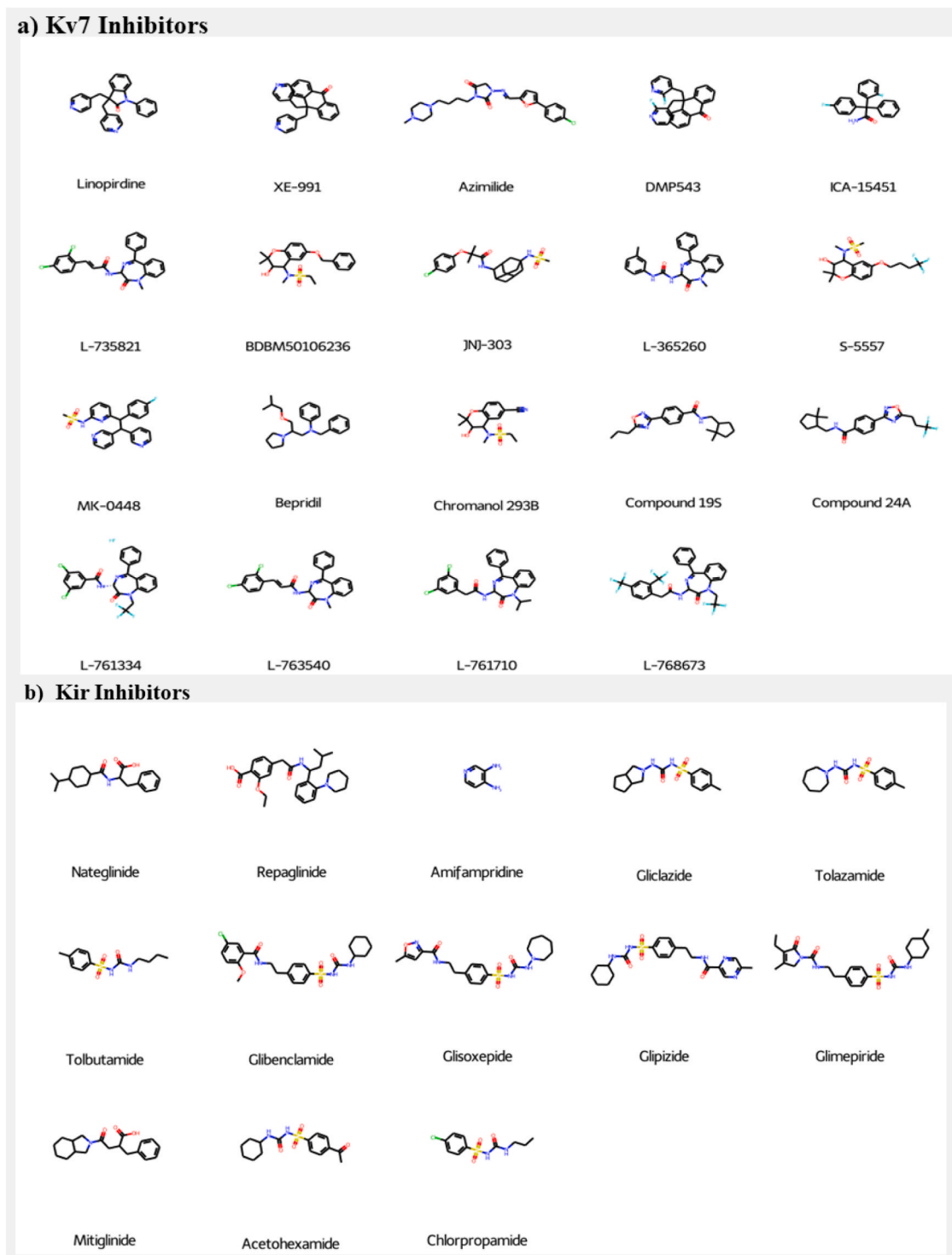
and as such should be considered carefully regarding any potential side effects before investigating other medical uses.

A series of compounds with a benzodiazepine scaffold (L-735821, L-768673, L-365260, L-761334, L-763540, L-761710), developed by Eli Lilly, induced an increase in the ventricular refractory period and a decrease in the sinus heart rate in a canine model (Stump et al., 2003; Lynch et al., 1999). ICA-15451 is a 2-Fluorophenyl-4-fluorophenyl-phenylacetamide  $I_{KS}$  blocker that inhibits the KCNQ1 current and has a binding affinity  $IC_{50}$  of 2  $\mu$ M for this  $K^+$ -channel (Coghlan, Carroll, and Gopalakrishnan, 2001). However, the compound showed  $\sim$  200-fold selectivity for KCNN4 ( $K_{Ca3.1}$ ) over KCNQ1 (Coghlan, Carroll, and Gopalakrishnan, 2001). Several other  $I_{KS}$  inhibitors (listed in Table 2) are promising in the preclinical phase, but none have yet completed clinical trials.

#### 5.4. $K_{ir}$ inhibitors

$K_{ir6.2}$  is an ATP-sensitive potassium channel consisting of a pore-forming subunit with a regulatory subunit, SUR. Blocking of the Kir

channel activity leads to membrane depolarization and stimulates insulin secretion in pancreatic  $\beta$ -cells (Trapp, Tucker, and Ashcroft, 1997). Diabetes treatment has changed greatly over the last two decades as it was discovered that oral sulfonylurea, which acts specifically on the  $K_{ATP}$  channel, could achieve better metabolic control than insulin injections (Sagen et al., 2004). Currently, high-dose glibenclamide (Fig. 8b), a second-generation sulfonylurea, is the first-choice treatment, being an effective and well-tolerated treatment in larger cohort studies (Pearson et al., 2006; Bowman et al., 2018) but to what extent this can treat DEND is still unclear. A concern is whether sulfonylurea can reach the brain in therapeutic doses since the drug is restricted by the blood-brain barrier and is also normally actively transported out of the brain (Lahmann, Kramer, and Ashcroft, 2015). Due to this uncertainty, early, high-dose sulfonylurea is still the recommended treatment as a neuroprotective measure (Hattersley, Greeley, Polak, Rubio-Cabezas, Njolstad et al., 2018). Early intervention may be more effective in targeting the brain as the blood-brain-barrier might be more permeable in the post-natal period, but the effect on early intervention is still not established. In a recent publication, sulfonylurea therapy was effective



**Fig. 8.** Inhibitors of  $K_v7$  and  $K_{ir}$  with chemical structure. a)  $K_v7$  inhibitors developed by industry and academia. L-768673 which showed promising results against  $K_v7.1$  but it has off-target activity against  $K_v11.1$  (hERG). b)  $K_{ir}$  inhibitors with chemical structure that are FDA approved except Mitiglinide which is approved in Japan. i The figures were generated using “RDKit: Open source chemoinformatics. <https://www.rdkit.org>”.

and tolerated even before term in a premature *KCNJ11* carrier (Walton-Betancourth et al., 2022). It has been proposed that inhibition of overactive neuronal  $K_{ATP}$  channels could mediate the therapeutic effect, as these ion channels are composed mainly of  $K_{ir}6.2/SUR1$  isoforms, and are sensitive to sulfonylurea (Koster et al., 2008). Several case reports have claimed that sulfonylurea treatment improves motor functions (Oka et al., 2014; Mlynarski et al., 2007; Mohamadi et al., 2010; Slingerland et al., 2006), supported by the observation of increased

cerebellar perfusion in one study (Mlynarski et al., 2007). However, two other larger multi-center studies following 115 *KCNJ11/ABCC8* carriers for more than ten years, revealed persistent CNS pathology and neuropsychiatric comorbidity in most of the patients (Bowman et al., 2018; Bowman et al., 2021). Interestingly, glibenclamide has also been shown to ameliorate Alzheimer’s pathology indirectly through the neurovascular  $K_{ATP}$  channels (Macauley et al., 2021).

## 6. Challenges and future outlook

K<sup>+</sup>-channels are important for regulating neuronal excitability, hormone secretion, and neurotransmitter release (Abbott and Goldstein, 2001; Miller, 2000). K<sup>+</sup>-channels can be homomeric or heteromeric, with functions modulated through interaction with different partner proteins and small molecules; for example, KCNQ channel functions are regulated by KCNE, phosphatidylinositol 4, 5-bisphosphate (PIP2) and calmodulin. Understanding their biological function and the effect of mutations is still challenging as the channel function is also dependent on the location and coupling to partner proteins. As detailed above, mutations in these channels have been linked to dysregulation and various diseases. With the application of next-generation sequencing, there has been a dramatic increase in information regarding the functional consequences of potassium channel mutations. Mutations in K<sup>+</sup>-channels have been observed in different locations from transmembrane to extracellular and cytoplasmic domains (S1-S6). Many K<sup>+</sup>-channel structures are available, but most are still at low resolution and detailed X-ray crystallography, or high-resolution cryo-EM studies are still missing for most channels and their ligand complexes.

Pharmacological targeting of K<sup>+</sup>-channels remains challenging, partially due to their critical physiological functions and risk of serious side effects. Ligand-based drug discovery and virtual screening programs are gradually emerging, but progress has been hampered by the shortage of high-resolution ligand-bound channel structures. However, recently published cryo-EM structures of channel complexes with ML277 and Retigabine, two agonists for modulating KCNQ function, may pave the way for future structure and ligand-based drug discovery targeting these proteins (Li, Zhang et al., 2021; Willegems et al., 2022). There is no antagonist-bound KCNQ structure available except linopirdine with KCNQ4 (Li, Wu et al., 2021).

## 7. Conclusion

Here, we have reviewed the function and regulation of the human K<sup>+</sup>-channel families. Establishing causality in relation to K<sup>+</sup>-channel functions in somatic and behavioural brain disorders is difficult especially given that many conditions are polygenic in nature and the K<sup>+</sup> related changes may be only one factor contributing to the phenotypes. Moreover, many expression profiling studies either on the transcriptome or proteome level in these behavioural brain disorders do not establish causal relationships but simply report patterns of up-/down-regulated expression. With the exception of certain (rare) monogenetic diseases and where loss/gain of function studies of a particular K<sup>+</sup> channel have been performed in animal models, it is difficult to establish the direction of causality. Where known, we have reported this, but we anticipate that it will be a focus on the next wave of research to examine these causal relationships more thoroughly, something which may be easier to establish in model systems.

We have summarized the involvement of these channels in diseases such as cardiac arrhythmias, diabetes, CHI, ataxia, epilepsy, and various neuropsychiatric conditions which may involve some common pathophysiological mechanisms. Recent progress in molecular genetics and pharmacology has improved our understanding of K<sup>+</sup>-channel functions and channelopathies. So far, development of new drugs targeting K<sup>+</sup>-channels has been challenging due to lack of specificity and off-target effects. With the introduction of new computational and experimental techniques in pharmacology and structural biology (e.g. genetic cell and animal models, machine learning protein folding algorithms and cryo-EM), we expect that structural and functional insights into these important drug targets will rapidly increase in the coming years, also paving the way for fundamentally new drugs targeting these channels.

## Conflicts of interest

The authors have no conflict of interest to disclose.

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## Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at [doi:10.1016/j.neubiorev.2023.105301](https://doi.org/10.1016/j.neubiorev.2023.105301).

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