

# Chronic Alcohol, Intrinsic Excitability, and Potassium Channels: Neuroadaptations and Drinking Behavior

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#### Abstract

Neural mechanisms underlying alcohol use disorder remain elusive, and this lack of understanding has slowed the development of efficacious treatment strategies for reducing relapse rates and prolonging abstinence. While synaptic adaptations produced by chronic alcohol exposure have been extensively characterized in a variety of brain regions, changes in intrinsic excitability of critical projection neurons are understudied. Accumulating evidence suggests that prolonged alcohol drinking and alcohol dependence produce plasticity of intrinsic excitability as measured by changes in evoked action potential firing and after-hyperpolarization amplitude. In this chapter, we describe functional changes in cell firing of projection neurons after long-term alcohol exposure that occur across species and in multiple brain regions. Adaptations in calcium-activated ( $K_{Ca}$ 2), voltagedependent ( $K_V$ 7), and G protein-coupled inwardly rectifying ( $K_{ir}$ 3 or GIRK) potassium channels that regulate the evoked firing and after-hyperpolarization parallel functional changes in intrinsic excitability induced by chronic alcohol. Moreover, there are strong genetic links between alcohol-related behaviors and genes encoding  $K_{Ca}^2$ ,  $K_V^7$ , and GIRK channels, and pharmacologically targeting these channels reduces alcohol consumption and alcohol-related behaviors. Together, these studies demonstrate that chronic alcohol drinking produces adaptations in K<sub>Ca</sub>2, K<sub>V</sub>7, and GIRK channels leading to impaired regulation of the after-hyperpolarization and aberrant cell firing. Correcting the deficit in the after-hyperpolarization with positive modulators of K<sub>Ca</sub>2 and K<sub>V</sub>7 channels and altering the GIRK channel binding pocket to block the access of alcohol represent a potentially highly effective pharmacological approach that can restore changes in intrinsic excitability and reduce alcohol consumption in affected individuals.

#### Keywords

After-hyperpolarization · Alcohol drinking · Alcohol use disorder · Intrinsic excitability · Potassium channels

#### 1 Introduction

The term addiction is commonly used to denote an unnatural or unbalanced amount of attention directed toward an object, substance, or activity. In clinical terms, the term addiction has largely been replaced by the phrase "use disorder" that reflects the understanding that these conditions are diseases or illnesses of the brain that result from some underlying alteration in normal physiology. Substance use disorders (SUDs) and more specifically those involving alcohol (ethanol) are operationally defined as the inability of the individual to control or reduce drug or alcohol intake even in the face of negative social, emotional, or health-related consequences (DSM-5 2013).

An emerging theme in the study of drug and alcohol addiction is that different neural systems and neurochemicals underlie various stages associated with drug and alcohol intake that contribute toward the progression of a drug-/alcohol- dependent state (Koob 2013). In one such model, a binge/intoxication stage is thought to

involve midbrain dopamine, opioid, and endocannabinoid reward pathways that are activated by acute ingestion of drugs/alcohol and induce positive and pleasurable feelings. Metabolic clearance of the drug or alcohol then induces a stage of acute withdrawal that may engage brain stress systems involving hypothalamic and extrahypothalamic circuits leading to negative or unpleasant symptoms that drive additional binge/intoxication stages. The desire to retake a drug or alcohol following some period of abstinence represents the preoccupation/anticipation stage and is associated with feelings of craving characterized as a need to seek out and consume the substance. This phase is thought to reflect activity in higher cortical areas including areas of the prefrontal and orbitofrontal cortex that are involved in guiding behavior by assessing risk and reward associated with making choices between competing activities.

While the brain circuitry underlying these three phases of the cycle is evolutionarily adapted for pursuing natural rewards, repeated episodes of drug or alcohol consumption may lead to an imbalance between these systems with reductions in reward signaling and altered activity in brain stress and preoccupation/anticipation pathways that combine to produce escalations in drug/alcohol use and the development of an SUD. The yearly incidence for developing an alcohol use disorder (AUD) varies among different populations and is approximately 6% for US adults age 18 and older (Substance Abuse and Mental Health Administration (SAMHSA) 2015). Multiple factors enhance an individual's susceptibility for developing an AUD including genetic and epigenetic mechanisms that influence the sensitivity of brain reward, stress, and cognitive systems to alcohol. Alcohol dependence disrupts systems designed to maintain and regulate excitability, and in this chapter, we focus on the role of three subtypes of K<sup>+</sup>-selective ion channels ( $K_{Ca}2$ ,  $K_V7$ , and  $K_{ir}3$ channels) in regulating intrinsic excitability and discuss how alcohol exposure alters the expression and function of these channels. We also highlight findings from recent studies showing how manipulating these channels with selective pharmacological agents can moderate alcohol consumption and facilitate extinction of cue-induced alcohol-seeking behaviors.

## 2 Alcohol and Intrinsic Excitability

Although several types of cells including those of skeletal and cardiac muscle are capable of generating action potentials, neurons have exploited this process to generate the complex set of electrical signals that underlie brain function. Action potentials reflect the opening of sodium permeable ion channels activated during periods of membrane depolarization elicited by excitatory synaptic inputs. The rapid entry of positively charged sodium ions drives the membrane potential toward the sodium equilibrium potential that is approximately +40 mV for most mammalian neurons. Voltage-dependent  $K^+$  ion channels are activated at these highly depolarized potentials and, combined with sodium channel inactivation, repolarize the neuronal membrane. Repolarization is often accompanied by an overshoot called the after-hyperpolarization (AHP) that briefly drives the membrane potential past its normal resting value. The AHP helps regulate the frequency of action potential

generation and is mediated by a variety of ion channels including those regulated by changes in intracellular calcium (e.g.,  $K_{Ca}1$  and  $K_{Ca}2$  channels). Neuronal firing is also regulated by activation of channels in the  $K_V7$  family whose activity is normally inhibited by G protein-coupled neurotransmitter receptors and by inwardly rectifying  $K^+$  channels ( $K_{ir}3$ ) that are activated by G proteins (also called GIRK channels).

Intrinsic excitability is a measure of a neuron's ability to fire and is experimentally determined by measuring the number of action potentials generated spontaneously or during a series of current pulses delivered to the neuron using the current-clamp mode of whole-cell electrophysiology. Importantly, plasticity of intrinsic excitability is a critical mechanism underlying synaptic integration and learning processes (Sehgal et al. 2013), and alterations in cellular firing by abused substances may facilitate drug-induced pre- and postsynaptic adaptations (Kourrich et al. 2015). The following section briefly reviews studies that have examined the effects of acute and chronic alcohol exposure on the firing properties of neurons (for review, see Harrison et al. 2017). Later sections focus on how alcohol-induced changes in the expression or function of  $K_{Ca}$ ,  $K_V$ 7, and GIRK channels may underlie changes in the current-spike relationship, thus altering the intrinsic excitability of neurons.

#### 2.1 Acute Alcohol and Spike Firing

Brain slice recordings have revealed that under basal conditions, neurons in ventral tegmental area (VTA), globus pallidus, cerebellum, and lateral habenula (LHb) are spontaneously active, while those from dorsal striatum, nucleus accumbens (NAc), hippocampus, and most cortical areas are silent although firing can be induced by direct current injection. Acute application of relatively high concentrations of alcohol (~40-80 mM) enhances firing of dopamine VTA neurons (Brodie et al. 1999), while a lower concentration (20 mM) was shown to increase firing of DA neurons located in the medial VTA (Mrejeru et al. 2015). Concentrations of alcohol as low as 1 mM increased spontaneous firing of glutamatergic neurons in the LHb, while 50 mM alcohol increased the frequency of action potential spiking in cerebellar Golgi neurons (Carta et al. 2004). In contrast, alcohol (10-80 mM) inhibits spontaneous firing of low-frequency (<30 Hz) globus pallidus neurons while having no effect on those that fire at higher frequencies (Abrahao et al. 2017). This effect was occluded by a blocker of  $K_{Ca}$  channels that are a known target for alcohol (Mulholland et al. 2009). Studies using current-evoked spiking report that alcohol also reduces firing of GABAergic neurons in the VTA (Gallegos et al. 1999), pyramidal neurons in the lateral orbitofrontal cortex (IOFC) (Badanich et al. 2013; Nimitvilai et al. 2016, 2017a), and serotonergic neurons of the dorsal raphe (Maguire et al. 2014). Alcohol inhibition of VTA GABAergic neuron firing may involve α6containing nicotinic acetylcholine receptors (Schilaty et al. 2014), while the alcoholinduced reduction in the firing of IOFC and dorsal raphe neurons requires activation of strychnine-sensitive glycine receptors (Badanich et al. 2013; Maguire et al. 2014).

#### 2.2 Chronic Alcohol and Spike Firing

Several studies have reported changes in intrinsic excitability following chronic exposure to alcohol (Table 1). Spike firing was increased in NAc medium spiny neurons (MSNs) recorded from rats following operant self-administration of alcohol (Hopf et al. 2010), and this was accompanied by reduced AHP amplitude and function of apamin-sensitive K<sub>Ca</sub>2 channels. Similarly, repeated systemic alcohol treatment and long-term drinking in an intermittent access model increased spontaneous action potentials and reduced AHP amplitude in LHb neurons (Agrawal et al. 2012). In contrast, no changes in spike firing or  $K_{Ca}^2$  channel currents were reported for NAc MSNs from rats given repeated oral doses of alcohol (Marty and Spigelman 2012). Following repeated cycles of chronic intermittent ethanol (CIE) vapor exposure in mice, spike firing of NAc medium spiny neurons and IOFC pyramidal neurons was increased along with reduced AHP and loss of apamin-sensitive currents (Nimitvilai et al. 2016; Padula et al. 2015). Renteria and colleagues reported that the increased firing after CIE exposure was observed only in D1R-expressing MSNs in the NAc shell (Renteria et al. 2017). The increase in spike firing in IOFC neurons persisted for up to 10 days and was associated with a loss of monoamine (DA, NE, 5HT) and GIRK channel modulation of firing and a tolerance to the acute inhibitory actions of alcohol (Harrison et al. 2017; Nimitvilai et al. 2016, 2017b). A similar attenuation of alcohol's inhibitory effect on spike firing was observed in IOFC neurons from long-term drinking (~9 months) monkeys, while current-evoked spiking was reduced in these animals (Nimitvilai et al. 2017a). In contrast, intrinsic excitability of putamen MSNs was increased in monkeys following prolonged drinking and repeated periods of abstinence (Cuzon Carlson et al. 2011). Regionspecific changes in spike firing following CIE treatment of mice have also been reported with increases for neurons in the ventral BNST (Marcinkiewcz et al. 2015; Pleil et al. 2015) and dorsal raphe (Lowery-Gionta et al. 2015), decreases in medial central nucleus of the amygdala (Pleil et al. 2015), and no change in infralimbic cortex (Pleil et al. 2015).

One key factor to consider from these types of studies is the time of recording relative to the last alcohol exposure. For example, in the mouse IOFC studies, CIE-exposed animals showed elevated spike firing by the 3-day withdrawal period, and excitability was still elevated at the 10-day withdrawal time point (Nimitvilai et al. 2016), while no change in excitability was seen in animals undergoing acute (<6 h) withdrawal (Nimitvilai et al. 2017a). Studies examining chronic alcohol-induced changes in intrinsic excitability in prelimbic cortical pyramidal neurons are inconsistent, with two studies showing no alterations in evoked firing in layer V neurons and one study reporting an increase in excitability of layer II/III neurons (Pleil et al. 2015; Hu et al. 2015; Trantham-Davidson et al. 2014). Changes in NAc neuron excitability in alcohol-exposed mice and rats were observed during early withdrawal (3–7 days; Padula et al. 2015) as well as following extended abstinence (Hopf et al. 2010). The increase in dorsal raphe neuron spiking following CIE exposure in mice was present 24 h after the last treatment but was lost after 1 week of withdrawal (Lowery-Gionta et al. 2015). Overall, these findings highlight

| Table 1 Chronic alcoh     | ol effects on intrinsic excitability, after- | hyperpolariz   | cation amplitude, a | nd $K_{Ca}$ 2 currents i | n rodents an  | d nonhuman primates               |
|---------------------------|--|----------------|---------------------|--------------------------|---------------|-----------------------------------|
|                           |  | AP             | AHP                 | $K_{Ca}2$                |               |                                   |
| Brain region              | Alcohol exposure model                       | firing         | amplitude           | amplitude                | Species       | Reference                         |
| BNST                      | CIE  | ←              | N/R                 | N/R                      | Mouse         | Pleil et al. (2015)               |
| BNST                      | CIE  | ←              | N/C                 | N/R                      | Mouse         | Marcinkiewcz et al. (2015)        |
| Central amygdala          | CIE  | $\rightarrow$  | N/R                 | N/R                      | Mouse         | Pleil et al. (2015)               |
| Dorsal raphe              | CIE  | <br>←          | N/R                 | N/R                      | Mouse         | Lowery-Gionta et al. (2015)       |
| Infralimbic cortex        | CIE  | N/C            | N/R                 | N/R                      | Mouse         | Pleil et al. (2015)               |
| Lateral habenula          | Repeated alcohol (IP); IAA<br>drinking       | ←              | $\rightarrow$       | N/R                      | Rat           | Kang et al. (2017)                |
| NAc                       | Operant self-administration                  | <i>←</i>       | $\rightarrow$       | $\rightarrow$            | Rat           | Hopf et al. (2010)                |
| NAc                       | Repeated alcohol (IG)                        | N/C            | <i>←</i>            | N/C                      | Rat           | Marty and Spigelman (2012)        |
| NAc                       | CIE  | ←              | $\rightarrow$       | $\rightarrow$            | Mouse         | Padula et al. (2015)              |
| NAc                       | CIE  | ←              | ←                   | N/R                      | Mouse         | Renteria et al. (2017)            |
| Orbitofrontal cortex      | CIE  | ←              | $\rightarrow$       | $\rightarrow$            | Mouse         | Nimitvilai et al. (2016)          |
| Orbitofrontal cortex      | 22 h drinking for 9 months                   | $\rightarrow$  | N/C                 | N/R                      | Monkey        | Nimitvilai et al. (2017a)         |
| Prelimbic cortex          | CIE  | ←              | N/R                 | N/R                      | Mouse         | Pleil et al. (2015)               |
| Prelimbic cortex          | CIE  | N/C            | N/R                 | N/R                      | Rat           | Trantham-Davidson et al. (2014)   |
| Prelimbic cortex          | CIE  | N/C            | N/R                 | $\rightarrow$            | Mouse         | Hu et al. (2015)                  |
| Putamen                   | 22 h drinking + repeated<br>abstinence       | ←              | N/R                 | N/R                      | Monkey        | Cuzon Carlson et al. (2011)       |
| Ventral tegmental<br>area | Repeated alcohol (IP)                        | →a             |                     | $\rightarrow$            | Rat           | Hopf et al. (2007)                |
| AP action potential, AHI  | after-hyperpolarization, BNST bed nucl       | leus of the st | ria terminalis, CIE | chronic intermitten      | tt ethanol, N | /C not changed, N/R not reported, |

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gou, AP action potential, AHP after-hyperpolarization, DNOS1 ded nuccieus ou ule suia terminaus, CLE NAc nucleus accumbens, IG intragastric, IP intraperitoneal, IAA intermittent access to alcohol <sup>a</sup>Denotes burst firing increased in alcohol-treated rats the dynamic nature of processes that regulate the intrinsic excitability of neurons across species and reveal that not all alcohol exposure models produce the same effect on cell firing, even within the same brain region.

## **3** Potassium Channels

The K<sup>+</sup> channel family is the largest known group of ion channels with at least 79 mammalian K<sup>+</sup> channel genes that encode the wide variety of channel subtypes. K<sup>+</sup> channels are highly conserved and ubiquitously expressed in almost all species (Kuo et al. 2005). Currently, there are several distinct categories of K<sup>+</sup> channels based on the mode of activation and gating, including calcium-activated (K<sub>Ca</sub>), voltage-gated (K<sub>V</sub>), inward rectifier (K<sub>ir</sub>), and two-pore domain K<sup>+</sup> channels (Table 2). Moreover, alternative splicing and co-assembly of varying K<sup>+</sup> channel subunits add to the diversity in K<sup>+</sup> channel subtypes and function (Zandany et al. 2015; King et al. 2016). Despite the large number of K<sup>+</sup> channel subtypes, all share the common feature of a highly selective K<sup>+</sup> ion-permeable transmembrane pore.

|       | IUPHAR protein              |                     |                |                  |
|-------|-----------------------------|---------------------|----------------|------------------|
| Gene  | name (common name)          | Description         | Activator      | Blockers         |
| Kcnn1 | K <sub>Ca</sub> 2.1 (SK1)   | Small-conductance,  | 1-EBIO, CyPPA, | Apamin           |
|       |                             | calcium-activated   | chlorzoxazone  |                  |
| Kcnn2 | K <sub>Ca</sub> 2.2 (SK2)   | Small-conductance,  | 1-EBIO, CyPPA, | Apamin           |
|       |                             | calcium-activated   | chlorzoxazone  |                  |
| Kcnn3 | K <sub>Ca</sub> 2.3 (SK3)   | Small-conductance,  | 1-EBIO, CyPPA, | Apamin           |
|       |                             | calcium-activated   | chlorzoxazone  |                  |
| Kcnq1 | K <sub>V</sub> 7.1          | Voltage-gated,      |                | XE-991           |
|       |                             | delayed rectifier   |                |                  |
| Kcnq2 | K <sub>v</sub> 7.2          | Voltage-gated,      | Retigabine     | XE-991           |
|       |                             | delayed rectifier   |                |                  |
| Kcnq3 | K <sub>v</sub> 7.3          | Voltage-gated,      | Retigabine     | XE-991           |
|       |                             | delayed rectifier   |                |                  |
| Kcnq4 | K <sub>V</sub> 7.4          | Voltage-gated,      | Retigabine     | XE-991           |
|       |                             | delayed rectifier   |                |                  |
| Kcnq5 | K <sub>V</sub> 7.5          | Voltage-gated,      | Retigabine     | XE-991           |
|       |                             | delayed rectifier   |                |                  |
| Kcnj3 | K <sub>ir</sub> 3.1 (GIRK1) | G protein-gated,    | ML297          | Ba <sup>2+</sup> |
|       |                             | inwardly rectifying |                | (nonselective)   |
| Kcnj6 | K <sub>ir</sub> 3.2 (GIRK2) | G protein-gated,    |                | Ba <sup>2+</sup> |
|       |                             | inwardly rectifying |                | (nonselective)   |
| Kcnj9 | K <sub>ir</sub> 3.3 (GIRK3) | G protein-gated,    |                | Ba <sup>2+</sup> |
|       |                             | inwardly rectifying |                | (nonselective)   |

**Table 2** HUGO Gene Nomenclature Committee (HGNC) designations with their InternationalUnion of Pharmacology (IUPHAR) protein names for the potassium channels discussed in thischapter

Also shown are the common protein names and the pharmacological agents used to probe alcoholrelated behaviors Given the high intracellular  $K^+$  concentration compared to that in the extracellular environment, channel opening leads to rapid  $K^+$  ion efflux and hyperpolarization/ repolarization of the cell membrane potential (Doyle et al. 1998).  $K^+$  channels thus act as an opposing force to cellular depolarization and excitability or as a modifying factor for the shaping of action potentials. Due to the immense number of  $K^+$  channel subtypes and the limited scope of this chapter, we will highlight only three of the  $K^+$  channel families, the  $K_{Ca}$  channels, the  $K_V$  channels, and the G protein-activated inward rectifier ( $K_{ir}$ 3) channels (Fig. 1). The structure and function of other  $K^+$  channel families and subtypes not mentioned here have been extensively reviewed by others and are referenced for the reader's consideration (Coetzee et al. 1999; Miller 2000; Gonzalez et al. 2012; Jenkinson 2006; Fonseca 2012; Vandenberg et al. 2015).

There are 12 subgroups ( $K_V 1-K_V 12$ ) in the family of voltage-gated K<sup>+</sup> channels.  $K_V$  channel subtypes are gated by varying voltage dependencies through a voltagesensing domain formed by four transmembrane segments (S1–S4) in each channel subunit, while the channel pore is comprised of two other transmembrane segments that form a loop (S5–S6).  $K_V 1$ ,  $K_V 4$ , and  $K_V 7$  channels are activated at relatively low membrane potentials and are critical in regulating the number of action potentials during early phases of membrane depolarization (Johnston et al. 2010). The transient A-type current is generated by  $K_V 4$  channels and has a unique feature



**Fig. 1** Activation of  $K_{Ca}^2$ ,  $K_V^7$ , and GIRK channels in neural membranes.  $K_{Ca}^2$  channels are activated by elevations in intracellular calcium via influx through voltage-gated calcium channels (VGCCs), NMDA receptors (NMDARs), or release from intracellular stores.  $K_V^7$  channels are activated near the resting membrane potential and during membrane depolarization. Ligand binding of G protein-coupled receptors (GPCRs) releases G proteins that bind to and activate GIRK channels. Opening of these  $K_{Ca}^2$ ,  $K_V^7$ , and GIRK channels allows potassium ions to flow outside of the cell causing hyperpolarization and shunting of neuronal excitability. *CaM* calmodulin, *RyR* ryanodine receptors. Images were acquired with permission from www.servier.com and subsequently modified

in which hyperpolarization is necessary for the removal of steady-state inactivation before activation (Maffie and Rudy 2008).  $K_V7$  voltage-gated K<sup>+</sup> channels produce the M-current, a slow-developing, low-voltage activated AHP current that is sensitive to muscarinic receptor activation (discussed in detail below).  $K_V2$  and  $K_V3$ currents are activated at high voltages, particularly during the firing of action potentials, and play an important role in membrane repolarization and regulation of firing in neurons with a fast-spiking phenotype. An important feature that differentiates  $K_V^2$  and  $K_V^3$  channels is the rate of activation with  $K_V^2$  channels showing much slower activation, while  $K_V3$  channels open rapidly contributing to their prominent role in regulating firing of fast-spiking neurons. Interestingly, K<sub>V</sub>5,  $K_V6$ ,  $K_V8$ , and  $K_V9$  are commonly named the silent electrical K<sup>+</sup> channel subunits. These subunits do not form functional channels as homomers but readily form heteromers with  $K_V 2$  channels with diverse functions within tissue types (Bocksteins 2016). The  $K_V 10$ - $K_V 12$  channels are referred to as ether-à-go-go (denoted  $K_V 10$ ), ether-à-go-go-related (erg, K<sub>V</sub>11), and ether-à-go-go-like (elk, K<sub>V</sub>12) and are members of the KCNH gene family. Few studies exist that directly characterize the exact function of these channels, but generally, these channels become activated at subthreshold voltages and display highly variable gating kinetics (Vandenberg et al. 2015; Zhang et al. 2009).

 $K_{Ca}$  channels are unique in that they are activated by increasing levels of intracellular calcium. Each member of this K<sup>+</sup> channel family is further distinguished by the level of single-channel conductance upon activation (Vergara et al. 1998). Large-conductance calcium-activated  $K_{Ca}$ 1 channels that are also voltage-gated have a single-channel conductance of ~100–300 pS, while intermediate ( $K_{Ca}$ 3; ~20–80 pS) and small ( $K_{Ca}$ 2; ~2–20 pS, Marty and Neher 1985) subtypes have more modest values. As discussed below, small-conductance calcium-activated  $K_{Ca}$ 2 channels are of particular interest due to their critical role in regulating intrinsic excitability in relation to alcohol addiction. Alcohol effects on large-conductance calcium-activated  $K_{Ca}$ 1 channels are discussed in the chapter by Dopico and colleagues in this volume (Dopico et al. 2017).

Inward-rectifying K<sup>+</sup> channels consist of seven subfamilies (K<sub>ir</sub>1-K<sub>ir</sub>7) and are distributed in multiple cell types, including cardiomyocytes, endothelial cells, kidneys, and neurons (for review, see Hibino et al. 2010). Among these, G protein-coupled inwardly rectifying K<sup>+</sup> (Kir3 or GIRK) channels are considered as important neuronal regulators and are associated with numerous neuropsychiatric diseases, including schizophrenia (Yamada et al. 2012), depression (Llamosas et al. 2015), epilepsy (Signorini et al. 1997), as well as drug and alcohol abuse disorders (Hill et al. 2003). Unlike K<sub>V</sub> and K<sub>Ca</sub>, GIRK channels are activated by ligandstimulated G protein-coupled receptors (GPCRs), including dopamine, serotonin, and GABA. Binding of an agonist to the GPCR triggers the dissociation of  $G_{\alpha i}$  and  $G_{\beta\gamma}$ . Once released from its bound  $G_{\alpha i}$ , the  $G_{\beta\gamma}$  dimeric protein can directly activate the GIRK channel (Logothetis et al. 1987; Reuveny et al. 1994) and increase its affinity for the membrane-bound phospholipid-phosphatidylinositol 4,5-bisphosphate (PIP2), which is required to stabilize the open state of the GIRK channel (Huang et al. 1998; Xiao et al. 2003). The activated GIRK channel is now permeable to  $K^+$  ions, leading to hyperpolarization of the cell membrane and inhibition of neuronal activity. Interestingly, concentrations of alcohol relevant to human consumption (18 mM alcohol or 0.08% blood alcohol level) directly activate GIRK channels independently from GPCR-dependent activation (Bodhinathan and Slesinger 2013; Kobayashi et al. 1999; Lewohl et al. 1999). As many therapeutic drugs that target GPCR-linked GIRK channels have been used to treat a number of neuropsychiatric diseases including alcoholism and alcohol itself directly activates GIRK channels, the role of these channels on neuronal activity and its involvement in alcohol addiction is also addressed in this chapter.

### 4 Intrinsic Excitability

 $K^{+}$  channel regulation of cellular excitability is among the most important functions related to proper neuronal activity. Excitability of neuronal activity is regulated in many ways including alteration of resting membrane potential (RMP) and limiting neuronal spike activity. The AHP that follows neuronal spiking is a manifestation of outward  $K^+$  current that regulates subsequent spiking episodes and, thus, establishes firing frequency. In addition, summation of the AHP after bursts of action potentials leads to spike-frequency adaptation that ultimately leads to the inhibition of spiking and is key for protecting neurons from over-excitation and epileptiform activity (Alger and Williamson 1988; Garduno et al. 2005; Schulz et al. 2012). The generation and regulation of action potentials by  $K^+$  channels are critical for neuronal encoding of input- and output-specific information and are mediated by the AHP. Intrinsic excitability is also crucial to processes such as spike timing-dependent plasticity in which changes in the strength of neuronal connectivity rely on the relative timing of synaptic events and back-propagating action potentials and is essential for certain types of learning (Debanne and Poo 2010). Therefore, K<sup>+</sup> channel regulation of excitability has important implications in establishing and mediating learning and memory processes.  $K_{Ca}2$ ,  $K_V7$ , and GIRK channels play significant roles in controlling intrinsic excitability by regulating RMP, spike frequency, and the AHP. Their functional roles and importance in alcohol-related neuroadaptations and behaviors are discussed in more detail below.

## 5 K<sub>Ca</sub>2, K<sub>V</sub>7, and GIRK Channel Regulation of Excitability

The small-conductance calcium-activated K<sup>+</sup> (K<sub>Ca</sub>2) channels play a key role in regulating intrinsic excitability and underlie the medium AHP (mAHP) that follows action potentials. *KCNN1–3* genes encode the pore-forming  $\alpha$  subunits of K<sub>Ca</sub>2.1, K<sub>Ca</sub>2.2, and K<sub>Ca</sub>2.3 channels that are predominantly expressed in the central nervous system (Stocker 2004). These channels are structurally similar to the K<sub>V</sub> channels in that they form tetramers and each  $\alpha$  subunit contains six transmembrane regions. K<sub>Ca</sub>2 channels are potently inhibited by the bee venom toxin apamin that produces an increase in cellular excitability and reduction in the amplitude of the mAHP (Blatz and Magleby 1986). Subunits of K<sub>Ca</sub>2 channels contain a calcium-sensitive calmodulin-binding domain formed by constitutively bound calmodulin (Schumacher et al. 2001; Xia et al. 1998) that senses changes in intracellular calcium concentration arising from activation of various calcium channel subtypes, NMDA receptors, and intracellular stores of the endoplasmic reticulum (Adelman et al. 2012). The increase in intracellular calcium concentration that occurs during membrane depolarization induces a conformational change in the calmodulin-binding domain of the  $K_{Ca}^2$  channel resulting in activation and  $K^+$  ion efflux (Xia et al. 1998). Thus,  $K_{Ca}^2$  channels are critical for monitoring and regulating intracellular calcium signaling and action potential generation.

Similar to other voltage-gated K<sup>+</sup> channels, K<sub>V</sub>7 channels are tetramers formed by assembly of six transmembrane  $K_V7$  protein subunits ( $K_V7.1-7.5$ ) that are encoded by the KCNO family of genes (KCNO1-5, respectively),  $K_V7.1$  subunits are found almost exclusively in cardiomyocytes and do not co-assemble with any of the other  $K_V7$  channel proteins and instead associate with KCNE proteins that act as ancillary modulatory subunits (Abbott and Goldstein 2001; McCrossan and Abbott 2004; Roura-Ferrer et al. 2010). The remaining four subunits are expressed throughout the nervous system and form functional homotetramers ( $K_V7.2$ ,  $K_V7.4$ , and  $K_V 7.5$ ) or heterotetramers with  $K_V 7.3$  (Howard et al. 2007; Jentsch 2000). These channels generate the M-current  $(I_M)$ , a voltage-sensitive K<sup>+</sup> current so named as it is suppressed by activation of muscarinic receptors (Wang et al. 1998; Shah et al. 2002). Subsequent research has demonstrated that the M-current can also be inhibited by a number of different neurotransmitters/hormones that act on G<sub>q</sub>and G<sub>11</sub>-coupled receptors, including, but not limited to, mGlu<sub>1/5</sub>, histamine H1, 5-HT2C, substance P, bradykinin, and angiotensin II (Brown and Passmore 2009; Zaika et al. 2006; Marrion 1997). Despite the abundance of K<sub>V</sub>7.2/7.3 channels and the physiological evidence that these heterotetramers contribute substantially to the native M-current, all  $K_V7$  channels produce M-like currents (Brown and Passmore 2009), with K<sub>V</sub>7.4-containing channels contributing to M-current in midbrain dopaminergic neurons (Hansen et al. 2008). Although  $K_V 7.5$ -containing channels show a less ubiquitous expression profile, they are nonetheless found in cortical, hippocampal, and striatal tissue (Shah et al. 2002; Schroeder et al. 2000). Regardless of composition, each M-channel subunit contains a voltage-sensor domain (transmembrane domains S1–S4), and the channels are slow-activating starting at subthreshold potentials of around -60 mV. Uniquely, M-channels do not inactivate, thus producing a sustained voltage-dependent outward current that stabilizes the membrane potential in the presence of depolarizing currents, thus regulating neuronal excitability by dampening repetitive or burst firing of action potentials (Jentsch 2000; Brown and Passmore 2009; Brown and Adams 1980). These channels also regulate interspike intervals and contribute substantially in determining whether neurons naturally fire tonically or phasically (Wang and McKinnon 1995; Lawrence et al. 2006). They also contribute to aspects of the AHP differentially depending on the brain region, channel composition, and presence/distribution of other  $K^+$ channels. In CA1 pyramidal neurons, M-channels almost exclusively mediate the mAHP (Gu et al. 2005), though not as much in other cell types (Mateos-Aparicio et al. 2014). In contrast, M-channels have been shown to mediate the fAHP and sAHP in VTA dopamine neurons (Koyama and Appel 2006). Suppression of the M-current by application of the K<sub>V</sub>7 channel blocker, XE-991, diminishes respective AHP components and increases cellular excitability and spike discharge (Brown and Passmore 2009; Gu et al. 2005; Koyama and Appel 2006). Thus, K<sub>V</sub>7 channels are an essential regulator of intrinsic excitability, the importance of which is underscored by the finding that a mere 25% reduction in function of K<sub>V</sub>7.2/7.3 channels induces seizures, as found in cases of benign familial neonatal convulsions caused by *KCNQ2* and *KCNQ3* mutations (Schroeder et al. 1998).

K<sub>Ca</sub>2 and K<sub>V</sub>7 channels play complementary roles in regulating neuronal excitability and the AHP.  $K_{Ca}^2$  channels within dentate gyrus granule cells have been identified as the central contributor to the mAHP and spike-frequency adaptation, while K<sub>V</sub>7 channels contribute minimally to the isolated mAHP and spikefrequency adaptation but strongly regulate the action potential threshold by activating at subthreshold potentials (Mateos-Aparicio et al. 2014). This complementary function is critical because dentate granule cell activity can regulate the output of interneurons and pyramidal cells through synaptic activity within hippocampal mossy fibers (Henze et al. 2002), and these channels also function to support stable long-term potentiation through facilitating protein synthesis (Barnes et al. 2010). In contrast, in CA1 hippocampal pyramidal cells, K<sub>Ca</sub>2 channels seem to contribute minimally to the mAHP following action potential bursts, whereas K<sub>V</sub>7 channels are the predominant regulators of the mAHP (Chen et al. 2014). Moreover, when K<sub>V</sub>7 channel function is inhibited or compromised in CA1 pyramidal cells, K<sub>Ca</sub>2 channels usurp regulation of the AHP and intrinsic excitability and function as a "fail-safe" to limit spike discharge (Chen et al. 2014). This has been proposed to have functional implications for conditions in which K<sub>V</sub>7 channel function may be disrupted including hyposmolarity-induced epileptiform seizures (Kobayashi et al. 2008), benign familial neonatal convulsions (Singh et al. 2008), or chronic alcohol exposure (Kang et al. 2017). There is limited understanding of how  $K_{Ca}^2$  and  $K_V^7$ channels may interact in other brain regions outside of the hippocampus. The diverse functional interactions within cellular subtypes of the hippocampus alone suggest that interplay between these channels may have varying influences on neuronal firing and AHP in other brain regions and/or cellular subtypes. Future studies are warranted to determine the full extent of K<sub>V</sub>7 and K<sub>Ca</sub>2 channel interactions to regulate cell firing, especially as disruptions in K<sub>V</sub>7-K<sub>Ca</sub>2 channel cross talk may influence plasticity of intrinsic excitability and alcohol-seeking behavior.

GIRK channels are comprised of four different subunits, GIRK1 to GIRK4. GIRK1–3 subunits (encoded by *Kcnj3*, *Kcnj6*, and *Kcnj9*, respectively, Table 2) are moderately or highly expressed throughout the brain, while expression of GIRK4 is low and is found only in a few brain regions such as the hypothalamus and cerebellum (Aguado et al. 2008; Karschin et al. 1996; Perry et al. 2008). Functional GIRK channels are heterotetramers of GIRK1/2, GIRK1/3, GIRK1/4 or GIRK2/3 subunits, or homotetramers of GIRK2 subunits (Luscher and Slesinger 2010). GIRK2 contains an endoplasmic reticulum (ER) export signal, enabling this subunit to form either homo- or heterotetramers. GIRK3 does not have an ER signal but contains a lysosomal targeting sequence that promotes degradation of GIRK channels. GIRK1 has neither an ER nor a lysosomal targeting signal so it must assemble with another GIRK subunit to express on the plasma membrane. GIRK currents are termed "inwardly rectifying" because current passes more easily in the inward direction than in the outward direction. Under physiological conditions where the RMP of neurons is positive to the equilibrium potential for K<sup>+</sup>, basal current or agonist-induced GIRK currents show large inward and small outward flow. The outward flow of GIRK-mediated K<sup>+</sup> currents near the RMP hyperpolarizes the membrane potential and thus decreases the excitability of the neuron. Dysfunction of GIRK channels has been implicated in several diseases. For example, loss of GIRK function results in excessive excitability found in epilepsy (Signorini et al. 1997), while over-activation of GIRK can reduce neuronal activity and may trigger cell death as postulated in Down's syndrome and Parkinson's disease, respectively (Patil et al. 1995).

## 6 K<sub>Ca</sub>2 Channels and Alcohol

#### 6.1 Genetics

AUD is a complex brain disease that likely results from interactions among genetic, epigenetic, and environmental factors that combine to promote heavy alcohol drinking and dependence phenotypes. Meta-analyses and twin studies estimated that 23-79% of the variance in alcohol addiction is heritable (Agrawal et al. 2012; NIAAA 2016). The limited success of the current FDA-approved drugs for treating excessive drinking may reflect the heterogeneous population of those with AUD. As precision medicine approaches are showing efficacy across a number of diseases (i.e., cancer and cardiovascular disease), recent clinical and preclinical studies have searched for genetic mutations as possible pharmacogenetic targets to treat alcohol addiction (Kranzler et al. 2017; Rinker and Mulholland 2017). While not all pharmacogenetic studies to treat alcohol addiction are reproducible (Kranzler et al. 2017), some studies have shown that matching genetic variation to pharmacotherapies can improve relapse rates and heavy drinking days (Kranzler and McKay 2012; Heilig et al. 2011; Sturgess et al. 2011). Thus, advances in precision medicine approaches offer a promising strategy for treating alcohol addiction, and a number of novel targets have been identified from preclinical models of alcohol seeking and dependence (Padula et al. 2015; Rinker and Mulholland 2017; Rinker et al. 2017).

A recent preclinical study employing an integrative functional genomics approach revealed that *KCNN* genes are present in multiple quantitative trait loci (QTL) and gene sets related to alcohol intake and dependence (Padula et al. 2015), including an alcoholism susceptibility QTL on human chromosome 1. Each member of the family of *Kcnn* genes is found in QTLs for alcohol consumption and preference in rats and mice (Padula et al. 2015; Bachmanov et al. 2002; Carr et al. 2003; Foroud et al. 2000; Radcliffe et al. 2004). BXD recombinant inbred (RI) strains of mice are an excellent resource to study the genetic diversity of

alcohol-related phenotypes (Philip et al. 2010). To gain a better understanding of Kcnn genes in controlling voluntary alcohol intake, the relationship between Kcnn and drinking was explored in BXD RI and their parental strains. Interestingly, Kcnn3 transcript levels in the NAc correlated negatively with voluntary drinking in a two-bottle choice limited-access and the drinking-in-the-dark model (Padula et al. 2015; Rinker et al. 2017). While there are some potential caveats of using BXD RI strains to study the genetic control of alcohol intake (such as the influence of taste and gene-environment interactions), Kcnn3 was also identified as a candidate signature gene that associated with alcohol preference in low- and high-alcohol-drinking rat lines (Lo et al. 2016). In alcohol-dependent BXD strains, the negative relationship between Kcnn3 and alcohol intake became more robust, suggesting that alcohol dependence alters Kcnn expression and that high levels of Kcnn expression protect against escalation of drinking in dependent mice (Padula et al. 2015). Thus, high expression levels of *Kcnn3* may be a protective factor against developing alcohol addiction and dependence. Although not identified in the NAc, reductions in KCNN2 expression were reported in the frontal cortex and amygdala of alcohol-dependent individuals (Ponomarev et al. 2012). As described below in detail, studies consistently demonstrate that chronic alcohol exposure reduces  $K_{Ca}^2$  channel function across multiple preclinical models and in divergent cell types, further demonstrating that KCNN is a mediator of voluntary and heavy alcohol drinking. This finding is supported by evidence showing that K<sub>Ca</sub>2 channel positive modulators reduce drinking in rodent models (see below). Lastly, KCNN genes are present in OTLs related to all abused substances and are altered in brains of addicts (Padula et al. 2015), suggesting that the KCNN family of genes is a common mechanism underlying addiction that spans multiple abused substances (Mulholland et al. 2016).

## 6.2 Alcohol and K<sub>Ca</sub>2 Channel Function

Alcohol has distinct effects on function and membrane trafficking of K<sub>Ca</sub>2 channels that may underlie some of the neuropathology associated with alcohol addiction (Fig. 2). Early studies in rats demonstrated that 20 weeks of chronic alcohol exposure significantly reduced inhibitory postsynaptic potentials and AHP currents in CA1 pyramidal neurons and dentate gyrus granule cells (Durand and Carlen 1984). Similar effects on K<sub>Ca</sub>2-mediated I<sub>AHP</sub> were later replicated in CA1 pyramidal neurons from organotypic hippocampal slices continuously exposed to alcohol in vitro (Mulholland et al. 2011). Interestingly, synaptic K<sub>Ca</sub>2 channels are part of a negative feedback loop with NMDA receptors within dendritic spine head nanodomains (Mulholland et al. 2011; Ngo-Anh et al. 2005). Mulholland and colleagues (2011) reported a loss of K<sub>Ca</sub>2 channel control of synaptic NMDA receptor activity after chronic alcohol that paralleled increases in excitotoxicity. This effect was attributed to reduced K<sub>Ca</sub>2.2 subunit expression at synaptic sites, and the hyperexcitability was rescued by treatment with 1-EBIO, a K<sub>Ca</sub>2 channel positive modulator. Together, these data demonstrate a relationship between prolonged alcohol exposure and deficits in hippocampal function that may underlie alcohol-induced cognitive impairments observed in clinical settings (Bartels et al. 2007).



**Fig. 2** Chronic alcohol reduces  $K_{Ca}^2$ ,  $K_V^7$ , and GIRK channel expression and signaling in the cortex and striatum.  $K_{Ca}^2$  and  $K_V^7$  potassium channels are expressed in dendrites, axons, and along the soma of neurons where they function to reduce the action potential threshold, increase the after-hyperpolarization (AHP) amplitude, and hyperpolarize the resting membrane potential. GIRK channels localize to synaptic and perisynaptic regions of glutamatergic neurons where they function to dampen neuronal excitation. Chronic alcohol exposure and alcohol dependence reduce expression and function of  $K_{Ca}^2$  and  $K_V^7$  potassium channels in neurons leading to increased intrinsic excitability and reduced AMP amplitude. GIRK channel signaling in the cortex is disrupted in alcohol-dependent mice. Images were acquired with permission from www.servier.com and subsequently modified

Alcohol exposure is also linked to reduced K<sub>Ca</sub>2 channel function within the VTA, a brain region that is the origin of dopamine cell bodies and that plays a significant role in regulating motivation and the rewarding properties of alcohol (Gonzales et al. 2004; Gorelova et al. 2012; Cook et al. 2014). Indeed, studies have shown that bath application of alcohol reduces K<sub>Ca</sub>2 channel function and increases excitability of dopaminergic neurons through modulation of the AHP (Brodie et al. 1999). It was later demonstrated that withdrawal from alcohol reduced AHP and  $K_{Ca}$ 2-mediated  $I_{AHP}$  amplitude in VTA neurons (Hopf et al. 2007). Similar effects have also been observed in the NAc and IOFC after induction of alcohol dependence (Nimitvilai et al. 2016; Padula et al. 2015) and voluntary consumption (Hopf et al. 2010). Decreases in NAc K<sub>Ca</sub>2 subunit expression and trafficking also accompany reductions in the AHP amplitude and are associated with increased excitability of the NAc. Interestingly, there was a complete loss of apamin-sensitive  $I_{AHP}$  current in NAc and IOFC neurons following chronic alcohol exposure (Nimitvilai et al. 2016; Padula et al. 2015), suggesting that alcohol may affect expression of apaminsensitive and apamin-insensitive isoforms of K<sub>Ca</sub>2.3 channels (Wittekindt et al. 2004). These data suggest that adaptations in K<sub>Ca</sub>2 channels underlie plasticity of intrinsic excitability and the motivation for alcohol-seeking behavior, particularly during a period of abstinence.

#### 6.3 K<sub>Ca</sub>2 Channel Ligands and Drinking

Several preclinical studies have shown that pharmacological modulation of K<sub>Ca</sub>2 channel activity alters alcohol consumption and seeking behavior. For example, chlorzoxazone is an FDA-approved K<sub>Ca</sub>2 channel activator (Syme et al. 2000; Cao et al. 2001) used as a muscle relaxant that dose-dependently reduced alcohol consumption in rats using the chronic intermittent access drinking protocol (Hopf et al. 2011). The chlorzoxazone-induced reduction in alcohol consumption was associated with the rescue of diminished K<sub>Ca</sub>2 channel activity in the NAc core as examined by ex vivo slice electrophysiology. In addition, infusion of 1-EBIO, a similar  $K_{Ca2}$  positive modulator, in the NAc core selectively reduced alcohol, but not sucrose operant self-administration after a period of forced abstinence (Hopf et al. 2010). Using a 24-h intermittent access procedure, investigators were able to show that CyPPA, another K<sub>Ca</sub>2 positive modulator, significantly reduced alcohol consumption in C57BL/6J mice (Padula et al. 2013). Taken together, these preclinical data indicate that treatment with  $K_{Ca}^2$  positive modulators is a potential promising pharmacotherapeutic approach to reduce alcohol consumption in individuals with alcohol use disorder (Mulholland 2012). Other studies have demonstrated that microinjection of apamin into the NAc significantly increased alcohol consumption in nondependent mice and also induced spontaneous seizure activity in dependent mice at high doses (Padula et al. 2015). These data indicate that there is a bidirectional role for K<sub>Ca</sub>2 channels to modulate alcohol consumption and further emphasize the role of reduced K<sub>Ca</sub>2 channel function in mediating excessive consumption.

In addition to its role in alcohol consumption,  $K_{Ca}^2$  channels are also involved in regulating responses to alcohol-associated cues. The prefrontal cortex is a key brain region that responds to the presentation of alcohol- and drug-associated cues (Otis et al. 2017), and  $K_{Ca}^2$  channels within this region have been linked with associative learning processes (Criado-Marrero et al. 2014). Recent evidence has shown that both systemic and local inhibition of infralimbic but not prelimbic cortex  $K_{Ca}^2$  channels with apamin facilitates extinction of alcohol-seeking behavior during cue extinction sessions (Cannady et al. 2017). This effect is hypothesized to be due to facilitation of newly formed extinction memories to compete with prior cue-associated memories that had once motivated alcohol-seeking behavior. These data demonstrate that  $K_{Ca}^2$  inhibition could act as a potential therapeutic target to facilitate cue-exposure therapy in problem drinkers.

# 7 K<sub>v</sub>7 Channels and Alcohol

## 7.1 Genetics

Similar to the relationship between *KCNN* genes and alcohol, integrative functional genomic analysis revealed that *Kcnq2* and *Kcnq3* lie within multiple alcohol-related QTLs in rodents, including those for alcohol consumption and preference (McGuier et al. 2016). Likewise, the remaining members of the *Kcnq* family of genes are present in alcohol preference-related QTLs in rodents (Table 3). In *Drosophila*, low doses of alcohol blocked *KCNQ* currents, and a loss-of-function mutation in *KCNQ* produced an increase in alcohol tolerance and sensitivity to its sedating effects (Cavaliere et al. 2012). *Kcnq2* was identified as a positional candidate within the cis-eQTL for alcohol consumption and withdrawal (Metten et al. 2014), and there

|       | GeneWeaver gene set |   |         | PubMed   |
|-------|---------------------|---|---------|----------|
| Gene  | ID                  | QTL or gene set                         | Species | ID       |
| Kcnq1 | GS128199            | Alcohol preference                      | Mouse   | n/a      |
|       | GS84196             | Alcohol preference QTL                  | Mouse   | 9880655  |
| Kcnq4 | GS223356            | Alcohol response QTL                    | Rat     | 16953387 |
|       | GS84162             | Chronic alcohol withdrawal severity QTL | Mouse   | 12925894 |
| Kcnq5 | GS84098             | Alcohol preference QTL                  | Mouse   | 10443995 |
|       | GS135279            | Alcohol preference QTL, male specific   | Mouse   | 10443995 |
|       | GS18838             | Differential expression                 | Rat     | 12462420 |
|       | GS223361            | Alcohol response QTL                    | Rat     | 15608595 |
|       | GS84096             | Alcohol consumption QTL                 | Mouse   | 11109025 |
|       | GS84097             | Alcohol preference QTL                  | Mouse   | 9880657  |
|       | GS84101             | Alcohol withdrawal QTL                  | Mouse   | 9655868  |

**Table 3** GeneWeaver.org gene sets that contain *Kcnq1*, *Kcnq4*, and *Kcnq5* genes in published QTL and curated genomic data sets for alcohol-related behaviors

are two single nucleotide polymorphisms (SNPs) in Kcnq2 that could account for the differences in drinking phenotypes across multiple mouse crosses (McGuier et al. 2016). In BXD RI strains, Kcnq transcript levels in the NAc and prefrontal cortex negatively correlated with voluntary alcohol drinking in a limited-access model (Rinker et al. 2017). Transcript expression levels of genes encoding  $K_V7.2$ ,  $K_V7.3$ , and  $K_V 7.5$  channel subunits are altered in key brain regions within the addiction circuitry in postmortem brain tissue from alcoholics and rodent models of chronic alcohol exposure or intake (Rinker and Mulholland 2017; Rinker et al. 2017; McGuier et al. 2016). In the NAc of BXD RI strains, adaptations in Kcnq1 and Kcnq5 transcript levels correlated with the change in voluntary drinking in alcoholdependent mice (Rinker et al. 2017). Moreover, a recent whole genome sequencing study identified Kcna5 as a gene associated with alcohol preference in rats (Lo et al. 2016). These preclinical findings are intriguing given that SNPs in KCNQ1 and KCNO5 are associated with early-onset alcoholism and symptoms of alcohol dependence (Kendler et al. 2011; Edenberg et al. 2010). Together, genetic findings linking alcohol action to the family of KCNQ genes across species as diverse as fruit flies and humans provide strong evidence that genetic diversity in KCNO influences heavy alcohol intake and contributes to risk factors for developing an AUD.

#### 7.2 Alcohol and K<sub>v</sub>7 Channel Function

There is accumulating evidence demonstrating that acute alcohol has direct effects on  $K_V7$  channel activity leading to alterations in the AHP and intrinsic excitability of neurons. In one of the first reports of this kind, Moore and colleagues showed that in rat hippocampal pyramidal cells, alcohol significantly reduced the M-current and blocked typical somatostatin-induced augmentation of the M-current (Moore et al. 1990). They also demonstrated that this effect of alcohol was mediated through mechanisms distinct from the muscarinic receptor, as bath application of atropine did not alter the alcohol-induced suppression of M-channel activity (Moore et al. 1990). More recent data in dissociated rat VTA dopaminergic neurons confirms that alcohol reduces M-current by acting directly on  $K_V7$  channels in a voltage-independent manner, suggesting that the site of action of alcohol is distinct from the voltagesensing regions of  $K_V7$  channel subunits (Koyama et al. 2007). Additionally, this effect is conserved across species, as the M-channel ortholog in *Drosophila*, *dKCNQ*, is a direct target of alcohol (Cavaliere et al. 2012, 2013).

While the majority of studies in this area have focused on the acute effects of alcohol on M-channel function, Kang and colleagues have recently examined the effects of more chronic alcohol administration on M-channel function. They demonstrate that repeated alcohol exposure results in increased excitability of neurons in the LHb, as evidenced by increased evoked spike firing, as well as a reduction in the mAHP and decreased ability of XE-991 to increase LHb cell firing (Kang et al. 2017). The authors argued that these effects of alcohol on neuron physiology are attributable to a loss of M-channel activity because of an overall reduction of both  $K_V 7.2$  and  $K_V 7.3$  subunit expression in LHb neurons (Kang et al. 2017; Shah et al.

2017). Similarly, K<sub>V</sub>7.2 subunits in the NAc are differentially trafficked between detergent soluble and insoluble membrane fractions after chronic alcohol consumption, possibly due to changes in K<sub>V</sub>7.2 SUMOylation that could alter M-channel function (McGuier et al. 2016). These changes in cellular expression profiles and function of M-channels following alcohol exposure (Fig. 2) provide support for using K<sub>V</sub>7 channel positive modulators to reduce alcohol consumption associated with AUD.

#### 7.3 Retigabine and Drinking

A number of preclinical studies demonstrate that increasing M-channel activity can alter alcohol-associated behaviors and, importantly, may represent a promising pharmacological target for treating AUD. Retigabine, a K<sub>v</sub>7 channel opener for treating epilepsy, has shown great promise in preclinical models as one such potential treatment. Initial demonstrations show that systemic retigabine administered acutely reduces alcohol consumption in rats in both a limited-access model of alcohol consumption (Knapp et al. 2014) and a more chronic alcoholdrinking model (McGuier et al. 2016). Interestingly, McGuier and colleagues demonstrated that retigabine was more effective in "high-drinking" rats than "lowdrinking" rats and that positive modulation of  $K_V7$  in the NAc was similarly effective in reducing alcohol consumption in "high-drinking" rats (McGuier et al. 2016). In a mouse model of chronic alcohol consumption, retigabine was highly effective at reducing consumption in mice showing a high-drinking phenotype (Rinker et al. 2017). Additionally, repeated, prophylactic administration of retigabine decreased hippocampal sensitivity to an acute intravenous injection of alcohol, i.e., retigabine decreased alcohol-induced changes in hippocampal EEG activity in rabbits (Zwierzynska et al. 2015). In a subsequent study, Zwierzynska and colleagues demonstrated that chronic retigabine administration blocked alcoholinduced changes in EEG activity both during forced alcohol administration and during abstinence, highlighting the potential of retigabine to prevent alcohol dependence-related functional changes in activity of the frontal cortex, hippocampus, and midbrain (Zwierzynska et al. 2016). As well, LHb M-channels are sensitive to repeated alcohol exposure, and Kang and colleagues determined that microinfusion of retigabine into the LHb, but not the nearby paraventricular nucleus of the thalamus or the mediodorsal thalamic nuclei, significantly reduced alcohol consumption and alcohol withdrawal-induced anxiety (Kang et al. 2017). Taken together, these preclinical studies demonstrate that retigabine, or other K<sub>V</sub>7 channel openers, holds great therapeutic potential for treating AUD. Despite these promising results, only one study to date has examined the effects of retigabine in a clinical population of moderate social drinkers to determine interactive effects of alcohol on retigabine pharmacodynamics and pharmacokinetics (Crean and Tompson 2013). Thus, future studies are essential to determine the efficacy of K<sub>V</sub>7 channel positive modulators in treating AUD.

## 8 GIRK Channels and Alcohol

#### 8.1 Genetics

A genome-wide OTL mapping study identified Kcni9 (a gene encoding the GIRK3 subunit) as one of the genetic determinants of alcoholism in mice (Buck et al. 2012). This gene was also associated with withdrawal from alcohol and other sedative hypnotics (Herman et al. 2015; Kozell et al. 2009), alcohol drinking (Tarantino et al. 1998), alcohol-conditioned aversion (Risinger and Cunningham 1998), and acute sensitivity to alcohol (Crabbe et al. 1994; Demarest et al. 1999). In BXD RI strains, *Kcnj3* (a gene encoding the GIRK1 subunit) transcript levels in the NAc positively correlated with voluntary alcohol drinking in nondependent mice, while Kcnj6 (a gene encoding the GIRK2 subunit) in the PFC negatively correlated with drinking in nondependent animals (Rinker et al. 2017), Following CIE exposure, significant adaptations in Kcnj3 and Kcnj6 transcript levels in the NAc have been detected (Rinker et al. 2017). In addition, there was a positive correlation between Kcnj9 and the change in voluntary drinking induced by alcohol dependence (Rinker et al. 2017). The genetic evidence in mice was correlated with behavioral studies in GIRK-knockout models. For example, GIRK2<sup>-/-</sup> mice showed reduced conditioned taste aversion and failed to develop a conditioned place preference for alcohol (Hill et al. 2003). Additionally, mice lacking GIRK3 exhibited excessive alcohol drinking (Herman et al. 2015) and demonstrated less severe withdrawal symptoms compared to their wild-type littermates (Kozell et al. 2009).

The involvement of KCNJ genes in the development of alcohol use disorders has also been identified in humans. One SNP, rs2836016 in KCNJ6, was found to be associated with alcohol dependence in adults. In addition, this KCNJ6 SNP was significantly associated with hazardous drinking, as defined by the Alcohol Use Disorders Identification Test (AUDIT), in adolescents but only in those exposed to early life stress (Clarke et al. 2011). Another study reported several SNPs in the promoter region of KCNJ6 in AUD subjects and in offspring at high risk to develop an AUD (Kang et al. 2012). In this study, electroencephalogram was used to record the theta event-related oscillations (EROs) that reflect processes underlying frontal inhibitory control, conscious awareness, and memory and processes that are often impaired in individuals with drug and alcohol use disorders. The results demonstrated a correlation between KCNJ6 SNPs and theta oscillations across the scalp, with the strongest associations for the frontal phenotype (Kang et al. 2012). A significant association of KCNJ6 SNP for nicotine dependence has also been reported (Saccone et al. 2007). Together, behavioral and genetic evidence in rodents and humans suggest the involvement of KCNJ family of genes with alcohol consumption and behaviors related to heavy drinking.

### 8.2 Alcohol and GIRK Channel Function

It is largely accepted that alcohol affects multiple neurotransmitters in the brain, many of which (i.e., dopamine and GABA) are linked to GIRK channel activation.

For example, alcohol enhances GABA<sub>B</sub>-mediated inhibitory postsynaptic transmission on rat VTA neurons by facilitating GIRK currents (Federici et al. 2009). Withdrawal from repeated in vivo alcohol exposure produced a profound decrease in D2-/GIRK-mediated inhibition in VTA neurons of mouse brain slice while having no effect on GABA<sub>B</sub>-/GIRK-mediated inhibition (Perra et al. 2011). Recent findings from our group demonstrated that monoamines, including dopamine, serotonin, and norepinephrine, decreased evoked firing of IOFC neurons in C57BL/6J mice via the activation of  $G_i$ -coupled D2, 5HT1A, and  $\alpha$ 2-adrenergic receptors, respectively (Nimitvilai et al. 2017b). This effect was GIRK-dependent as blocking GIRK channel with barium attenuated monoamine inhibition, and the GIRK1-subunit selective activator, ML297, by itself reduced evoked spiking. Following CIE exposure, however, the inhibitory effects of each monoamine or ML297 were blunted (Nimitvilai et al. 2017b), indicating the importance of monoamine/GIRK system as a modulator of IOFC excitability and suggesting that disruption of this process could contribute to various deficits associated with alcohol use disorder. As mentioned earlier, alcohol at intoxicating concentrations in humans can directly activate GIRK channels independently from GPCR signaling pathway. In Xenopus oocytes co-injected with mRNAs encoding GIRK1/GIRK2 subunits or GIRK1/GIRK4 subunits, alcohol (100-200 mM) induced strong K<sup>+</sup> currents, and this effect was blocked by barium, suggesting a direct action of alcohol on GIRK channels (Kobayashi et al. 1999). A similar finding was reported for GIRK-mediated currents in cerebellar granule cells (Lewohl et al. 1999). Recently, a high-resolution crystal structure of a GIRK channel (Aryal et al. 2009) combined with an alcohol-tagging approach (Bodhinathan and Slesinger 2013) revealed that GIRK channels contain an alcohol binding pocket located at the interface between two adjoining subunits within the cytoplasmic domains. The presence of alcohol in the pocket induces conformational changes and increases the affinity of PIP2 that helps stabilize the open state of the GIRK channel. Mutation of a leucine (L257) within the alcohol binding pocket significantly decreases alcohol-induced GIRK currents (Aryal et al. 2009). Therefore, changes in physical and chemical nature of the alcohol binding pocket could interfere with alcohol action on GIRK channels.

#### 8.3 GIRK Channel Ligands and Drinking

Imbalance or dysfunction of GIRK channels has been implicated in altering neuronal excitability and is linked to many neuropsychiatric diseases and SUDs. As mentioned above, a number of studies demonstrate that GIRK channels can be activated directly by acute alcohol (Bodhinathan and Slesinger 2013; Kobayashi et al. 1999; Lewohl et al. 1999) and that GIRK function is blunted following chronic alcohol exposure (Nimitvilai et al. 2017b). In addition, the action of many G<sub>i</sub>-coupled neurotransmitters, including dopamine, serotonin, and GABA, that are linked to GIRK channel activation is modulated by alcohol (Nimitvilai et al. 2017b; Federici et al. 2009; Perra et al. 2011). Genetic studies also depict the association of *Kcnj* genes encoding GIRK channels in alcohol use disorder and dependence (Rinker and

Mulholland 2017; Rinker et al. 2017; Buck et al. 2012; Clarke et al. 2011). Therefore, selective manipulation of GIRK channels may represent a promising target for treating excessive drinking and relapse.

In 2012, baclofen, a GABA<sub>B</sub> agonist that is linked to GIRK channel activation, was approved as a treatment for alcohol addiction in France and is currently under clinical trials in the USA. It shows promising effects in managing alcohol withdrawal symptoms, reducing alcohol craving and consumption, and promoting alcohol abstinence in alcoholic animal models and humans, without serious or severe side effects (Addolorato et al. 2012; Maccioni and Colombo 2009; Morley et al. 2014). An increase in sedation on the BAES scale was reported in human subjects; however, no clinically significant sedative side effects, including sedation, tiredness, and sleepiness, were reported during the treatment session, confirming the safety of baclofen in alcohol-dependent patients (Evans and Bisaga 2009; Leggio et al. 2012). Despite these positive findings, other studies reported a lack of efficacy of baclofen in some alcohol-dependent individuals (Garbutt et al. 2010; Leggio et al. 2010) and a severe sedative effect of the drug (Garbutt et al. 2010). One clinical trial study examined the possible role of DRD4, a genetic modulator associated with risk of alcohol dependence (AD), on the effect of baclofen (Leggio et al. 2013). There is evidence of a robust relationship between urge for alcohol and the DRD4 or 5-HTTLPR polymorphisms, i.e., the presence and absence of the DRD4 allele 7-repeat or the short and long allele in the 5-HTTLPR promoter region (Kenna et al. 2012; McGeary 2009). When baclofen was given to AD participants, less drinking was observed in subjects with  $\geq$ 7 DRD4 repeats, while the opposite was observed in AD patients with <7 DRD4 repeats. Baclofen caused a reduction in alcohol consumption regardless of 5HTTLPR form; however, individuals with a homozygous LL genotype drank significantly less than those with SS/SL genotype (Leggio et al. 2013). Therefore, the ability of baclofen to reduce alcohol consumption might be limited to specific endophenotypes of AD individuals. At present, there is no treatment for alcohol dependence that directly targets GIRK channels. One compound, ML297, has been recently designed to directly activate GIRK1containing GIRK channels (Kaufmann et al. 2013) and has been shown to decrease anxiety-related behavior and exhibit antiepileptic properties without affecting locomotor activity or conditioned place preference (Kaufmann et al. 2013; Wydeven et al. 2014). It will be interesting to examine whether ML297 can also be used to alleviate symptoms related to alcohol withdrawal that are thought to contribute to the risk of relapse. Although both ML297 and alcohol enhance GIRK channel activity, ML297 may help restore normal GIRK channel tone that is lost following chronic alcohol exposure and reduce craving for alcohol.

#### 9 Conclusions and Future Directions

In this chapter, we have summarized the effects of chronic alcohol exposure on intrinsic excitability and adaptations in expression and function of  $K_{Ca}$ ,  $K_v7$ , and GIRK channels across different alcohol exposure models and species (*Drosophila*,

rodent, monkey, and humans). In general, transcript levels of genes in these K<sup>+</sup> channel families negatively correlate with higher levels of alcohol intake. Evidence presented here suggests that downregulation of  $K_{Ca}^2$  and  $K_V^7$  channel function underpins the reduction in AHP amplitude and increased evoked cell firing after chronic alcohol exposure. In many cases, positive modulators of these channels restore or prevent aberrant physiology and behaviors that result from prolonged alcohol exposure, including alcohol-seeking and withdrawal- and anxiety-related behaviors (Table 4). Indeed,  $K_{Ca}^2$  and  $K_V^7$  channel positive modulators reduce alcohol intake across many preclinical models of drinking and seeking, and both channels play a critical role in heavy alcohol drinking in dependent and nondependent rodents (Padula et al. 2013, 2015; Rinker et al. 2017; McGuier et al. 2016). Together, these findings reveal genetic variations and adaptations in  $K_{Ca}^2$  and  $K_V^7$  channels that are important for the plasticity of intrinsic excitability and a heavy drinking phenotype.

The goal of preclinical studies is to identify neural mechanisms that underpin aberrant drug-seeking and relapse-like behaviors. As presented in this chapter, K<sub>Ca</sub>2,  $K_V7$ , and GIRK channels emerged from these preclinical studies as promising "translational" therapeutic targets for treating alcohol use disorder. The next step in the progression to FDA approval is to determine the efficacy of compounds that target K<sub>Ca</sub>2, K<sub>V</sub>7, and GIRK channels in clinical trials of treatment-seeking individuals diagnosed with alcohol use disorder. Because activators of these channels have anticonvulsive properties, sedation and cognitive impairments may be an unwanted side effect. A small-scale trial in social and moderate drinkers (ClinicalTrials.gov record number: NCT01342341) was recently completed with chlorzoxazone, an FDA-approved drug prescribed as a skeletal muscle relaxant (Chou et al. 2004) that acts as a K<sub>Ca</sub>2 channel positive modulator (Cao et al. 2001). Although chlorzoxazone was well tolerated in this moderate social drinking population, the dosing schedule used in this trial did not reduce the number of alcohol drinks across 2 weeks of treatment. These findings are in stark contrast to the preclinical studies showing that K<sub>Ca</sub>2 channel positive modulators decrease consumption. The reasons for the discrepancy between the preclinical studies and this clinical trial are unclear but may relate to the short half-life, low EC<sub>50</sub> for  $K_{Ca2}$ channels, off-target actions of chlorzoxazone, conservative dosing approach, or population of drinkers that were recruited for the trial.

Similar to  $K_{Ca}^2$  channels, an FDA-approved drug, retigabine, acts as a positive modulator of  $K_V^7$  channels and is used to treat partial-onset seizures, and acute doses are well tolerated in moderate social drinkers (Crean and Tompson 2013). However, extended retigabine use produces pigment changes in the retina and skin due to accumulation of retigabine dimers with low solubility. Although the pigment changes are reversible, GlaxoSmithKline withdrew retigabine from the market in 2017. While these findings are somewhat discouraging, there are analogs of retigabine with selectivity for brain-specific  $K_V^7$  channel subtypes with chemical scaffolds that appear not to form insoluble dimers. Thus, despite some setbacks, there is continued enthusiasm for developing additional  $K_{Ca}^2$  and  $K_V^7$  channel positive modulators as pharmacotherapeutics for treating alcohol use disorder,

| Table 4 Summary             | of effects of $K_{\rm Ca}2$ and $K_{\rm V}7$ chai | nnel ligands | on alcohol-related | behaviors               |                                     |                              |
|-----------------------------|---|--------------|--------------------|-------------------------|-------------------------------------|------------------------------|
| Alcohol-related<br>behavior | Model   | Species      | Drug               | Route of administration | Ligand outcome                      | Reference                    |
| $K_{Ca}2$ channels          |   |              |                    |                         |                                     |                              |
| Alcohol-                    | Alcohol self-administration                       | Rat          | 1-EBIO             | NAc                     | ↓ Breakpoint for responding         | Hopf et al.                  |
| seeking                     |   |              |                    | microinfusion           |                                     | (2010)                       |
| Alcohol                     | Chronic intermittent alcohol                      | Mouse        | 1-EBIO             | IP                      | ↓ HICs                              | Mulholland                   |
| withdrawal                  |   |              |                    |                         |                                     | et al. (2011)                |
| Voluntary                   | IAA   | Rat          | Chlorzoxazone      | IP                      | ↓ Intake                            | Hopf et al.                  |
| ui liikiiig                 |   |              |                    |                         |                                     | (1107)                       |
| Voluntary<br>drinking       | IAA   | Mouse        | CyPPA              | Ы                       | ↓ Intake                            | Padula et al.<br>(2013)      |
| Voluntary                   | 2-bottle, limited-access                          | Mouse        | Apamin             | NAc                     | 1 Intake                            | Padula et al.                |
| drinking                    | drinking  |              | 4                  | microinfusion           |                                     | (2015)                       |
| Extinction                  | Extinction and reinstatement                      | Rat          | Apamin             | IP and IL-mPFC          | f Extinction learning and           | Cannady et al.               |
| learning                    | of alcohol-seeking                                |              |                    | microinfusion           | ↓ spontaneous recovery              | (2017)                       |
| $K_V7$ channels             |   |              |                    |                         |                                     |                              |
| Acute                       | Clinical laboratory study                         | Human        | Retigabine         | PO                      | N/C in alcohol-induced              | Crean and                    |
| intoxication                |   |              |                    |                         | deficits                            | Tompson (2013)               |
| Voluntary                   | IAA   | Rat          | Retigabine         | IP and NAc              | ↓ Intake                            | McGuier et al.               |
| drinking                    |   |              |                    | microinfusion           |                                     | (2016)                       |
| Alcohol-                    | 2-bottle, limited-access                          | Rat          | Retigabine         | IP                      | ↓ Intake                            | Knapp et al.                 |
| seeking                     | drinking  |              |                    |                         |                                     | (2014)                       |
| Alcohol<br>dependence       | Forced alcohol access                             | Rabbit       | Retigabine         | PO                      | ↓ Alcohol-induced changes in EEGs   | Zwierzynska<br>et al. (2016) |
| Convulsions                 | IAA   | Rat          | XE-991             | ΓĿ                      | ↑ Spontaneous seizure-like activity | McGuier et al.<br>(2016)     |
| Voluntary<br>drinking       | IAA   | Mouse        | Retigabine         | IP                      | ↓ Intake                            | Rinker et al.<br>(2017)      |

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| Anxiety-like<br>behaviors | Repeated IP alcohol        | Rat        | Retigabine       | LHb<br>microinfusion         | ↓ Anxiety-like behaviors           | Kang et al. (2017)    |
|---------------------------|----------------------------|------------|------------------|------------------------------|------------------------------------|-----------------------|
| Voluntary<br>drinking     | IAA                        | Rat        | Retigabine       | LHb<br>microinfusion         | ↓ Intake                           | Kang et al.<br>(2017) |
| Voluntary<br>drinking     | IAA                        | Rat        | Retigabine       | MDT and PVN<br>microinfusion | N/C in intake                      | Kang et al.<br>(2017) |
| UIC handling indu         | Infu: DEG II Sucielumo per | ibom oidmi | androntel contox | ID intronomitonool IA        | A intermittent access to clocked E | EC alaatioonoonb      |

*HICs* handling-induced convulsions, *IL-mPFC* infralimbic medial prefrontal cortex, *IP* intraperitoneal, *IAA* intermittent access to alcohol, *EEG* electroencephalogram, *MDT* mediodorsal thalamic nucleus, *PO* per os, *PVN* paraventricular nucleus of the thalamus

especially in light of the vast preclinical genetic, functional, and pharmacological evidence supporting a role for these channels in alcohol-seeking behaviors. Finally, based on the compelling preclinical and human genetic evidence, future clinical studies are necessary to validate *KCNQ* SNPs as pharmacogenetic targets for a precision medicine approach for treating alcohol addiction.

In addition, although this chapter was focused on the role of discrete K<sup>+</sup> channel subtypes in alcohol addiction, emerging evidence reveals that plasticity of intrinsic excitability contributes to addiction of all abused substances (Kourrich et al. 2015; Kourrich and Thomas 2009) and neuropsychiatric disorders (Beck and Yaari 2008). For example, protracted withdrawal from chronic morphine exposure increased the intrinsic excitability of NAc shell medium spiny neurons in rats (Wu et al. 2013), and this was accompanied by an attenuation of the apamin-sensitive AHP current in the morphine-withdrawn rats. Interestingly, members of the KCNN family of genes have links with opioid and alcohol addiction (Padula et al. 2015), and multiple studies have implicated KCNN3 mutations in schizophrenia (Bowen et al. 2001; Cardno et al. 1999; Chandy et al. 1998). A rare frameshift mutation in KCNN3 that generates a dominant-negative form of this channel was reported in a patient with schizophrenia (Bowen et al. 2001), and longer polyglutamine repeat alleles in K<sub>Ca</sub>2.3 channels associate with negative symptoms and cognitive performance in schizophrenics (Cardno et al. 1999; Grube et al. 2011). Importantly, the rare frameshift mutation and longer polyglutamine repeats in KCNN3 suppress K<sub>Ca</sub>2 channel surface expression and function (Grube et al. 2011; Miller et al. 2001). These findings are consistent with the overlap of some genes with abused substances and psychiatric diseases (Agrawal et al. 2012) and suggest that neural mechanisms that underlie adaptations in intrinsic excitability are critical factors that drive the risk for and emergence of neuropsychiatric disorders.

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