ORIGINAL RESEARCH



# Integrative Analyses Identify *KCNJ15* as a Candidate Gene in Patients with Epilepsy

Shitao Wang ₀ · Zongyou Li · Xiangqian Ding · Zongyou Zhao · Mengen Zhang · Hui Xu · Jinghong Lu · Lili Dai

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### ABSTRACT

*Introduction*: Although there is accumulating evidence that genetic factors play a vital role in the pathogenesis of epilepsy, few epilepsy-associated genes have been identified. Additionally, the role of *KCNJ15* in epilepsy has not been evaluated so far.

*Methods*: Here, we performed differentially expressed gene analysis, expression quantitative trait loci analysis, gene co-expression analysis, and protein–protein interaction analysis to evaluate the role of *KCNJ15* in epilepsy.

*Results*: Analysis of gene expression and expression quantitative trait loci data revealed

X. Ding

Department of Neurosurgery, Qilu Hospital of Shandong University, Shandong, China

Z. Zhao

Department of Geriatrics, Funan County People's Hospital, Funan, Anhui, China e-mail: dailili19880418@163.com that *KCNJ15* was significantly downregulated in patients with epilepsy (adjusted P = 0.0146 and  $log_2$  Fold change = -1.0025), and an epilepsyassociated polymorphism (rs2833098) was linked to altered *KCNJ15* expression level in human temporal lobe brain tissue (P = 0.0036). Gene co-expression analysis revealed that *KCNJ15* was co-expressed with genes that have been reported to be associated with epilepsy in human brain tissue. Furthermore, protein–protein interaction analysis revealed strong supportive evidence for the role of *KCNJ15* in epilepsy.

*Conclusion*: Our results show that *KCNJ15* may be a candidate target for epilepsy. Functional analysis of *KCNJ15* may provide novel insights for epilepsy treatment.

Keywords: Epilepsy; Gene; KCNJ15; Therapy

S. Wang  $(\boxtimes) \cdot Z$ . Li  $\cdot$  M. Zhang  $\cdot$  H. Xu  $\cdot$  J. Lu Department of Neurology, Affiliated Fuyang People's Hospital of Anhui Medical University, Fuyang, Anhui, China e-mail: wangshitaomd@163.com

Department of Neurology, Funan County People's Hospital, Funan, Anhui, China

L. Dai (🖂)

# Key Summary Points

Epilepsy is one of the nervous system diseases with complex inheritance. However, the role of *KCNJ15* in epilepsy remains unknown.

About 30% of patients do not respond well to current antiepileptic drugs. Furthermore, current antiepileptic drugs are often correlated with multiple adverse reactions. Considering the limitations of current therapeutic strategies, gene therapy may be a promising option.

The protein encoded by *KCNJ15*, ATPsensitive inward rectifier potassium channel 15, is an integral membrane protein. Its physiological function is to act as an inward potassium channel that allows potassium to flow into the cell through the cell membrane.

By an integrative analysis with data on *KCNJ15* expression, expression quantitative trait locus (eQTL), gene coexpression, and protein–protein interaction (PPI), we hypothesize that *KCNJ15* has an active role in epilepsy.

# INTRODUCTION

Epilepsy is the most prevalent nervous system disease [1], and it is characterized by episodes of excessive synchronized neuronal activity. About 30% of patients do not respond well to current antiepileptic drugs [2, 3]. Furthermore, these drugs often have multiple adverse side effects [4, 5]. Although surgery is an effective option for drug-resistant epilepsy, it is suitable only for a few patients [6] and might also affect other brain tissues surrounding the epileptic focus [7]. Considering the limitations of current therapeutic strategies, gene therapy may be a promising option [8]

K<sup>+</sup> channels play an important role in membrane repolarization of active

neurons. Therefore, K<sup>+</sup> channels may be potential targets for epilepsy treatment [9]. The protein encoded by KCNJ15, ATP-sensitive inward rectifier potassium channel 15, is an integral membrane protein. Its physiological function is to act as an inward potassium channel that allows potassium to flow into the cell through the cell membrane. The expression of KCNJ15 has been observed in glial cells [10]. Knockdown of KCNJ15 can result in compromised electrotaxis [11]. KCNI15 is associated with Parkinson's disease [12], and it also plays a vital role in Alzheimer's disease pathogenesis [13], suggesting that it is involved in the pathogenesis of central nervous system diseases more broadly. However, the association between KCNI15 and epilepsy has not been evaluated so far. Therefore, we conducted a study including differentially expressed gene (DEG) analysis, expression quantitative trait locus (eQTL) analysis, gene coexpression analysis, and protein-protein interaction (PPI) analysis, to systematically investigate the role of KCNJ15 in epilepsy.

# **METHODS**

# Differentially Expressed Genes Identified in Human Brain Tissue

The GSE6834 data set was downloaded from NCBI (https://www.ncbi.nlm.nih.gov), and R software was used to screen the DEGs between epilepsy and controls. The GSE6834 data set is divided into temporal lobe brain tissue samples from patients with epilepsy and temporal lobe brain tissue samples from the control group. Specifically, ten epilepsy temporal lobe brain tissue samples were obtained from patients undergoing therapeutic surgery for drug-resistant mesial temporal lobe epilepsy according to routine clinical protocols and controls from ten nonepileptic temporal lobe samples. Patients in the case group were between 18 and 60 years old, and those in the control group were between 56 and 90 years old. An adjusted P  $\leq 0.05$  and  $|\log_2$  Fold change|  $\geq 1$  were considered statistically significant.

This article is based on previously conducted studies and does not contain any new studies

with human participants or animals performed by any of the authors.

#### Expression Quantitative Trait Locus Analysis in Human Brain Tissue

Rs2833098 has been reported to be associated with the risk of epilepsy [14]. To explore if rs2833098 regulates the expression level of *KCNJ15* in human temporal lobe brain tissue, we conducted eQTL analysis in the BRAINEAC database (http://www.braineac.org/), which provides gene expression values across ten brain tissues. *KCNJ15* expression was measured using RNA sequencing, and a linear regression analysis under an additive model was used to explore the association of rs2833098 with *KCNJ15* expression levels.

#### Gene Co-expression Analysis in Human Brain Tissue

We queried the Coexpedia database (https:// www.coexpedia.org/), a database for studying gene co-expression in mice and humans, to evaluate the co-expression network of *KCNJ15* for genes with co-expression scores greater than 1 with *KCNJ15* in the brain. This database was supported by the National Research Foundation of Korea.

#### Protein-Protein Interaction Analysis

PPI networks can be used to develop new drugs and discover novel drug targets. To explore the association between *KCNJ15* and epilepsy drug therapy, we identified 115 genes (Table 1) targeted by approved antiepileptic drugs from two databases, Therapeutic Target Database 2020 and DrugBank 5.0 [15, 16]. These drug databases include molecular information about drugs, as well as their mechanisms, interactions, and targets. The PPI analysis was conducted using the STRING database (https://string-db.org/cgi/ input.pl) [17]. Finally, the PPI network was built using Cytoscape software [18]. **Table 1** The 115 identified genes whose encoded proteinsare targeted by epilepsy drugs

Drug	Gene
Phenobarbital	NR112, GRIA2, GABRA1, CHRNA4, CHRNA7, GRIK2, GRIN1, GRIN2A, GRIN2B, GRIN2C, GRIN2D, GRIN3A, GRIN3B
Primidone	CHRNA4, GRIK2, GABRA1, GABRA3, GABRA6, GABRA2, GABRA4, GABRA5, CHRNA7, GRIA2, GABRB1, GABRB2, GABRB3, GABRD, GABRE, GABRG1, GABRG2, GABRG3, GABRP, GABRQ
Phenytoin	SCN5A, SCN3A, CACNA1C, CACNA1D, CACNA1F, CACNA1S, CACNB1, CACNB2, CACNB3, CACNB4, CACNA1A, SCN8A, KCNH2, SCN1A, NR112, SCN1B, SCN2A, GABRA1, GABRA3, GABRA6, GABRA2, GABRA4, GABRA5, GABRB1, GABRB2, GABRB3, GABRD, GABRE, GABRG1, GABRG2, GABRG3, GABRP, GABRQ, SCN5A
Carbamazepine	SCN1A, SCN2A, SCN3A, SCN4A, SCN5A, SCN7A, SCN8A, SCN9A, SCN10A, SCN11A, CHRNA4, NR112
Valproate	ALDH5A1, HDAC2, PPARA, PPARD, OGDH, SCN1A, SCN2A, SCN3A, SCN4A, SCN5A, SCN7A, SCN8A, SCN9A, SCN10A, SCN11A, SCN1B, SCN2B, SCN3B, SCN4B, PPARG, HDAC9, ACADSB, GSK3A, ABAT
Clonazepam	TSPO, NR1I2, GABRA1, GABRA3, GABRA6, GABRA2, GABRA4, GABRA5, GABRB1, GABRB2, GABRB3, GABRD, GABRE, GABRG1, GABRG2, GABRG3, GABRP, GABRQ

#### Table 1 continued

Drug	Gene			
Clobazam	GABRA1, GABRA3, GABRA6, GABRA2, GABRA4, GABRA5, GABRB1, GABRB2, GABRB3, GABRD, GABRE, GABRG1, GABRG2, GABRG3, GABRP, GABRQ			
Gabapentin	CACNA2D1, KCNQ5, ADORA1, Cacna1b, Cacna1b, Cacna2D2, KcNQ3, Cacna2D1, Cacna2D2, GABBR1, GABBR2, SLC5A6			
Lamotrigine	HTR3A, CACNA1E, ADRA2A, HRH1, OPRK1, ADORA1, ADORA2A, ADRA1A, DRD2, GABRA1, GABRA3, GABRA6, GABRA2, GABRA4, GABRA5, GABRG1, GABRG2, GABRG3, SCN2A, ADRB1, DRD1, DRD5, GABRA1, GABRA3, GABRA6, GABRA2, GABRA4, GABRA5, GABRB1, GABRB2, GABRB3, GABRD, GABRE, GABRG1, GABRQ, CHRM1, CHRM2, CHRM3, CHRM4, CHRM5, HTR2A, SCN11A			
Topiramate	CA2, GRIK1, GRIK2, GRIK3, GRIK4, GRIK5, CA3, CA4, CA1, CACNA1E, GABRA1, SCN1A, SCN2A, SCN3A, SCN4A, SCN5A, SCN7A, SCN8A, SCN9A, SCN10A, SCN11A, CACNA1C, CACNA1D, CACNA1F, CACNA1S, CACNB1, CACNB2, CACNB3, CACNB4			
Oxcarbazepine	SCN1A, SCN2A, SCN3A, SCN4A, SCN5A, SCN7A, SCN8A, SCN9A, SCN10A, SCN11A, SCN1B, SCN2B, SCN3B, SCN4B			
Tiagabine	SLC6A1			
Levetiracetam	SV2A, CACNA1B			

Table 1	continued	ł
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Drug	Gene
Zonisamide	CA5B, CA10, CA11, CA12, CA13, SCN3A, SCN4A, SCN3B, MAOB, CA2, CA4, CA7, CA9, CACNA1H, SCN9A, SCN1B, SCN2B, SCN1A, CA1, CACNA1G, CA3, CA5A, CA6, CA8, CA14, CACNA1I, SCN2A, SCN5A, SCN11A, SCN4B, MAOA
Felbamate	GRIN3A, GRIN2A, GRIN2B
Pregabalin	CACNA2D1
Vigabatrin	ABAT, GABBR1

### RESULTS

# Differentially Expressed Genes Identified in Human Brain Tissue

On the basis of the DEG analysis, *KCNJ15* was identified as differentially expressed in one microarray data set (GSE6834). As shown in the volcano plot (Fig. 1), the results showed that the expression level of *KCNJ15* in epileptic temporal lobe brain tissue was significantly downregulated compared with that in controls (adjusted P = 0.0146 and  $\log_2$  Fold change = -1.0025) (Table 2).

#### Expression Quantitative Trait Locus Analysis in Human Brain Tissue

eQTL analysis in the BRAINEAC database indicated that rs2833098 is associated with *KCNJ15* expression level in human temporal lobe brain tissue (P = 0.0036), providing evidence that this polymorphism is involved in modifying *KCNJ15* expression in human temporal lobe brain tissue. Specifically, the AA genotype is associated with downregulated *KCNJ15* expression compared with that of the GG and GA genotypes in the human temporal lobe (Fig. 2).



**Fig. 1** Volcano plot illustrating differentially expressed genes (DEGs) between controls and patients with epilepsy in the analysis of the GSE6834 data set

**Table 2** Comparison of the expression of KCNJ15 in thebrain tissue of the epilepsy group and the control group

Adjusted <i>P</i> value	P value	t	В	log <sub>2</sub> FC
0.0146	9.00E-05	_	1.5103	_
		4.7501		1.0025

FC fold change

# Gene Co-expression Analysis in Human Brain Tissue

As shown in the co-expression network map (Fig. 3), the genes with co-expression scores greater than 1 with *KCNJ15* in brain tissue are *A1CF*, *RABAC1*, *CYP2A6*, *SIGLEC6*, and *CRHR2*. Thus, these genes are likely to be functionally associated with *KCNJ15*.

#### **Protein–Protein Interaction Analysis**

PPI analysis was performed for 115 genes targeted by epilepsy drugs and *KCNJ15*. The PPI network indicated that the protein encoded by *KCNJ15* directly interacts with two epilepsy drug targets encoded by *GABBR1* and *GABBR2* (Fig. 4). GABBR1 is the target of vigabatrin and







Fig. 3 Gene co-expression analysis. Genes with a coexpression score greater than 1 with *KCNJ15* in brain tissue are *A1CF*, *RABAC1*, *CYP2A6*, *SIGLEC6*, and

gabapentin, and GABBR2 is the target of gabapentin.

### DISCUSSION

Although genetic factors play a vital role in the pathogenesis of epilepsy [19], the genetic

*CRHR2.* These genes are highly likely to be functionally associated with *KCNJ15.* Data were retrieved from the Coexpedia database (https://www.coexpedia.org/)

association between polymorphisms of *KCNJ15* and epilepsy has not yet been evaluated. Here, we conducted an association study to explore the role of *KCNJ15* in contributing genetic risk to epilepsy. By an integrative analysis with data on *KCNJ15* expression, eQTLs, gene co-expression, and PPI, we hypothesize that *KCNJ15* has an active role in epilepsy. To our knowledge,





RIA

GABRA3

G<mark>ABRA</mark>6

Fig. 4 Protein-protein interaction (PPI) network of *KCNJ15* and genes targeted by approved epilepsy drugs. The red node represents *KCNJ15*, and green nodes indicate genes targeted by approved epilepsy drugs. The

this is the first report evaluating the genetic association of *KCNJ15* with epilepsy.

In this study, *KCNJ15* was highly downregulated in the temporal brain tissue of drug-resistant mesial temporal lobe patients with epilepsy (Fig. 1), suggesting an important role of *KCNJ15* in epilepsy. *KCNJ15* encodes the ATPsensitive inward rectifier potassium channel 15, which is involved in the activation of microglia [20, 21]. Previous studies indicated that epilepsy is linked to microglial activation [22, 23]. There may be various mechanisms by which glia are

red lines represent direct interactions between the protein encoded by *KCNJ15* and the targets of approved epilepsy drugs

involved in the pathogenesis of epilepsy. However, the major mechanisms include increased excitability and inflammation [24]. Furthermore, the transcript level of *KCNJ15* has been positively associated with Alzheimer's disease [13], and epilepsy and Alzheimer's disease may share similar pathogenic mechanisms [25], further suggesting a role of *KCNJ15* in epilepsy.

We also explored the association between single nucleotide polymorphisms (SNPs) that have been reported to be associated with epilepsy and *KCNJ15* expression in human temporal lobe brain tissue. Rs2833098, which is located in a noncoding region, was previously associated with the risk of epilepsy in a genomewide meta-analysis [14]. Additionally, eQTL analysis showed that the AA genotype of rs2833098 is associated with decreased KCNI15 mRNA level in human temporal lobe brain tissue (Fig. 2). SNPs in non-coding regions often confer risk of disease by regulating the expression of their target genes [26]. Furthermore, we also found that KCNJ15 was significantly downregulated in the temporal lobe brain tissue of patients with epilepsy. Therefore, we speculate that rs2833098 may be a marker of epilepsy risk by regulating the expression level of KCNI15 in human temporal lobe brain tissue.

Gene co-expression networks can be used to identify regulatory genes [27]. Gene expression and regulation are highly tissue-specific, and most disease-related genes have different expression levels in different tissues [28, 29]. Gene co-expression analysis revealed that KCNJ15 is co-expressed with multiple genes, including A1CF, RABAC1, CYP2A6, SIGLEC6, and CRHR2, in human brain tissue (Fig. 3), suggesting that these genes are functionally associated. Previous studies have identified that CYP2A6 is associated with the efficacy of antiepileptic drug treatment in patients with epilepsy [30, 31], so we speculate that CYP2A6 may play an important role in epilepsy, and KCNJ15 may be a candidate target for epilepsy treatment. However, CYP2A6 has many substrates and interactors, not only antiepileptic drugs, so the role of KCNJ15 in epilepsy still needs further verification.

Considering the limitations of current therapeutic strategies, it is necessary to discover new targets for epilepsy treatment. Understanding the association between genes and drug targets will facilitate the translation of clinical utility in the future. The PPI network is an effective tool to discover drug targets and drugs [32]. Our study demonstrated that KCNJ15 is more likely to interact with targets of approved epilepsy drugs, including GABBR1 and GABBR2 (Fig. 4), indicating that these proteins may be functionally associated. By querying the DrugBank database and the Therapeutic Target Database, we found that GABBR1 is the target of vigabatrin and gabapentin, and GABBR2 is the target of gabapentin, further supporting a role of *KCNJ15* in epilepsy.

Although no patients with epileptic syndrome with de novo mutations in this gene have yet been found, we found that a SNP associated with the risk of epilepsy is associated with the expression level of KCNJ15 in brain tissue. Therefore, we speculate that KCNJ15 may not affect the risk of epilepsy through mutations in the amino acid sequence, but through altered expression level in human brain tissue, thereby affecting the risk of epilepsy. Therefore, this study may contribute to the discovery of new targets for epilepsy treatment. However, this is a future prospect that requires further indepth studies. Knockdown or overexpression of the gene in epilepsy animal models can help to further validate the role of the gene in epilepsy, and epilepsy pharmacogenomics can help genetic findings translate into clinical treatment.

Although we identified *KCNJ15* as a potential biological target by integrative analysis, some limitations of our study should be acknowledged. First, the sample size of the temporal lobe brain tissue samples in our study is relatively small. Second, we did not validate our conclusions with animal models, so more investigations are necessary to confirm our findings. Third, the association of *KCNJ15* with epilepsy has not been evaluated by other studies, so it is important to validate our results in different populations.

# CONCLUSIONS

Our study suggests that *KCNJ15* may be a potential therapeutic target for epilepsy. Additional functional analysis of *KCNJ15* may provide novel insights for epilepsy treatment.

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**Disclosures.** Shitao Wang, Zongyou Li, Xiangqian Ding, Zongyou Zhao, Mengen Zhang, Hui Xu, Jinghong Lu, and Lili Dai declare that they do not have any personal, financial, commercial, or academic conflicts of interest.

*Compliance with Ethics Guidelines.* This article is based on previously conducted studies and does not contain any new studies with human participants or animals performed by any of the authors.

*Data Availability.* The data sets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

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