

ORIGINAL ARTICLE

Mutational analysis of *GABRG2* in a Japanese cohort with childhood epilepsies

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A few mutations in the gene encoding the gamma 2 subunit of the gamma-aminobutyric acid receptor type A (*GABRG2*) have been reported in various types of epilepsy. The aim of this study is to investigate the role of *GABRG2* in the pathogenesis of childhood epilepsy in a large Japanese cohort. Genetic analysis of *GABRG2* was performed on 140 Japanese patients with various childhood epilepsies largely including Dravet syndrome and genetic epilepsy with febrile seizures plus. The mutational analysis identified one novel missense mutation of *GABRG2* (c.236A > G: p.N40S) in a patient with generalized tonic-clonic seizures (GTCS). The mutation was heterozygous and replacing a highly conserved Asn residue with a Ser. The affected amino acid was located at residue 40 of the mature *GABRG2* protein, which was near the first one of two high-affinity benzodiazepine-binding domains of the $\gamma 2$ subunit (Lys-41-Trp-82). This mutation in such an important position may hamper the function of the channel and contribute to the case's pathogenesis of GTCS.

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INTRODUCTION

Epilepsy is a group of heterogeneous disorders characterized by paroxysms resulting from bioelectric hyperexcitation of neuronal networks of the brain. Recently, it has been well recognized that dysfunctions of ion channels expressed in the brain contribute to such hyperexcitation and hence closely associate with the pathogenesis of epilepsy. Accordingly, to date, a number of mutations of the genes encoding ion channels have been identified in various types of epilepsy.

Gamma-aminobutyric acid receptor type A ($GABA_A$ receptor) is one such ion channel where mutations have been identified in several epilepsy phenotypes. $GABA_A$ receptor, which is a ligand-gated chloride ion channel, serves as a major component of the neuronal inhibitory system in adult brain. It is considered that majority of the receptors in the brain function as a pentamer consisting of $\alpha 1$, $\beta 2$ and $\gamma 2$ subunits.

Mutations of the genes encoding the subunits of $GABA_A$ receptors were so far found in the genes encoding $\alpha 1$ (*GABRA1*), δ (*GABRD*) and $\gamma 2$ subunits (*GABRG2*).^{1–4} A mutation of *GABRA1* was found in autosomal dominant juvenile myoclonic epilepsy, a rare inherited idiopathic epilepsy phenotype.² Several variants of *GABRD* were not reported as causes of epilepsy but suggested to associate with suscept-

ibility to genetic epilepsy with febrile seizures plus (GEFS+).³ In contrast, mutations in *GABRG2* have been reported as causes of a wide spectrum of epilepsies, from Dravet syndrome to milder conditions such as childhood absence epilepsy, GEFS+ and FS+.^{1,4–8}

Although major progress has been made in tying *GABRG2* to some categories of epilepsy (that is, GEFS+, childhood absence epilepsy and Dravet syndrome), its role in most kinds of childhood epilepsy such as benign epilepsy of childhood with centrotemporal spikes, generalized tonic-clonic seizures (GTCS), partial epilepsy and so on remains poorly understood. Accordingly, this study further investigates the role of *GABRG2* in the pathogenesis of childhood epilepsies.

MATERIALS AND METHODS

Patients

Our study included 140 pediatric patients who had been diagnosed with epilepsy at various departments of neurology in regional tertiary pediatric hospitals (Table 1). The epilepsy phenotypes included Dravet syndrome, GEFS+, GTCS, partial epilepsy, juvenile myoclonic epilepsy, benign familial neonatal seizures, childhood absence epilepsy, benign epilepsy of childhood with centrotemporal spikes, epilepsy with continuous spikes and waves during slow sleep and progressive myoclonus epilepsy (PME). We also recruited 48 healthy Japanese volunteers as the ethnic matched control group. Each patient

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Table 1 Clinical and genetic characteristics of the patients

Diagnosis	Number	GABRG2 variants				
		c.236 A>G	c.315 C>T	c.588 C>T	c.1254C>T	IVS1+18del T
Dravet syndrome	55	0	33	38	2	1
GEFS+, FS+	36	0	14	27	0	0
BECCT	2	0	1	2	0	0
BFNC	7	0	3	5	0	0
CAE	5	0	2	3	1	0
CSWS	1	0	1	1	0	0
GTCS	6	1	3	4	0	0
JME	9	0	5	9	0	0
PME	1	0	1	0	0	0
PS	12	0	6	11	0	0
WEST syndrome	6	0	5	5	0	0
Control	48	0	22	39	0	0

Abbreviations: BECCT, benign epilepsy of childhood with centrotemporal spikes; BFNC, benign familial neonatal convulsions; CAE, childhood absence epilepsy; CSWS, epilepsy with continuous spikes and waves during slow sleep; FS+, febrile seizures plus; GEFS+, genetic epilepsy with febrile seizures plus; GTCS, generalized tonic-clonic seizures; JME, juvenile myoclonic epilepsy; PME, progressive myoclonus epilepsy; PS, partial epilepsy.

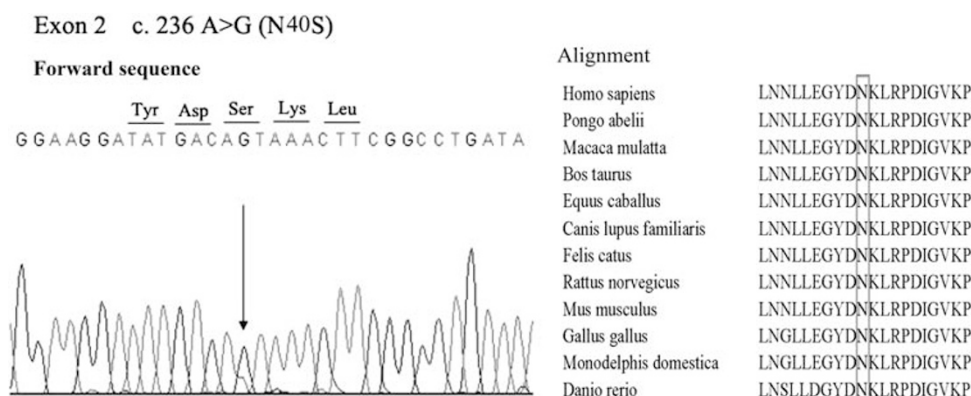


Figure 1 GABRG2 mutation and alignment of affected amino acid. Arrow indicates where mutation occurs. Rectangular box represents the corresponding amino acid to the amino acid where the mutation occurs, that is highly conserved throughout different species.

or parent/guardian signed an informed consent form approved by the Ethics Review Committee of Fukuoka University or similar committees of the participating institutions.

Genetic analysis

Using QIAamp DNA Blood kit (Qiagen, Hilden, Germany), genomic DNAs were prepared from ethylenediaminetetraacetic acid-treated whole blood samples. Genetic abnormalities were sought within all 10 exons of GABRG2 and their flanking intronic splice sites by a direct sequencing method with an automatic sequencer as described earlier.^{9,10} Details of the PCR conditions and the primers used are available on request. Reference sequences of mRNA were based on information available from RefSeq, accession numbers: Human GABRG2, NM_198904.

Statistical analysis

To determine whether the polymorphisms were involved in the pathogenesis of epilepsy, we determined the genotype and allele frequency of the polymorphisms in our patients and in the control population. Data analysis was performed by Fisher's exact test using an SPSS software package (version 13.0). All *P*-values were two-tailed. The significance level was considered to be 5%.

RESULTS

Mutational analysis for the 140 patients revealed one novel missense mutation (c.236A>G: p.N40S, Figure 1) in one of six patients with GTCS. The mutation was heterozygous and not found in other patients of the cohort or in the 48 ethnic matched control individuals. The DNA of the parents of the patient was not available. The patient was a girl whose first seizure occurred when she was 15-years old, and after that re-occurred once a month. She exhibited the typical seizure and electroencephalographic phenotype and susceptibility to anti-epileptic drugs of GTCS supporting that the diagnosis of GTCS. She had no mental retardation or other neurological disorder. Family history of febrile seizures or epilepsy was not found in parents of the patient. The Asn residue at the position of 40, which was replaced with Ser by the mutation, is a highly conserved amino acid throughout many species (Figure 1).

Three exonic variants were found on exon 3 (rs11135176, *n*=74), exon 5 (rs211037, *n*=105) and exon 10 (c.1254 C/T: p.D379D, *n*=3), and one intronic variant (IVS1+18delT, *n*=1) was found (Figure 2; Table 1). Variants of rs11135176 and rs211037 were also found in the control population. None of the variants led to any amino-acid changes in the protein sequence. Fisher's exact test showed no

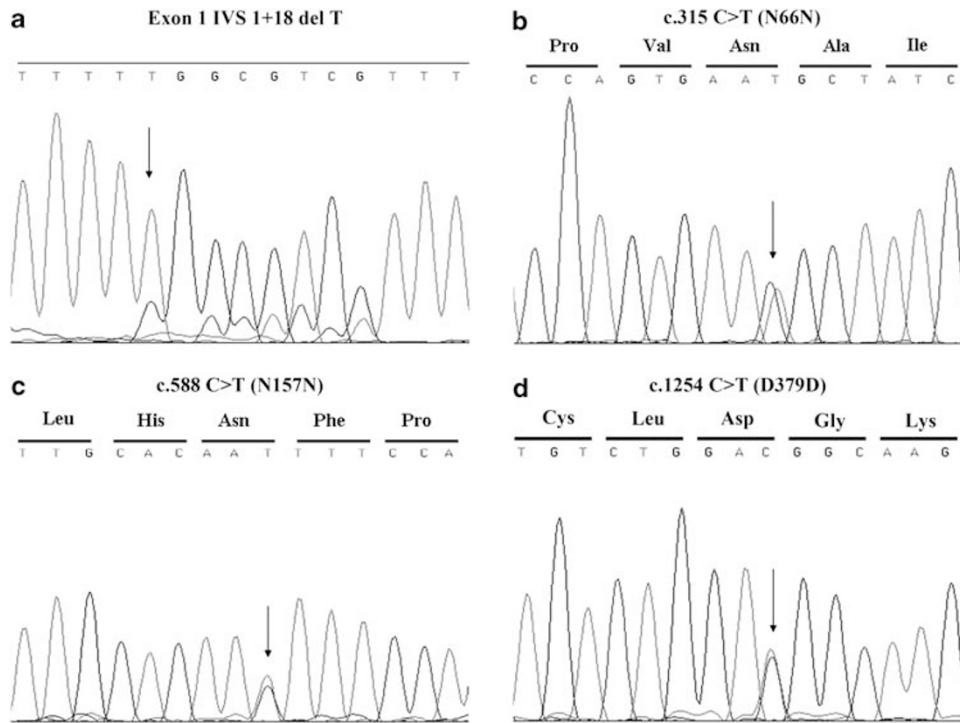


Figure 2 Four *GABRG2* variants are identified. Arrows indicate where variants occur. (a) Variant in intron 1. Among these variants there are two known SNPs (b, c) (rs211037 and rs11135176) and one new SNP (d) (c.1254 C>T).

Table 2 Distribution of polymorphisms in the *GABRG2* gene in patients and controls

cDNA nucleotide	Population	Genotype count (frequency)			P-value ^a	Allele count (frequency)		P-value ^b
		CC	CT	TT		C	T	
c.315C>T	Patients	66 (0.47)	61 (0.44)	13 (0.09)	0.49	193 (0.69)	87 (0.31)	0.30
	Control	26 (0.54)	20 (0.42)	2 (0.04)		72 (0.75)	24 (0.25)	
c.588C>T	Patients	35 (0.25)	67 (0.48)	38 (0.27)	0.69	137 (0.49)	143 (0.51)	0.41
	Control	9 (0.19)	24 (0.50)	15 (0.31)		42 (0.44)	54 (0.56)	
c.1254C>T	Patients	137 (0.98)	3 (0.02)	0 (0.00)	0.57	277 (0.99)	3 (0.01)	0.57
	Control	48 (1.00)	0 (0.00)	0 (0.00)		96 (1.00)	0 (0.00)	

^aGenotype counts.

^bAllele counts are compared between patients and control population by Fisher's exact test.

significant differences ($P > 0.05$) in the genotype and allele frequency between the two groups (Table 2).

DISCUSSION

This study reports one novel missense mutation of *GABRG2* (c.236 A>G: p.N40S) in a female with the typical GTCS phenotype. The mutation was heterozygous and not found in 48 ethnic matched control samples. No other relevant genetic variations were found in the 140 patients. To our knowledge, this is the first report of *GABRG2* mutation in GTCS providing compelling evidence of the involvement of *GABRG2* in epilepsies.

GABA_A receptors are the major inhibitory neurotransmitter receptors in the central nervous system, and several anti-epileptic drugs including benzodiazepines, barbiturates and neurosteroids act by enhancing GABA_A receptor currents. These inhibitory receptors are pentamers formed by assembly of multiple subunit subtypes and the $\alpha 1\beta 2\gamma 2$ receptor is the most abundant receptor isoform. The $\gamma 2$

subunit contributes to receptors involved in both phasic and tonic inhibition and underlies the benzodiazepine sensitivity of both modes of inhibition.¹¹ It is also critical for receptor trafficking, clustering and synaptic maintenance.^{12,13} Up to date, at least seven mutations of *GABRG2* including missense mutations, nonsense mutations and splice-site mutation have been associated with a broad spectrum of epilepsies.^{1,4-8,14}

The N40S mutation identified in this study affects a highly conserved Asn at residue 40 of the mature $\gamma 2$ subunit, thus, the mutation is adjacent to the first one of the two high-affinity benzodiazepine-binding domains of the $\gamma 2$ subunit (Lys-41-Trp-82 in the mature $\gamma 2$ subunit). Wallace *et al.*¹⁵ had suggested that R43Q mutation in the benzodiazepine-binding site can attenuate benzodiazepine sensitivity of GABA_A receptor. Another study on this mutation was shown to accelerate deactivation of the receptor.¹⁶ These lines of evidence support that the N40S mutation should attenuate the GABA_A receptor functions whereby increasing the intracortical

excitability of the brain. This notion accords with the recent findings with the *GABRG2* mutations in the N-terminal domain.¹⁷

In addition, Kang and Macdonald¹⁸ suggest that with heterozygous expression, the R43Q mutation may result in impaired receptor trafficking and increased retention of the receptor in intracellular compartments, including the ER. This reduced cell surface expression would result in decreased inhibitory GABA_A receptor current *in vivo*, and consequently, an increase in neuronal excitability and epilepsy. Several subsequent studies have identified the retention of mutant receptors in the ER¹⁴ and shown that *GABRG2* mutations have reduced trafficking either to the membrane surface with relatively normal function^{18,19} or to the surface with impaired function.^{15,20} It is believed that the main electrophysiological deficit of GABA_A receptor resulting from the mutation is due to intracellular trafficking abnormality of channel molecules. Thus, the N40S mutation may result in an aberrant trafficking of the GABA_A receptor. We anticipate that this mutation N40S may contribute to the patient's pathogenesis of GTCS.

Recently, Wang *et al.*²¹ reported that the *GABRG2* polymorphism rs211014A allele was higher in the febrile seizures group ($P < 0.005$), suggesting that *GABRG2* polymorphisms may predict susceptibility of febrile seizures. Another study²² found that children with the *GABRG2* (SNP:rs211037)-C allele had a higher incidence of idiopathic generalized epilepsies, indicating that the *GABRG2* (SNP:rs211037)-C allele is a candidate genetic marker for idiopathic generalized epilepsies. In this study, three exonic variants and one intronic variant are identified. Among these variants, c.1254C/T is a novel polymorphism. None of these variants leads to any amino-acid changes in the protein sequence. However, in this study, there are no significant differences for these polymorphisms in genotype and allele frequency between patients and control population, suggesting that they are not involved in the etiology of Japanese childhood epilepsy.

In summary, one novel missense mutation of *GABRG2* (N40S) was identified in a patient with GTCS. To our knowledge, there have been no previous reports of mutation of *GABRG2* in GTCS. This finding indicates that mutation *GABRG2* can underlie the pathogenesis of GTCS and thus reinforces the involvement of GABA_A receptors in epilepsy. However, the contribution of mutations of *GABRG2* *per se* to the pathogenesis of epilepsy remains unclear because we do not have sufficient patients. Further studies will involve gathering more cases especially GTCS, progressive myoclonus epilepsy patients and performing the *GABRG2* analysis.

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