OBSERVATION

Novel SCN1A Mutation in a Proband With Malignant Migrating Partial Seizures of Infancy

Emily R. Freilich, MD; Julie M. Jones, MS; William D. Gaillard, MD; Joan A. Conry, MD; Tammy N. Tsuchida, MD, PhD; Christine Reyes, MD; Sulayman Dib-Hajj, PhD; Stephen G. Waxman, MD; Miriam H. Meisler, PhD; Phillip L. Pearl, MD

Objective: To characterize a novel SCN1A mutation in a proband with malignant migrating partial seizures of infancy.

Design: Genomic DNA was isolated from blood and submitted for commercial testing. The identified missense mutation was confirmed in brain DNA obtained at autopsy. Genomic DNA from the brain of the proband was analyzed by comparative genome hybridization, and the coding exons of SCN9A were amplified. Quantitation studies of the mutant transcript were performed.

Setting: Children’s National Medical Center and Yale University School of Medicine.

Proband: A full-term female infant who experienced seizure onset at age 10 weeks, with progression of hemi-clonic, apneic, and multifocal migrating partial seizures leading to recurrent status epilepticus and death at age 9 months.

Main Outcome Measures: Electroencephalographic and magnetic resonance imaging results, quantitative RNA expression, and secondary mutation test results.

Results: The heterozygous missense mutation c.C5006C>A was identified by sequencing genomic DNA from blood and was confirmed in brain DNA. The resulting amino acid substitution p.A1669E alters an evolutionarily conserved residue in an intracellular linker of domain 4 of the SCN1A sodium channel protein Na1.1. The mutant transcript is found to be expressed at levels comparable to the wild-type allele in brain RNA. No variation in copy number was detected in the chromosome region 2q24 containing SCN1A or elsewhere in the genome. No mutations were detected in the linked sodium channel gene SCN9A, which has been reported to act as a modifier of SCN1A mutations.

Conclusion: This report expands the spectrum of SCN1A epileptic channelopathies to include malignant migrating partial seizures of infancy.

Arch Neurol. 2011;68(5):665-671

INCE ITS INITIAL DESCRIPTION in 1995, the syndrome of malignant migrating partial seizures of infancy has become increasingly well recognized, with approximately 50 cases reported worldwide.1,2 The main features are normal development before seizure onset, seizure onset before 6 months of age, migrating focal motor seizures at onset with progression to multifocal seizures that are intractable to conventional antiepileptic drugs, and generally unfavorable outcome, with death usually occurring in the first 1 to 2 years of life.1,8 The cause remains elusive despite extensive neurometabolic, biochemical, and neuroradiologic investigations.3 Certain features of the syndrome suggest a genetic basis, including early age at onset, progressive psychomotor retardation, acquired microcephaly, and multifocality of seizures. Prior studies2,3 of candidate genes associated with infantile epilepsy syndromes failed to detect mutations. We now describe a novel mutation in the SCN1A (OMIM *182389) sodium channel in an infant who met clinical and electroencephalographic criteria for the syndrome of malignant migrating partial seizures of infancy.

METHODS

ELECTROENCEPHALOGRAPHY

Continuous digital video electroencephalographic recordings were acquired using the internationally standard 10-20 Electrode Placement System on several occasions, the lengths of which ranged from 30 minutes to several days. The recordings were then analyzed at 24-hour increments and were interpreted by board-certified staff clinical neurophysiologists (W.D.G., J.A.C., T.N.T., and P.L.P.).

MAGNETIC RESONANCE IMAGING

Magnetic resonance imaging (MRI) results were obtained using a 1.5-T GE scanner (GE Healthcare, Buckinghamshire, England) with a standard infant epilepsy protocol,10 including sagittal and axial T1 images, axial...
diffusion-weighted images, axial spin-echo proton density and T2-weighted images, coronal fast spin-echo T2 images with fat saturation, coronal high-resolution T2 images, and sagittal fast spin-echo T2 images at 3 separate time points (2 months, 5 months, and 7 months of age). Single-voxel short echo time and long echo time spectroscopic imaging was performed in the left basal ganglia of the proband at age 7 months.

HIGH-RESOLUTION KARYOTYPE AND COPY NUMBER VARIATION

Peripheral blood from the proband was analyzed at a banding level of 650 G-bands or more. Genomic DNA from proband brain cells and a DNA strand from a female control individual were analyzed by comparative genome hybridization with the 244 K Agilent array in the Molecular Medical Genetics Core at the University of Michigan (Ramaswamy Iyer, PhD, oral communication, January 8, 2010), as described herein.

SCN1A AND SCN9A SEQUENCES

Genomic DNA was isolated from blood and submitted for commercial testing by sequence of exons and splice sites (Athena Diagnostics Inc, Worcester, Massachusetts). The missense mutation in exon 26 was confirmed by polymerase chain reaction (PCR) amplification from phenol-chloroform–extracted DNA obtained from the brain at autopsy, followed by gel purification and sequencing, as previously described. Total RNA was prepared from brain tissue obtained at autopsy (22 hours after death) using Trizol Reagent (Invitrogen Corp, Carlsbad, California). Reverse transcription (RT)–PCR products were sequenced in the University of Michigan Sequencing Core. The coding exons of SCN9A were amplified from brain genomic DNA. Sequencing was then performed, as previously described.12

Figure 1. Two separate episodes of status epilepticus with different originating hemispheres. A, First episode originating in the left centrotemporal region on July 7, 2009. ECG indicates electrocardiogram. B, Second episode originating in the right posterior quadrant on July 13, 2009.
QUANTITATION OF THE MUTANT TRANSCRIPT

A 571-base pair (bp) fragment of the SCN1A complementary DNA containing the proband’s mutation was amplified by RT-PCR from brain RNA using a 25-mer forward probe end-labeled with the fluorescent dye 6-FAM (Eurofins MWG Operon, Huntsville, Alabama). The product was digested with the endonuclease Ddel (New England Biolabs Inc, Ipswich, Massachusetts), and the resulting fragments were separated on an automated sequencer (3730 DNA Analyzer; Applied Biosystems Inc, Foster City, California). The fluorescent-labeled 5’ end fragments were quantitated using GeneMapper, version 4.0 (Applied Biosystems Inc) and Genemarker (Softgenetics LLC, State College, Pennsylvania) software in the University of Michigan Sequencing Core.

RESULTS

CLINICAL FEATURES

The proband was a female infant (the firstborn of twins) born at 37.5 weeks, whose conception had resulted from in vitro fertilization with a donor ovum. No history of seizures was documented in the family of the father or that of the ovum donor. A paternal half-brother had had normal development but had died at age 4 years; his diagnosis was sudden unexplained death in childhood.

The proband had mild hypotonia within the first month of life with otherwise normal early development. Seizure onset at 10 weeks of age was manifest by left arm clonic activity of 3 hours’ duration despite multiple doses of lorazepam. Five days later, the proband had a clonic seizure of her right arm, which responded to a loading dose of phenobarbital. Results of routine analysis of electrolytes, calcium, and glucose levels were normal. The initial electroencephalographic recording showed prolonged sleep spindles on an otherwise normal background, and brain MRI results were normal. The proband remained clinically seizure free for 2½ months while taking phenobarbital.

At 5 months of age, the proband developed recurrent episodic status epilepticus that was refractory to conventional therapy. Seizure characteristics were hemi- clonic, multifocal clonic, and apneic. Status epilepticus recurred on average every 5 to 8 days. A 5-week seizure-free interval occurred while the proband was being treated with supratherapeutic levels of phenobarbital (levels of 60-90 μg/mL), valproic acid, fosphenytoin sodium, topiramate, levetiracetam, and lorazepam. Her seizures returned when she was aged 7 months and they became increasingly refractory to intervention. She developed profound encephalopathy and became progressively unresponsive. Her head circumference decelerated from the mean at age 2 months to the second percentile by age 9 months. Despite therapy with several pentobarbital infusions and trials of clobazam, rufinamide, stiripentol, vigabatrin, felbamate, high-dose corticosteroids, and intravenous immunoglobulin, the proband deteriorated clinically and died at age 9 months. Microcephaly was confirmed on autopsy, with a brain weight of 613 g, compared with an expected 750 g.\(^13\)

ELECTROPHYSIOLOGY AND IMAGING

The electroencephalographic recordings obtained during episodes of status epilepticus initially suggested seizure onset from the right posterior hemisphere. Within days, a transition originated in the left posterior hemisphere and subsequently broadened to multifocal onset (Figure 1). Over time, the ictal and interictal recordings became indistinguishable, ultimately showing virtually continuous migratory ictal loci (Figure 2).

When the proband was aged 5 months, MRI scans revealed restricted diffusion of the right hippocampus, which did not persist on follow-up and was attributed to peri-ictal activity. A subsequent MRI scan at 7 months demonstrated absence of callosal growth and myelination, as well as cerebral atrophy. Magnetic resonance spectroscopy using a single voxel over the basal ganglia suggested decreased N-acetylaspartate levels (Figure 3).

BIOCHEMICAL ANALYSIS

No abnormalities were detected by metabolite analysis that included plasma amino acids, urine organic acids, pipercolic acid, plasmalogens, fatty acids, acylcarnitine profile, isoelectric focusing of transferrin, and cerebrospinal fluid analysis of neurotransmitters, lactate, and amino acids. Results of DNA methylation analysis for Angelman syndrome did not detect abnormalities.

GENOMEWIDE MUTATION ANALYSIS

The high-resolution karyotype was normal. Copy number analysis by comparative genome hybridization using the Affymetrix 244K chip (Affymetrix, Santa Clara, California) did not detect any novel deletions or insertions.

MUTATION OF SODIUM CHANNEL SCN1A

SCN1A gene sequencing from blood DNA was obtained from the proband at age 5 months because of her initial presentation with frequent hemi- clonic status epilepticus. A heterozygous cytosine to adenosine transversion, c.C5006C>A, was detected. The mutation was confirmed in brain DNA obtained post mortem (Figure 4A). Paternal SCN1A test results were negative; maternal DNA was unavailable.

The mutation is predicted to change the hydrophobic amino acid alanine at residue 1669 to the acidic residue glutamic acid (p.A1669E). Alanine 1669 is located within a short cytoplasmic linker between transmembrane segments 4 and 5 of domain 4 of the sodium channel (Figure 4B). Alanine 1669 is evolutionarily conserved in the human paralogs of SCN1A and in vertebrate and invertebrate sodium channel genes (Figure 4C). The evolutionary conservation, together with the alteration in chemical properties, strongly predicts that A1669E is a pathogenic variant. This theory is supported by analysis with the protein prediction programs Polycln (http://genetics.bwh.harvard.edu/pph/ and SIFT (http://sift.jcvi.org/), which predict that A1669E is highly likely to be a deleterious mutation. Three other pathologic mutations located in the same linker region have previously been reported.\(^14-16\)
EXPRESSION OF MUTANT AND WILD-TYPE SCN1A TRANSCRIPTS IN THE HETEROZYGOUS PROBAND

Brain RNA was amplified by RT-PCR. The overall abundance of the SCN1A transcript in proband and control brain matter was comparable (Figure 5A). Sequencing of the RT-PCR product of the proband demonstrated that the mutant transcript is expressed (not shown). To quantify the relative expression of mutant and wild-type (WT) transcripts, we developed an assay based on the introduction of a novel Ddel restriction site (CTNAG) by the c.C5006C>A mutation, which changes the WT sequence CTGCG to the Ddel consensus CTGAG (Figure 4A). A 571-bp RT-PCR product containing the mutation was 5’ end-labeled with the fluorescent tag 6-FAM. Digestion of the labeled PCR product with Ddel generated 5’ fragments of 528 bp from the WT transcript and 280 bp from the mutant transcript (Figure 5A and B). These fragments were size-separated on an automated DNA sequencer and detected by fluorescence (Figure 5C). Quantitation of the areas corresponding to

Figure 2. Alternating foci of seizures that occurred 1 minute apart when the proband was aged 9 months. A, Electrographic seizure in the left centrotemporal area at 18:31:47. B, Onset of electrographic seizure from the right centrotemporal area at 18:33:20.
the 2 fragments demonstrated a ratio of approximately 60:40 of WT to mutant transcript (Figure 5D). This result demonstrates that the wild-type allele is expressed in the proband, eliminating the possibility of an unrecognized regulatory mutation that could reduce overall channel expression. In addition, the stability of the mutant transcript is demonstrated.

SEQUENCE OF SCN9A

Amplification and sequencing of the exons and adjacent splice sites of SCN9A from brain DNA detected no novel variants of SCN9A affecting amino acid sequence or splice sites. The proband is heterozygous for the polymorphic variant R1150W, which has an allele frequency of approximately 0.15 and may be associated with hypersensitivity to pain.17,18

**COMMENT**

The clinical course of our proband is more severe than the typical course of epilepsy caused by mutations of SCN1A and fulfills the original proposed criteria for malignant migrating partial seizures in infancy: normal development before seizure onset, seizure onset before age 6 months, migrating focal motor seizures, multifocal seizures that became intractable and refractory to therapy, and profound psychomotor delay.1-8 Other typical features include prominent apneic seizures, acquired microcephaly, and decreased N-acetylaspartate as quantified by spectroscopy.1,9 The electroencephalographic recording evolved to exhibit multiple foci, characteris-

tic overlap of ictal and interictal recordings, and migratory ictal foci. The migratory pattern is described as rhythmic theta activity beginning in 1 region and progressively involving adjacent areas, with independent discharges appearing in other regions although the original patterns persist or fade, producing complex electrographic multifocal status epilepticus.2 Our proband meets the clinical and electroencephalographic diagnostic criteria for this malignant syndrome, for which no cause has been elucidated. Mutational analysis of SCN1A had been performed in 3 prior patients with malignant migrating partial seizures in infancy, and no mutations were detected.9

We identified a novel mutation affecting an evolutionarily conserved amino acid residue of the sodium channel protein Na,1.1 encoded by the gene SCN1A. More than 600 mutations of SCN1A have been reported, most of them in patients with the sporadic syndrome severe myoclonic epilepsy of infancy, also known as Dravet syndrome.15,16,17,20 Mutations also have been reported in patients with the related syndrome severe myoclonic epilepsy borderland, a variant that lacks the generalized spike-wave and myoclonus of Dravet syndrome, and in the typically milder inherited epilepsy syndrome known as generalized epilepsy with febrile seizures plus other seizure types (GEFS+).14,16,20 Most variants associated with the more severe phenotypes occur de novo, in contrast
the patients were studied between the ages of 5 and 20 years. Difficulty often occurs with respect to classifying patients with cryptogenic epilepsies that begin in the first year of life.\textsuperscript{21,22} Patients with severe myoclonic epilepsy in infancy may initially be classified as having cryptogenic localization-related epilepsy, which may lead to misguided surgical procedures.

The phenotype of the proband described herein was more severe than that typically seen in individuals with severe myoclonic epilepsy of infancy, many of whom are homozygous for mutations that cause complete loss of function of SCN1A.\textsuperscript{14} The novel amino acid substitution A1669E in our proband changes the charge of a short cytoplasmic linker joining the S4 and S5 transmembrane segments in domain 4 of the channel (Figure 4). This 12-residue linker is the site of 3 previously described mutations in patients with severe myoclonic epilepsy borderland or severe myoclonic epilepsy of infancy: T1658R, F1661S, and P1668A.\textsuperscript{14-16} The functional effects of these substitutions on Na,1.1 channel function have not been determined. However, the pathogenic mutation A1632E introduces the identical amino acid substitution into the corresponding residue of SCN9A.\textsuperscript{23} This SCN9A mutation was identified in a patient with a complex pain disorder. Functional characterization of this mutation in SCN9A revealed multiple biophysical abnormalities, including a 7-mV hyperpolarizing shift in the voltage dependence of channel activation.\textsuperscript{24} In addition, the pathogenic mutation A1071T substitutes a polar residue into the S4-S5 linker of domain 3 in mouse SCN8A and results in a 14-mV shift in voltage dependence of activation.\textsuperscript{24} The biophysical alterations resulting from these mutations in closely related sodium channels support the pathogenicity of the SCN1A mutation in our proband.

We performed several experiments to attempt to explain the severe phenotype associated with the A1669E mutation. Using comparative genome hybridization, we found no unusual copy number variant in our proband. The severity of SCN1A mutations has been reported to be exacerbated by deleterious variants in the closely linked sodium channel gene SCN9A.\textsuperscript{25} Because of the clinical severity of the proband’s disease, we tested the possibility of an additional mutation in SCN9A, and no such mutation was identified. Quantitative analysis of brain RNA demonstrated that wild-type and mutant alleles are expressed at comparable levels, indicating that no deficiency of wild-type protein exists. The mutant protein could have a dominant negative effect on the wild-type channel, but such effects of mutant sodium channels only rarely have been observed.\textsuperscript{26} Other potential explanations for the severe phenotype in this proband include unidentified factors in her genetic background, such as variation in other ion channels\textsuperscript{27} or stochastic processes that can exacerbate the effects of any mutation during development.

This case extends the spectrum of SCN1A-associated epileptic encephalopathic syndromes described as severe infantile multifocal epilepsy.\textsuperscript{28} SCN1A mutations were identified in 3 of 5 patients with this disorder, although the phenotype appears to be milder than malignant migratory partial seizures of early infancy because developmental slowing occurred between the ages of 16 months and 6 years, and the autosomal dominant inheritance pattern with variable penetrance seen in GEFS+\textsuperscript{15,16,19}.

The spectrum of SCN1A-associated infantile epileptic encephalopathic conditions also has been reported to include a syndrome described as severe infantile multifocal epilepsy.\textsuperscript{28} SCN1A mutations were identified in 3 of 5 patients with this disorder, although the phenotype appears to be milder than malignant migratory partial seizures of early infancy because developmental slowing occurred between the ages of 16 months and 6 years, and the autosomal dominant inheritance pattern with variable penetrance seen in GEFS+.\textsuperscript{15,16,19}
Accepted for Publication: September 29, 2010.
Correspondence: Phillip L. Pearl, MD, Department of Neurology, Children’s National Medical Center, 111 Michigan Ave NW, Washington, DC 20010-2970 (pppearl@cnmc.org).

Author Contributions: Study concept and design: Freilich, Gaillard, Tsuchida, Reyes, Dib-Hajj, Waxman, Meisler, and Pearl. Acquisition of data: Freilich, Jones, Gaillard, Conry, Meisler, and Pearl. Analysis and interpretation of data: Freilich, Jones, Gaillard, Conry, Dib-Hajj, Waxman, Meisler, and Pearl. Drafting of the manuscript: Freilich, Tsuchida, Reyes, Meisler, and Pearl. Critical revision of the manuscript for important intellectual content: Jones, Gaillard, Conry, Dib-Hajj, Waxman, Meisler, and Pearl. Obtained funding: Waxman and Meisler. Administrative, technical, and material support: Jones, Gaillard, Conry, Tsuchida, Reyes, Dib-Hajj, Waxman, Meisler, and Pearl. Study supervision: Conry, Dib-Hajj, Waxman, Meisler, and Pearl.

Financial Disclosure: Dr Gaillard receives grant support from the National Institute of Neurological Disorders and Stroke, the National Institute of Mental Health, and the National Institute of Child Health and Development. He has lectured at an education symposium supported by H. Lundbeck A/S. His department conducts industry-sponsored (Ovation Pharmaceuticals Inc, Eisai Co Ltd, and Schwarz Pharma Inc) trials for which no individual derives personal income. Dr Conry is an institutional sponsor for studies conducted by H. Lundbeck A/S, Eisai Co Ltd, UCB S.A., and grant 1R01NS045911-01A1 from the National Institutes of Health (Childhood Absence Epilepsy Study) and is a consultant to H. Lundbeck A/S. Research by Dr Waxman is funded by the Rehabilitation Research Service and the Medical Research Service, Department of Veterans Affairs. Dr Meisler receives grant support from the National Institute of Neurological Disorders and Stroke and National Institute of General Medical Sciences and has lectured with support from Athena Diagnostics. Dr Pearl receives grant HD58553 R01 from the National Institutes of Health (National Institute of Neurological Disorders and Stroke).

Funding/Support: This work was supported in part by grant NS34509 from the National Institutes of Health (Dr Meisler).

Additional Information: Dr Freilich and Ms Jones served as co-first authors. The contributions of Dr Meisler’s laboratory were equal to those of the authors affiliated with the Children’s National Medical Center. Guy Lenk, PhD, performed the protein prediction program analysis. We thank Robert Lyons, PhD, Director of the University of Michigan Sequencing Core. We thank the family of the proband for their cooperation, patience, and understanding.

REFERENCES


