



Investigating the genetic basis of fever-associated syndromic epilepsies using copy number variation analysis

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SUMMARY

Fever-associated syndromic epilepsies ranging from febrile seizures plus (FS+) to Dravet syndrome have a significant genetic component. However, apart from *SCN1A* mutations in >80% of patients with Dravet syndrome, the genetic underpinnings of these epilepsies remain largely unknown. Therefore, we performed a genome-wide screening for copy number variations (CNVs) in 36 patients with *SCN1A*-negative fever-associated syndromic epilepsies. Phenotypes included Dravet syndrome (n = 23; 64%), genetic epilepsy with febrile seizures plus (GEFS+) and febrile seizures plus (FS+) (n = 11; 31%) and unclassified fever-associated epilepsies (n = 2; 6%). Array comparative genomic hybridization (CGH) was performed using Agilent 4 × 180K arrays. We identified 13 rare CNVs in 8 (22%) of 36 individuals. These included known pathogenic CNVs in 4 (11%) of 36 patients: a 1q21.1 duplication in a proband with Dravet syndrome, a 14q23.3 deletion in a proband with FS+, and two deletions at 16p11.2 and 1q44 in two individuals with fever-associated epilepsy with concomitant autism and/or intellectual disability. In addition, a 3q13.11 duplication in a patient with FS+ and two de novo duplications at 7p14.2 and 18q12.2 in a patient with atypical Dravet syndrome were classified as likely pathogenic. Six CNVs were of unknown significance. The identified genomic aberrations overlap with known neurodevelopmental disorders, suggesting that fever-associated epilepsy syndromes may be a recurrent clinical presentation of known microdeletion syndromes.

KEY WORDS: Copy number variation, Fever-associated syndromic epilepsy, Febrile seizures plus, Dravet syndrome, *SCN1A*-negative.



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Febrile seizures (FS) are a major manifestation of fever-associated syndromic epilepsies such as febrile seizures plus (FS+), genetic epilepsy with febrile seizures plus (GEFS+), and Dravet syndrome. As opposed to simple FS, which usually occur as isolated events, fever-associated syndromic epilepsies present with recurrent FS, FS persisting beyond the age of 6 years, additional afebrile seizures, additional features such as intellectual disability (ID), autism, or congenital anomalies (CGAs), and in cases of GEFS+, with family members also affected with FS or fever-associated epilepsy.

Although fever acts as the precipitating factor, the etiology of fever-associated syndromic epilepsies shows a significant genetic contribution. Investigation of classic FS did not reveal any major causative genes, but progress was

made examining patients with fever-associated syndromic epilepsies. Known genes include *SCN1A*, *SCN1B*, *SCN2A*, and *GABRG2*.¹

Sequence mutations in *SCN1A* are the most common genetic variant in Dravet syndrome, accounting for at least 70% of cases.² In addition, deletions or duplications of *SCN1A* can be detected in 2–3% of patients with Dravet syndrome.³ Rare copy number variants (CNVs) identified in one of 19 Dravet⁴ and 2 of 15 patients with severe idiopathic generalized epilepsy of infancy (SIGEI)⁵ and 17q12 duplications in 0.45% (1/222) of patients with familial FS/GEFS+⁶ suggest that CNVs play a role, but the overall significance of CNVs remains unclear. CNVs are deletions and duplications larger than 1 kb, and rare CNVs have been established as an important source of genetic morbidity in a range of neurodevelopmental phenotypes including ID, schizophrenia, and autism.^{7–9} Rare recurrent microdeletions in 15q13.3, 15q11.2, and 16p13.11 are important risk factors in 3% of patients with idiopathic/genetic generalized epilepsy (IGE/GGE).⁵ Rare structural genomic variations have been identified as a frequent cause of epileptic encephalopathies.⁴

In this study, we performed a genome-wide CNV analysis in patients with fever-associated syndromic epilepsy and identified pathogenic CNVs in 11% of patients.

METHODS

Patient selection

This study has been approved by the ethics committee of the Christian-Albrechts-University of Kiel, the Antwerp University Hospital, and the University of Washington.

Thirty-six patients with fever-associated syndromic epilepsies were selected from the biobanks of the Department of Neuropediatrics at the Christian-Albrechts-University of Kiel and the Vlaams Instituut voor Biotechnologie (VIB) Department of Molecular Genetics at the University of Antwerp. All 36 samples were negative for sequence mutations in *SCN1A*; 18 (50%) of 36 were negative for *SCN1A* deletions and duplications using multiplex ligation-dependent probe amplification (MLPA) or multiplex amplification quantification (MAQ).

All patients had fever-related seizures or status epilepticus as the most prominent clinical features in the first years of life. Patient phenotypes were classified in three large groups (Table 1). The first group consisted of 13 patients with typical and 10 with atypical Dravet syndrome ($n = 23$; 64%). Most patients with atypical features were classified as having severe idiopathic generalized epilepsy of infancy (SIGEI) as described by Doose,¹⁰ with predominant generalized tonic-clonic seizures (GTCS), but without the alternating hemiclonic seizures of typical Dravet syndrome.

The second group comprised 11 patients ($n = 11$; 31%) with GEFS+/FS+. All patients had simple FS with addi-

tional seizure types or FS persisting beyond the usual age of remission.

The third group included two patients ($n = 2$; 6%) with “unclassified” epilepsy who had additional syndromic features including profound ID, autism, short stature, dysmorphic features, macrocephaly, or hypotonia, although a diagnosis of Dravet/SIGEI or FS+ would be justifiable from the epileptology point of view. These patients were included because the clinical features of fever-induced epilepsy were prominent.

A diagnosis of ID was present in 26 (72%) of 36 patients, autism was diagnosed in 5 (14%) of 36 individuals, and 6 (17%) of 36 patients had CGA; 18 (69%) of 26 of the patients with ID had normal development before seizure onset and cognitive impairment started with epileptic activity in terms of an epileptic encephalopathy.

Array Comparative Genomic Hybridization

Genomic DNA of all patients was screened for CNVs using array comparative genomic hybridization (array CGH). We applied Agilent 4 × 180K arrays with an overall median probe spacing of 13 kb.

Labeling and hybridization were performed following standard protocols. Microarray slides were scanned on a G2505C DNA Microarray Scanner (Agilent Technologies, Santa Clara, California, U.S.A.) using Agilent Scan Control (version A.8.4.1) with the preset Agilent G3 CGH/CNV/ChIP scan profile (resolution 3 μm), then processed by the Agilent Feature Extraction software (version 10.7.3.1) using the default CGH_107_Sep09 protocol. The Derivative Log Ratio Spread (DLRS) was used for quality control. All arrays had a DLRS ≤ 0.3 and 26 of 36 arrays had a DLRS < 0.2.

CNV analysis

Further data processing and analysis were performed using Agilent Genomic Workbench (standard edition, version 5.0.14). Log₂ ratios for each array were normalized (centralization algorithm with bin size 10, centralization threshold 6.0). CNVs were called applying the Aberration Detection Method 2 (ADM-2) algorithm (threshold 6.0). In addition, arrays were visually inspected for CNVs. Only CNVs containing at least five probes with a minimum average absolute log ratio of 0.5 were reported. Variants were filtered as described previously⁴: CNVs were eliminated from analysis if they did not overlap any RefSeq genes, lay entirely within segmental duplications, or had a >50% overlap with a CNV detected in 4,519 published controls.^{11,12} The last criterion was not applied to established hotspot CNVs known to rarely occur in healthy controls. All filtered CNVs were assessed by visual analysis in Genomic Workbench. Where available, parental DNA was investigated to determine whether the CNV had arisen de novo. Patients with pathogenic and likely pathogenic variants underwent detailed phenotyping including review of available clinical documentation, imaging, and electroencephalography.

Table 1. Phenotypes of patients included in the current study

Epilepsy phenotype	No. patients	No. patients with				
		ID with onset			Autism	CGA
		Prior to epilepsy	After epilepsy	Unknown		
SCN1A-negative Dravet syndrome	23 (64%)	2	18	3	4	4
Typical Dravet syndrome	13					
Atypical Dravet syndrome/SIGE1	10					
GEFS+/FS+	11 (31%)	1 ^a	0	0	0	0
FS+ afebrile	4					
FS+ prolonged	4					
FS+ absence	1					
FS+ other	2					
Unclassified fever-associated epilepsy	2 (6%)	2	0	0	1	2
Total	36	5 (14%)	18 (50%)	3 (8%)	5 (14%)	6 (17%)

CGA, congenital anomalies; FS+, febrile seizures plus; GEFS+, genetic epilepsy with febrile seizures plus; ID, intellectual disability; SIGE1, severe idiopathic generalized epilepsy of infancy.

According to the presentation, patients were classified as "FS+ afebrile" if additional afebrile GTCS occurred, "FS+ prolonged" if FS persisted beyond the age of 6 years, "FS+ absence" if additional absence seizures were noted, and "FS+ other" if other seizure types were found. In the two patients of this category, atastic and tonic seizures were observed.

^aPatient with borderline ID (full scale intelligence quotient of 75 in the Hamburg Wechsler Intelligenztest für Kinder IV as the German adaption of Wechsler Intelligence Scale for Children IV).¹⁶

Evaluation of pathogenicity

Pathogenicity of rare CNVs was evaluated based on guidelines for the interpretation of clinical array CGH results in patients with ID, autism, or multiple CGAs¹³ and as performed previously.⁴ In brief, CNVs were classified as pathogenic if they were de novo deletions, or were previously described in neurodevelopmental phenotypes or included known epilepsy genes. CNVs were evaluated as likely pathogenic if they were de novo duplications or CNVs >1 Mb regardless of inheritance. All remaining CNVs were classified as variants of unknown significance.

Deletion break point mapping, microsatellites

Deletion break points were refined in patient 2 using long-range polymerase chain reaction (PCR) as described in the Appendix S1 and Table S1.

Microsatellite analysis (patient 5, PowerPlex S5 System, Promega, Madison, WI, U.S.A.) or CNV segregation studies (patient 2) were used to confirm maternity and paternity.

RESULTS

CNV screening

We identified eight patients with a total of 13 rare CNVs (Table 2) including four patients with a single, three patients with two, and one patient with three CNVs. To determine the inheritance pattern of rare CNVs, parental DNA was available for both parents in two patients, for one parent in three patients, and unavailable in three patients. However, two of these patients carried hotspot CNVs at 1q21.1 and 16p11.2, which were considered pathogenic regardless of inheritance. In total, we identified three de novo, three maternally inherited and one

paternally inherited variant. Six CNVs were of unknown inheritance.

All CNVs were then classified according to pathogenicity. Four patients carried pathogenic CNVs (Fig. 1), two patients carried likely pathogenic duplications (Supporting Information, Fig. S1), and in two patients CNVs were of unknown significance. All pathogenic CNVs in our study had additional supportive data for pathogenicity, as some assessment criteria suggest caution when interpreting CNVs as pathogenic due to a single de novo deletion.

All pathogenic variants have been described previously in neurodevelopmental disorders. They comprised two rare recurrent CNVs or hotspot variants of unknown inheritance, namely a 1q21.1 duplication in patient 8 with Dravet syndrome and a distal 16p11.2 deletion in patient 3 with unclassified fever-associated epilepsy, ID, autism, generalized muscular hypotonia, and macrocephaly. Furthermore, a de novo 1q44 deletion was identified in patient 2 with unclassified fever-associated epilepsy, ID, dysmorphic features, and short stature. This patient also carried two additional rare inherited CNVs of unknown significance, including a duplication of 6q23.3 and a deletion of 7p22.1. Patient 1 with FS+ presented with a maternally inherited pathogenic 14q23.3 deletion interrupting *GPHN* and a 4q28.3 deletion of unknown significance. Overall, three likely pathogenic CNVs were discovered. Patient 4 with FS+ carried a 1.6 Mb likely pathogenic duplication at 3q13.11 including *ALCAM* and *CBLB*. Patient 5 carried two likely pathogenic de novo CNVs, a 191 kb duplication at 7p14.2 including the *ELMO1* gene and a 217 kb duplication at 18q12.2 comprising five zinc finger genes. Three additional CNVs in two patients were duplications of unknown significance in the chromosomal regions 11p15.1, 1p22.3, and 4p15.31.

Table 2. Rare CNVs identified in 36 patients with SCN1A-negative fever-associated syndromic epilepsies

Patient no.	Epilepsy phenotype	ID, autism, CGA	CNV, chr location	Coordinates (Build 36, Mb)	Size (kb)	RefSeq genes included	Inheritance	Evaluation of pathogenicity
1	FS+ afebrile	-	del, 4q28.3	139.29–139.49	197	SLC7A11	Not in mother	Of unknown significance
2	Unclassified fever-associated epilepsy	ID, short stature, dysmorphic features	del, 14q23.3	66.18–66.27	85	GPHN	M	Pathogenic
			del, 1q44	243.11–244.41 ^a	1301 ^a	HNRNPU ^a , EFCAB2, KIF26B, SMYD3	De novo	Pathogenic
3	Unclassified fever-associated epilepsy	ID, autism, generalized muscular hypotonia, macrocephaly	dup, 6q23.3	135.89–136.07	184	MIR548H4, C6orf217	M	Of unknown significance
			del, 7p22.1	4.88–4.97	85	RADIL, MMD2	F	Of unknown significance
4	FS+ prolonged SCN1A-negative atypical Dravet syndrome	ID, autism, generalized muscular hypotonia, macrocephaly	del, 16p11.2	28.73–28.95	218	ATXN2L, TUFM, SH2B1, ATP2A1, RABEP2, CD19, NFATC2IP, SPNS1, LAT	Unknown	Pathogenic
			dup, 3q13.11	106.11–107.73	1623	ALCAM, CBLB	Not in mother	Likely pathogenic
5	SCN1A-negative atypical Dravet syndrome	ID	dup, 7p14.2	36.93–37.12	191	ELMO1	De novo	Likely pathogenic
			dup, 18q12.2	31.02–31.24	217	ZNF397, ZNF397OS, ZNF271, ZNF24, ZNF396	De novo	Likely pathogenic
6	SCN1A-negative Dravet syndrome	ID, autism	dup, 11p15.1	21.30–21.39	92	NELI	M	Of unknown significance
7	SCN1A-negative Dravet syndrome	ID, microcephaly	dup, 1p22.3	87.17–87.28	115	HS2ST1	Unknown	Of unknown significance
			dup, 4p15.31	21.87–22.73	855	GPR125, GBA3	Unknown	Of unknown significance
8	SCN1A-negative Dravet syndrome	ID	dup, 1q21.1	144.53–146.27	1744	GPR89A, GPR89C, PDZK1P1, LOC200030, NBPFL1, LOC728989, PRKAB2, PDIA3P, FMO5, CHD1L, BCL9, ACP6, GJA5, GJA8, GPR89B	Unknown	Pathogenic

CGA, congenital anomalies; chr, chromosome; del, deletion; dup, duplication; F, inherited from father; FS+, febrile seizures plus; ID, intellectual disability; M, inherited from mother.

^aHNRNPU was shown to be interrupted by the deletion by refining the break points with long-range PCR and gel electrophoresis to chr1: 243090300–243093300 and chr1: 244408023–244411023 (NCBI Build 36).

^bfull scale intelligence quotient of 75 in the Hamburg Wechsler Intelligenztest für Kinder IV as the German adaptation of Wechsler Intelligence Scale for Children IV.¹⁶

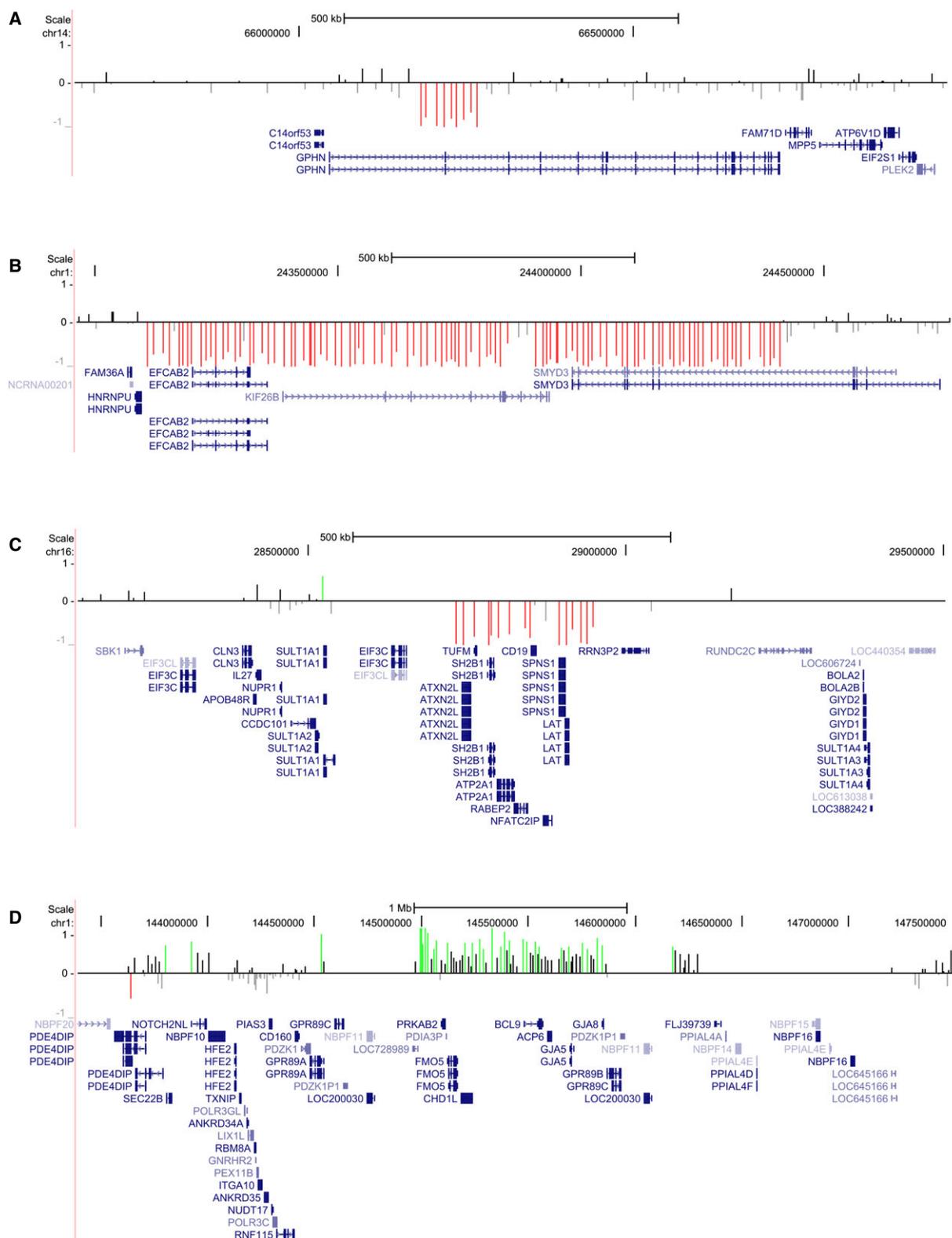


Figure 1.

Array CGH results are shown for all pathogenic CNVs detected in 36 patients: Patient 1, del 1q23.3 (**A**); patient 2, del 1q44 (**B**); patient 3, distal del 16p11.2 (**C**); patient 8, dup 1q21.1 (**D**). Probe log₂ ratios are plotted against the loci of probes and depicted by vertical lines: between -0.5 and 0 colored gray, between 0 and 0.5 colored black, <-0.5 colored red, >0.5 colored green. RefSeq genes are shown in blue.

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The break points of the 1q44 deletion in patient 2 were narrowed down to chr1: 243090300-243093300 and chr1: 244408023-244411023 (NCBI Build 36), interrupting *HNRNPU* by deleting the first exon of the gene.

Microsatellite and CNV segregation analysis confirmed maternity and paternity for the parents of patients 5 and 2.

Patient phenotypes

Phenotypes of patients carrying pathogenic or likely pathogenic CNVs are described in Appendix S2.

DISCUSSION

We performed genome-wide array CGH in 36 patients with *SCN1A*-negative fever-associated syndromic epilepsies and identified 13 rare CNVs in 8 individuals including pathogenic CNVs in 11% (4/36) of patients and likely pathogenic CNVs in 6% (2/36) of patients. These CNVs and the corresponding phenotypes are discussed in Appendix S3.

The investigated cohort included several patients with ID, autism, and CGAs in addition to fever-associated epilepsy. Because CNVs are found more frequently in patients with epilepsy and additional neurodevelopmental phenotypes than in patients with epilepsy alone, a diagnosis of ID, autism, or CGA might upwardly bias the diagnostic yield in our study. Spreiz et al.¹⁴ identified rare CNVs in 9 (21%) of 43 patients with epilepsy, ID, and minor dysmorphisms including causative CNVs in 3 (7%) of 43 individuals. Mullen et al.¹⁵ detected rare CNVs in 17 (28%) of 60 patients with GGE and ID. These findings are consistent with 8 (22%) of 36 patients from our study carrying rare and 4 (11%) of 36 patients carrying pathogenic CNVs. However, most of our patients with ID (18/26; 69%) had normal development before seizure onset and cognitive impairment occurred in terms of an epileptic encephalopathy. Considering prior studies, the diagnostic yield of chromosomal microarrays in epileptic encephalopathies is lower than in GGE with ID (8% vs. 28%)^{4,15} and about equals the diagnostic yield in GGE alone (8% vs. 9%),^{4,5} indicating that ID linked to epileptic encephalopathies does not relevantly increase the amount of CNV findings. When comparing patients with fever-associated epilepsy and ID present before epilepsy onset or with an unknown starting point, autism, or CGA to patients with fever-associated epilepsy without these additional features, there is no significant difference in the amount of rare CNVs (5/14 and 3/22, $p = 0.22$, Fisher's exact test). However, as we investigated a small cohort, replication of our investigations in a larger cohort will help to provide a more accurate estimate of diagnostic yields in these subgroups.

The pathogenic CNVs detected in this study were not specific for fever-associated syndromic epilepsies but are known to occur in patients with different neurodevelopmental disorders.

Collectively, our findings indicate that several known microdeletion syndromes can present as fever-associated epilepsy syndromes, either in isolation or in association with other neurodevelopmental features. In conclusion, our study suggests that array CGH represents a useful diagnostic tool for identification of the genetic basis in fever-associated syndromic epilepsies negative for prime candidate genes such as *SCN1A*, even though we cannot know from our sample whether the frequency of pathogenic CNVs is higher than in other epilepsy cohorts. This conclusion cannot be generalized to individuals with simple FS, as these were not investigated in this study. In a clinical setting, array CGH analysis may be the next step of the diagnostic work-up in patients with fever-associated syndromic epilepsies and overlapping neurodevelopmental phenotypes, once common genetic causes have been excluded.

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DISCLOSURE

None of the authors has any conflict of interest to disclose. We confirm that we have read the Journal's position on issues involved in ethical publication and affirm that this report is consistent with those guidelines.

REFERENCES

1. Baulac S, Gourfinkel-An I, Nabbout R, et al. Fever, genes, and epilepsy. *Lancet Neurol* 2004;3:421–430.
2. Marini C, Scheffer IE, Nabbout R, et al. The genetics of Dravet syndrome. *Epilepsia* 2011;52(Suppl. 2):24–29.
3. Marini C, Scheffer IE, Nabbout R, et al. *SCN1A* duplications and deletions detected in Dravet syndrome: implications for molecular diagnosis. *Epilepsia* 2009;50:1670–1678.
4. Mefford HC, Yendle SC, Hsu C, et al. Rare copy number variants are an important cause of epileptic encephalopathies. *Ann Neurol* 2011;70:974–985.
5. Mefford HC, Muhle H, Ostertag P, et al. Genome-wide copy number variation in epilepsy: novel susceptibility loci in idiopathic generalized and focal epilepsies. *PLoS Genet* 2010;6:e1000962.
6. Hardies K, Weckhuysen S, Peeters E, et al. Duplications of 17q12 can cause familial fever-related epilepsy syndromes. *Neurology* 2013;81:1434–1440.

7. de Vries BB, Pfundt R, Leisink M, et al. Diagnostic genome profiling in mental retardation. *Am J Hum Genet* 2005;77:606–616.
8. International Schizophrenia Consortium. Rare chromosomal deletions and duplications increase risk of schizophrenia. *Nature* 2008;455:237–241.
9. Sebat J, Lakshmi B, Malhotra D, et al. Strong association of de novo copy number mutations with autism. *Science* 2007;316:445–449.
10. Doose H, Lunau H, Castiglione E, et al. Severe idiopathic generalized epilepsy of infancy with generalized tonic-clonic seizures. *Neuropediatrics* 1998;29:229–238.
11. Itsara A, Cooper GM, Baker C, et al. Population analysis of large copy number variants and hotspots of human genetic disease. *Am J Hum Genet* 2009;84:148–161.
12. Shaikh TH, Gai X, Perin JC, et al. High-resolution mapping and analysis of copy number variations in the human genome: a data resource for clinical and research applications. *Genome Res* 2009;19:1682–1690.
13. Miller DT, Adam MP, Aradhya S, et al. Consensus statement: chromosomal microarray is a first-tier clinical diagnostic test for individuals with developmental disabilities or congenital anomalies. *Am J Hum Genet* 2010;86:749–764.
14. Spreiz A, Haberlandt E, Baumann M, et al. Chromosomal microaberrations in patients with epilepsy, intellectual disability, and congenital anomalies. *Clin Genet* 2014;86:361–366.
15. Mullen SA, Carvill GL, Bellows S, et al. Copy number variants are frequent in genetic generalized epilepsy with intellectual disability. *Neurology* 2013;81:1507–1514.
16. Daseking M, Petermann U, Petermann F. (2007) Intelligenzdiagnostik mit dem HAWIK-IV [Assessment of intelligence with the HAWIK-IV]. *Kindheit und Entwicklung* 16:250–259.

SUPPORTING INFORMATION

Additional Supporting Information may be found in the online version of this article:

Appendix S1. Supplementary Methods. Deletion break point mapping.

Appendix S2. Phenotypes of patients with pathogenic and likely pathogenic CNVs.

Appendix S3. Discussion of pathogenic and likely pathogenic CNVs.

Table S1. Deletion break point mapping: Primer pairs and length of PCR fragments.

Figure S1. Array CGH results for all likely pathogenic CNVs detected in 36 patients.