De Novo Loss-of-Function Mutations in CHD2 Cause a Fever-Sensitive Myoclonic Epileptic Encephalopathy Sharing Features with Dravet Syndrome

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Dravet syndrome is a severe epilepsy syndrome characterized by infantile onset of therapy-resistant, fever-sensitive seizures followed by cognitive decline. Mutations in SCN1A explain about 75% of cases with Dravet syndrome; 90% of these mutations arise de novo. We studied a cohort of nine Dravet-syndrome-affected individuals without an SCN1A mutation (these included some atypical cases with onset at up to 2 years of age) by using whole-exome sequencing in proband-parent trios. In two individuals, we identified a de novo loss-of-function mutation in CHD2 (encoding chromodomain helicase DNA binding protein 2). A third CHD2 mutation was identified in an epileptic proband of a second (stage 2) cohort. All three individuals with a CHD2 mutation had intellectual disability and fever-sensitive generalized seizures, as well as prominent myoclonic seizures starting in the second year of life or later. To explore the functional relevance of CHD2 haploinsufficiency in an in vivo model system, we knocked down chd2 in zebrafish by using targeted morpholino antisense oligomers. chd2-knockdown larvae exhibited altered locomotor activity, and the epileptic nature of this seizure-like behavior was confirmed by field-potential recordings that revealed epileptiform discharges similar to seizures in affected persons. Both altered locomotor activity and epileptiform discharges were absent in appropriate control larvae. Our study provides evidence that de novo loss-of-function mutations in CHD2 are a cause of epileptic encephalopathy with generalized seizures.

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Epileptic encephalopathies (EEs) are severe, intractable childhood epilepsies with concomitant cognitive impairment and other associated comorbidities. Although a broad range of exogenous factors can lead to EE, in a significant subset of affected individuals the etiology remains unidentified and might be endogenous. Consequently, a genetic cause is assumed. Among the various EEs of genetic origin, Dravet syndrome (MIM 607208) has emerged as one of the best-defined phenotypes and the one with the highest mutation detection yield. Children with Dravet syndrome are prone to repetitive and prolonged epileptic seizures in the setting of fever. Although these fever-induced seizures start around the age of 6 months (range = 3–16 months), other seizure types occur during the course of the disease, and developmental plateauing is typical in the second year of life.

Taking into account SCN1A abnormalities due to single or multiple exons deletions, de novo mutations in SCN1A (MIM 182389) are known to cause Dravet syndrome in ~75% of affected probands. Despite this high probability of identifying a mutation in an individual with a typical phenotype, up to 25% of affected persons do not carry SCN1A mutations, suggesting the involvement of other genes. Mutations in PCDH19 (MIM 300460) can result in a Dravet-syndrome-like phenotype in females and explain some of the cases without an SCN1A mutation. For a relevant subset of probands, however, a causative mutation cannot be identified in either gene. We therefore explored the involvement of mutations in additional genes in these probands by using whole-exome sequencing in proband-parent trios. This approach provides the possibility of querying the entire exome for de novo mutations in simplex cases, which has been proven to be successful for intellectual disability, schizophrenia, autism, and some forms of epilepsy or epilepsy-related disorders.

We first studied nine Dravet-syndrome-affected individuals in whom SCN1A sequence mutations or copy-number variations had been excluded. These probands were selected on the basis of broad inclusion criteria, extending the onset age of seizures to an age between 3 months and 2 years of life. Further inclusion criteria consisted of (1) the presence of both febrile and afebrile seizures; (2) multiple seizure types including tonic-clonic, hemi-clonic, myoclonic, absence, and/or focal seizures; (3) pharmacoresistant epilepsy at least during childhood or frequent status epilepticus; (4) normal development prior to epilepsy onset, although some minor degree of developmental delay could be present; and (5) slowing or stagnation of development after onset of seizures and absence of epileptogenic lesions on brain MRI.

Signed informed consent was obtained from all study participants or their legal representatives. The local ethical committees of the University of Antwerp and Antwerp University Hospital, University of Kiel, and other collaborating centers approved this study. Genomic DNA was extracted from peripheral blood according to standard procedures.

We performed whole-exome sequencing on genomic DNA of the nine selected individuals with Dravet syndrome and both unaffected parents at the Wellcome Trust Sanger Institute (Hinxton, Cambridgeshire). In brief, genomic DNA (~3 μg) was fragmented by sonication, and fragments with a length of 150–200 bp were purified. After a paired-end DNA library was prepared from the DNA fragments (with the TruSeq DNA Sample Preparation Kit from Illumina), targeted enrichment was performed with the SureSelect Human All Exon 50Mb Kit (Agilent Technologies). Captured DNA was then sequenced on a HiSeq2000 (Illumina) as paired-end 75 bp reads according to the manufacturer’s protocol. Sequencing reads passing quality filtering were aligned to the human reference genome (hg19, UCSC Genome Browser) with the Burrows-Wheeler Aligner. The Genome Analysis Toolkit (GATK) was used to recalibrate base quality scores, realign around indels, and mark duplicate reads. Independent variant calling was performed on the mapped reads with SAMtools (pipempileup, GATK UnifiedGenotyper, and Dindel. The GenomeComb program was used for annotating, comparing, and filtering the data. For de novo variant calling, the DeNovoGear program by Conrad and colleagues was used and double-checked by GenomeComb analysis.

Our analysis revealed a heterozygous de novo mutation in CHD2 (MIM 302119; RefSeq accession number NM_001271.3), encoding chromodomain helicase DNA binding protein 2 (CHD2; RefSeq NP_001262.3), in two out of nine probands. One individual carried a nonsense mutation, c.4971G>A (p.Trp1657*), in exon 38; the second person carried a splice-site mutation, c.1810–2A>C, affecting the splice acceptor site of exon 16. Presence or absence of the mutations was confirmed on genomic DNA of the probands or parents, respectively, by bidirectional Sanger sequencing using the ABI BigDye Terminator v.3.1 cycle sequencing kit on an ABI 3730xl automated DNA Analyzer (Applied Biosystems).

To obtain further genetic evidence of pathogenicity, we performed a mutation analysis of all 39 coding exons and intron-exon boundaries of CHD2 by using bidirectional sequencing (primer sequences are available upon request) in a cohort of 150 EE probands similar to the two individuals carrying a CHD2 mutation: all selected probands had infantile- or childhood-onset epilepsy with subsequent developmental delay. All individuals had normal brain MRI and at least one of the following seizure types: tonic-clonic seizures, myoclonic seizures, (atypical) absence seizures, or atomic seizures. In this cohort, we identified a third person carrying a de novo mutation in CHD2 (c.1396C>T [p.Arg466*]) in exon 13.

The two identified premature stop codons are predicted to result in degradation of the mutant transcript by means of nonsense-mediated mRNA decay (NMD). The effect of the splice-site mutation on transcript level is unclear, given that both exon skipping and (partial) intron retention are possible. Most likely, the splice acceptor mutation results in skipping of exon 16 and a subsequent out-of-frame

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deletion of exon 16, leading to a premature stop codon in exon 17 (p.Thr604Valfs2*). Therefore, NMD could also be active in this case. To test the NMD hypothesis, we extracted RNA from fresh blood (Qiagen RNeasy Micro Kit) of the three probands and a parent as a control individual, removed contaminated DNA by Ambion DNA-free DNase treatment (Life Technologies), and synthesized cDNA by Superscript III reverse transcriptase (Life Technologies). For the two nonsense mutations, we performed bidirectional sequencing on cDNA with primers flanking the mutation. With these experiments, we were able to detect the mutation with a 50/50 ratio, proving that the aberrant allele was not degraded by NMD. These results were confirmed by Sybr-Green-based quantitative PCR (qPCR) experiments (Sigma-Aldrich) with six primer pairs complementary to CHD2 cDNA (data not shown). For the splice-site mutation, we performed qPCR and developed sequencing primers flanking exon 16 on cDNA. Also here, qPCR showed the presence of both alleles. Additionally, the sequencing experiment showed an abundance of alternative splicing events in the probands compared to the control individual, but the consequence of the alternative splicing remained unknown. Although skipping of exon 16 appeared to be a logical consequence, additional investigations revealed more complex alternative splicing events. Whereas definite identification of all alternatively spliced transcripts was not possible, we were able to rule out NMD. We assumed that either the aberrant proteins were degraded by the proteasome or the shorter proteins were not fully functional; both of these cases would result in loss of function. In support of the pathogenicity of these mutations, none of the identified mutations have been observed in the 1000 Genomes Project, National Heart, Lung, and Blood Institute Exome Sequencing Project Exome Variant Server (EVS), or dbSNP (build 137). Furthermore, splice-site, frameshift, or nonsense variations are absent in the EVS and 1000 Genomes Project cohorts.

Between the age of 14 months and 3.5 years, the three persons carrying a de novo CHD2 mutation presented with febrile seizures followed by therapy-resistant generalized seizures (Table 1). Frequent myoclonic seizures, generalized tonic-clonic seizures (GTCSs), and absences were seen in all three individuals. Proband 1 developed normally during the first year of life. The first febrile seizure occurred when he was 14 months old and was soon followed by afebrile head drops occurring several times a day. When he was 2 years old, therapy-resistant myoclonic seizures, atypical absences, and GTCSs rarely associated with fever developed. On one occasion, he had a status epilepticus. Electroencephalography (EEG) showed generalized polyspike wave discharges and, later, focal epileptic discharges. He has been treated with valproic acid, levetiracetam, phenytoin, topiramate, bromide, phenobarbital, ethosuximide, topiramate, vitamin B6, and prednisolone. He now has moderate intellectual disability (ID), dystarthis, and ataxia. Proband 2 had a normal early development. At the age of 2 years, she had a cluster of febrile seizures followed by therapy-resistant generalized seizures. Frequent myoclonic seizures, GTCSs, and absences were seen in all three individuals. Proband 3 had a normal early development and a cluster of febrile seizures. Frequent myoclonic seizures, GTCSs, and absences were seen in all three individuals.
seizures. At the age of 2.5 years, she developed therapy-resistant absence seizures accompanied by eyelid myoclonias, myoclonic seizures, and febrile and afebrile GTCSs. EEG showed frequent generalized spike-wave complexes and polyspikes. She has been treated with vigabatrin, valproate, bromide, ethosuximide, lamotrigine, and levetiracetam and is currently taking a combination of topiramate and valproic acid. She still has afebrile GTCSs and moderate ID. Proband 3 had slightly delayed early motor and speech development, given that he walked at the age of 1.5 years and produced his first words at the age of 2 years. At the age of 3.5 years, he had two GTCSs during an episode of high fever. During the following 2 years, he had pharmacoresistant febrile and afebrile GTCSs, hemiconic, atonic, and myoclonic seizures, and atypical absences. He was treated with valproic acid, topiramate, and levetiracetam. After the start of clobazam at the age of 5.5 years, he became seizure free. EEG showed generalized (poly)spike-wave complexes. After seizure onset, a cognitive decline was seen but partially improved when seizures were controlled. He now has mild ID, autism spectrum disorder (ASD), attention deficit hyperactivity disorder, and mild ataxia. Brain MRI was normal in probands 1 and 2 and showed atrophic changes in proband 3.

In addition to our three individuals with a CHD2 mutation, one simplex case with ID and absence epilepsy and one simplex ASD case both carrying a mutation in CHD2 have been reported in the literature.\(^{14,15}\) Recently, two other research groups have also shown the involvement of CHD2 mutations in EEs.\(^{16,17}\) Furthermore, several individuals affected by ID and generalized epilepsy and carrying a multigenic chromosomal deletion of 15q26.2, including CHD2, have been described (Table 2).\(^{18-22}\) The presumed haploinsufficiency of CHD2 in these probands prompted us to screen all individuals without a previous detected mutation from both studied cohorts for copy-number variants in CHD2 with the multiplex amplicon quantification (MAQ) technique, an in-house-developed technique based on a semiquantified multiplex PCR. The multiplex PCR reaction consisted of six target amplicons located in the genomic region of CHD2 and four reference amplicons randomly located on different chromosomes. The MAQ analysis was performed as described previously.\(^{21}\) A partial or full deletion or duplication of the gene was not identified in any of the remaining studied persons (7 of the initial cohort and 149 of the second-stage cohort).

To establish additional evidence of the implication of CHD2 in the development of epilepsy, we examined the functional consequence of CHD2 haploinsufficiency by knocking down chd2 in zebrafish by using targeted morpholino (MO) antisense oligomers.\(^{24}\) All zebrafish experiments carried out were approved by the ethics committee of the University of Leuven (Ethische Commissie van de KU Leuven, approval number P05090) and by the Belgian Federal Public Service of Health, Food Chain Safety, and Environment (Federale Overheidsdienst Volksgezondheid, Veiligheid van de Voedselketen en Leefmilieu, approval number LA1210199). In order to mimic loss-of-function mutations, we designed a MO (E212 MO, 5′-GATCGAG CTTGCTTTTGTGACC-3′) to target the splice donor site of exon 2 and interfere with normal pre-mRNA splicing of zebrafish chd2 (ENSDART00000127730). Targeting of the exon 2-intron 2 boundary should result in abnormal exon 2 splicing, leading to its complete or partial deletion together with its flanking introns. This should result in an mRNA shorter than the wild-type transcript (Figure 1). A control MO (randomized 25 N oligomer) was used as a negative control (ctrl MO). All MOs were designed and synthesized by GeneTools. Gene knockdowns were achieved through microinjection of MOs into 1- to 2-cell-stage embryos from the AB (wild-type) strain according to the method previously described.\(^{25}\) In order to mimic haploinsufficiency, we titrated the amount of E212 MO to 9 ng per injection so as to reduce correctly spliced chd2 mRNA levels by approximately 50%. The same amount of ctrl MO was injected into sibling control embryos. To evaluate the level of knockdown in zebrafish embryos and larvae, we performed qPCR on splice-blocked pre-mRNA. Total mRNA was purified from each of 10 ctrl-MO- and E212-MO-injected embryos and larvae between 1 and 5 days postfertilization (dpf) with TRizol reagent (Life Technologies) according to the recommended protocol. Reverse transcription of 2 μg total RNA to single-stranded cDNA was performed with the High Capacity cDNA Reverse Transcription Kit (Applied Biosystems). The PCR reaction was performed with Phusion Polymerase (ThermoScientific) and chd2-specific primers (5′-AAGAGGCTCGACTCAA-3′ and 5′-TGCAAGGCTCCTTTGCTATA CTGC-3′) for detecting the amplicon with or without the partially deleted exon 2. PCR products were visualized with standard agarose gel electrophoresis. As expected, the ctrl MO did not have any effect on splicing and resulted in the predicted wild-type mRNA corresponding to a 384 bp PCR product (Figure 1). chd2 knockdown using the E212 MO resulted in two products: (1) a 384 bp band corresponding to the wild-type mRNA and (2) a shorter product (~300 bp) probably corresponding to an abnormally spliced mRNA, suggesting a partial knockdown. The discrepancy between the length of predicted (149 bp) versus observed (~300 bp) abnormally spliced mRNA was most likely a result of the activation of a cryptic splice site in exon 2 instead of splicing to the 5′ end of the upstream splice site (this could cause a partial deletion of exon 2). This abnormal product appeared after 1 dpf and was sustained until 5 dpf. Adult zebrafish (Danio rerio) of the AB strain (Zebrafish International Resource Center, Eugene) were maintained at 28.5°C on a 14/10 hr light/dark cycle under standard aquaculture conditions, and fertilized eggs were collected via natural spawning. Embryos were raised in embryo medium consisting of 1.5 mM HEPES, pH 7.6, 17.4 mM NaCl, 0.21 mM KCl, 0.12 mM MgSO\(_4\), and 0.18 mM Ca(NO\(_3\))\(_2\) in an incubator on a 14/10 hr light/dark cycle at 28.5°C. For all experiments described, larvae of 1–5 dpf were used.
**Table 2. Clinical Phenotype of Probands Reported in Literature with CHD2 Deletions or Mutations**

<table>
<thead>
<tr>
<th>Reference</th>
<th>Number of individuals</th>
<th>Genetic findings</th>
<th>Age at seizure onset</th>
<th>Seizure type at onset</th>
<th>Development prior to epilepsy</th>
<th>Developmental outcome</th>
<th>Other clinical findings</th>
<th>Fever sensitivity</th>
<th>EEG</th>
<th>MRI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Capelli et al.</td>
<td>1</td>
<td>de novo 0.5 Mb deletion including CHD2 and RGMA</td>
<td>2 years</td>
<td>CPSs</td>
<td>normal</td>
<td>globally delayed, severe speech impairment</td>
<td>ataxia, relative microcephaly, mild facial dysmorphisms</td>
<td>not specified</td>
<td>generalized spike waves and focal discharges</td>
<td>normal</td>
</tr>
<tr>
<td>Dhamija et al.</td>
<td>1</td>
<td>de novo 0.9 Mb deletion including CHD2 and three other genes</td>
<td>3.5 years</td>
<td>febrile generalized clonic SE</td>
<td>delayed</td>
<td>mild ID</td>
<td>microcephaly, short stature, mild facial dysmorphisms</td>
<td>yes</td>
<td>generalized spike waves</td>
<td>normal</td>
</tr>
<tr>
<td>Veredice et al.</td>
<td>1</td>
<td>de novo 5 Mb deletion including CHD2 and 55 other genes</td>
<td>6 months</td>
<td>two episodes of FSs</td>
<td>normal</td>
<td>normal</td>
<td>microcephaly, congenital hypothyroidism, bicuspid aortic valve, hyponatonia</td>
<td>yes</td>
<td>irregular generalized spike waves, PPR</td>
<td>normal</td>
</tr>
<tr>
<td>Li et al.</td>
<td>1</td>
<td>3.3 Mb deletion including CHD2 and 17 other genes (no segregation analysis)</td>
<td>not specified</td>
<td>atypical ASs, MSs</td>
<td>partial agenesis of vermis</td>
<td>mild to moderate ID, speech impairment</td>
<td>microcephaly, congenital dysmorphism</td>
<td>no</td>
<td>not specified</td>
<td>normal</td>
</tr>
<tr>
<td>Lund et al.</td>
<td>1</td>
<td>2 Mb deletion including CHD2 and seven other genes. Also carried five additional deletions and duplications, including a total of 100 genes (paternal DNA not available)</td>
<td>4 years</td>
<td>generalized slow spike waves and runs of fast spikes</td>
<td>delayed</td>
<td>severe ID</td>
<td>microcephaly, short stature, mild facial dysmorphism</td>
<td>not specified</td>
<td>generalized slow spike waves and runs of fast spikes</td>
<td>normal</td>
</tr>
<tr>
<td>Rauch et al.</td>
<td>1</td>
<td>de novo frameshift mutation c.1809 del (p.Thr604Leufs*19)</td>
<td>5 years</td>
<td>FSs, MSs, atypical ASs, GTCs, FSs, FDs</td>
<td>delayed</td>
<td>mild ID</td>
<td>microcephaly, congenital dysmorphism, bicuspid aortic valve, hyponatonia</td>
<td>not specified</td>
<td>generalized slow spike waves and runs of fast spikes</td>
<td>normal</td>
</tr>
<tr>
<td>Carvill et al.</td>
<td>6</td>
<td>four de novo frameshift and two de novo nonsense alterations: p.Glu1412Glyfs<em>64, p.Arg121</em>, p.Gly491Valfs<em>13, p.Arg1644Lysfs</em>22, p.Trp548Arg, p.Leu823Pro</td>
<td>1–3 years</td>
<td>therapy-resistant MSs with eyelid flutter, TSs, MSs, GTCs</td>
<td>delayed</td>
<td>normal or delayed</td>
<td>microcephaly, congenital dysmorphism, bicuspid aortic valve, hyponatonia</td>
<td>unknown</td>
<td>not specified</td>
<td>normal</td>
</tr>
<tr>
<td>Allen et al.</td>
<td>1</td>
<td>de novo splice mutation c.1502+1G&gt;A</td>
<td>6 months</td>
<td>one patient</td>
<td>normal</td>
<td>normal or delayed</td>
<td>microcephaly, congenital dysmorphism, bicuspid aortic valve, hyponatonia</td>
<td>no</td>
<td>generalized slow spike waves, slow spike waves, multifocal discharges, generalized paroxysmal fast activity, diffuse slowing</td>
<td>normal</td>
</tr>
</tbody>
</table>

**Abbreviations are as follows:** AS, absence seizure; AtS, atonic seizure; CPS, complex partial seizure; FDS, focal dyscognitive seizure; FS, febrile seizure; GTCs, generalized tonic-clonic seizure; HS, hemiclonic seizure; ID, intellectual disability; MA, myoclonic absence; MS, myoclonic seizure; NCS, nonconvulsive status epilepticus; PPR, photo paroxysmal response; SE, status epilepticus; and TS, tonic seizure.
E2I2-MO-injected larvae exhibited prominent morphological and behavioral alterations. The E2I2-MO-injected larvae showed from 2 dpf onward multiple developmental abnormalities: pericardial edema, microcephaly, body curvature, absent swim bladder, and stunted growth (Figure 2). The ctrl-MO-injected larvae were morphologically indistinguishable from the uninjected ones. Visual observation of chd2 knockdown larvae by means of high-magnification stereomicroscopy revealed that all 4 dpf larvae displayed abnormal movement patterns with frequent

Figure 1. chd2 Knockdown: E2I2 MO Causes Missplicing of Zebrafish chd2
(A) Schematic cartoon showing predicted splicing events in the pre-mRNA of chd2 E2I2-MO- and ctrl-MO-injected fish. The exons are represented by colored boxes (E1, E2, and E3), and the introns are represented by solid black lines (I1 and I2). The splice MO binding site (E2I2 MO) and the primer binding sites (P1 and P2) used for qPCR are indicated. According to the predictions, PCR products of 384 and 149 bp were expected for ctrl-MO- and E2I2-MO-injected larvae, respectively. In case of a partial knockdown, both products should be present.
(B) qPCR analysis of MO-knockdown larvae. Normal splicing in ctrl-MO-injected larvae resulted in the predicted 384 bp product, indicating the presence of wild-type mRNA. Abnormal splicing in E2I2-MO-injected larvae resulted in two products: 384 bp (corresponding to the wild-type mRNA) and ~300 bp (an abnormal mRNA), indicating partial knockdown. The larger-than-expected size of the PCR product could have been a result of the activation of a cryptic splice site. The aberrant mRNA was present from 1–5 dpf and was accompanied by the wild-type 384 bp fragment.

E2I2-MO-injected larvae exhibited prominent morphological and behavioral alterations. The E2I2-MO-injected larvae showed from 2 dpf onward multiple developmental abnormalities: pericardial edema, microcephaly, body curvature, absent swim bladder, and stunted growth (Figure 2). The ctrl-MO-injected larvae were morphologically indistinguishable from the uninjected ones. Visual observation of chd2 knockdown larvae by means of high-magnification stereomicroscopy revealed that all 4 dpf larvae displayed abnormal movement patterns with frequent

Figure 2. Representative Pictures of 4-Day-Old chd2 Knockdown and Control Larvae
chd2 E2I2-MO-injected larvae displayed pericardial edema, microcephaly, body curvature, absent swim bladder, and stunted growth (A). Ctrl-MO-injected (B) and uninjected (C) larvae developed normally. The experiment was performed at least three times with 100 embryos injected per condition.
whirlpool-like events. Occasionally, we also noticed pectoral-fin and jaw twitching and whole-body trembling. To confirm whether this behavior could have been a result of seizure activity, we performed field-potential recordings on larval tecta as described previously.\textsuperscript{26} Already from 4 dpf, E2I2-MO-injected larvae displayed epileptiform discharges (Figure 3). Discharges consisted of multiple upward spikes of amplitudes several times larger than those of ctrl-MO-injected or uninjected larvae and with occasional ictal-like patterns. This spiking pattern resembled preictal discharges observed in immature hippocampi of a mouse model of temporal lobe epilepsy.\textsuperscript{27} These experimental findings suggest that loss of CHD2 results in an epilepsy phenotype.

CHD2 encodes CHD2, a protein that does not have an established link to neuronal function or hyperexcitability. CHD proteins are assumed to modify gene transcription by affecting chromatin structure through helicase function. A Chd2-deficient mouse model has been reported to show spinal abnormalities, renal dysfunction, growth retardation, and susceptibility to tumors, but not epileptic seizures.\textsuperscript{28,29} None of the features described in the mouse model were seen in the probands with de novo CHD2 mutations, suggesting that in contrast to the zebrafish model presented here, the existing mouse model insufficiently replicates the human phenotype. On the other hand, in addition to showing electrographic seizures observed in zebrafish chd2 knockdowns, these larvae displayed edemas, body curvature, and stunted growth that could be considered equivalent to the cardiovascular and renal defects, lord kyphosis, and postnatal stunted-growth phenotypes described in Chd2 mouse mutants.\textsuperscript{28,30,31} Thus, the zebrafish phenocopies aspects of both the human and the mouse spectra. Why no seizure phenotype has been reported for Chd2 mutant mice remains to be determined. Perhaps these mice have to be monitored with EEG for seizure detection and/or challenged before (presumably) spontaneous seizure behavior can be detected. Additionally, mutations in other genes encoding members of the CHD family have been identified, such as CHD7 mutations in persons with CHARGE syndrome\textsuperscript{32} and de novo mutations in CHD3, CHD7, and CHD8 in individuals with ASD.\textsuperscript{33,34} Although the exact role of CHD2 in neuronal hyperexcitability remains to be determined, our findings suggest that helicase dysfunction might be a mechanism involved in epileptogenesis and neurodevelopment.

In summary, we identified CHD2 nonsense mutations as the underlying genetic defect for a fever-sensitive myoclonic EEG. In our study, individuals carrying a CHD2 mutation displayed a spectrum of fever-sensitive generalized seizures similar to those in Dravet syndrome, but seizure onset was clearly later, and unlike in Dravet syndrome, developmental delay could be seen prior to epilepsy onset. Future studies will reveal whether CHD2 mutations also account for a subset of individuals with more typical Dravet syndrome. We showed that a MO-based knockdown of chd2 in zebrafish resulted in clinical and electrographic seizures paralleling the human phenotype. Our study further suggests that helicase dysfunction in humans might specifically result in neuronal hyperexcitability in the absence of syndromic or dysmorphic features.

Consortia

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Web Resources

The URLs for the data presented herein are as follows:

1000 Genomes Project, http://www.1000genomes.org
Beyond the Ion Channel (EuroEPINOMICS blog), http://channelopanlist.net
Decipher, http://decipher.sanger.ac.uk
DeNovoGear, http://sourceforge.net/projects/denovogear
Dindel, http://www.sanger.ac.uk/resources/software/dindel
Genome Analysis Toolkit (GATK), http://www.broadinstitute.org/gatk/
Multiplex Amplicon Quantification (MAQ), http://www.multiplicom.com/multiplex-amplicon-quantification-maq

References


