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Abstract

Dravet syndrome is devastating infantile-onset epilepsy, often accompanied by severe intellectual disabilities, hyperactive behavior, autistic traits, and ataxia. The discovery in 2001 of the SCN1A mutation as a primary cause of this syndrome has accelerated our understanding of the pathophysiological processes underlying Dravet syndrome. SCN1A mutations are genetically heterogeneous, and the forebrain may be involved in the seizure susceptibility, fever sensitivity of seizures, premature death, and autistic traits characteristic of Dravet syndrome. More recently, human cellular models of Dravet syndrome have been established using patient-derived induced pluripotent stem cells (iPSCs) from three groups including ours. By taking advantage of these human disease models, functional vulnerabilities in GABAergic neurons have been revealed. Here, we review recent advances in Dravet syndrome research, particularly focusing on the development of iPSC models, and their future directions.

Keywords Epilepsy; -aminobutyric acid; Disease modeling; Genetics; Induced pluripotent stem cells; Mechanism; Mouse model; SCN1A

Abbreviation: DS: Dravet Syndrome; GABA: -amino Butyric Acid; iPSCs: Induced Pluripotent Stem Cells

Introduction

Dravet syndrome (DS) is a devastating epilepsy syndrome, which was first described by Dr. Charlotte Dravet in 1978 [1]. Generalized or unilateral clonic seizures appear in previously healthy infants, and are frequently associated with fever [2]. These seizures tend to evolve into status epilepticus and occur frequently especially during the early phases of DS. Other seizures, including focal, absence, and myoclonic seizures appear later. Seizures are refractory to most currently available treatments, and severe intellectual disabilities develop after seizure onset, often accompanied by hyperactive behavior and autistic traits. Ataxia worsens with age, resulting in significant gait disturbance. Furthermore, 10–20% of the affected children experience premature death [3,4]. Thus, the development of new treatment is urgently needed.

Mutations in the SCN1A gene in patients with DS were first reported in 2001 [5]. Subsequent studies supported the hypothesis that the SCN1A defect is the primary cause of DS [6,7]; these findings have triggered a number of studies attempting to uncover the pathogenic mechanisms underlying DS. These studies have employed electrophysiological functional analysis of forcedly expressed Na_v1.1 mutants [8,9], mouse models based on heterozygotes or knock-out/knock-in mouse [10,11], and more recently, human cellular models using patient-derived induced pluripotent stem cells (iPSCs) [12–14]. First, we briefly review previous research on DS and then describe our recent research on generating an iPSC model for DS.

Genetic alteration in SCN1A

SCN1A encodes the α -subunit of the voltage-gated sodium channel Na_v1.1 (Figure 1) [15]. Abnormalities in the SCN1A gene were first reported in patients with genetic epilepsy febrile seizures plus (GEFS+) [15], and have been also identified in patients with other clinical phenotypes, including cryptogenic focal/generalized epilepsies [16].

However, DS is the primary phenotype in which a robust correlation with SCN1A defects has been confirmed [17,18]: 70–80% of patients with DS carry SCN1A abnormalities [19,20].

Nearly 700 mutations in the SCN1A gene that are associated with DS have so far been identified [21], and most of them are novel. These mutations include nonsense, missense, splice site, and frameshift mutations, and are distributed throughout the gene. Specific genotype–phenotype correlations remain unclear, but truncation mutations, harbored by half of the patients with DS, appear to be associated with a more severe phenotype than missense mutations [22]. Exonic or micro chromosomal deletions involving SCN1A or its promoter region have also been identified in patients with DS [23–27]. Other genes potentially associated with DS or similar phenotypes include SCN1B [28], SCN2A [29], GABRG2 [30], and PCDH19 [31,32]. However, mutations in the former three occur rarely, and only a minority of patients with PCDH19 mutations present with the DS phenotype [33,34].

Functional alterations of mutated Na_v1.1

Electrophysiological studies examining the functions of mutated Na_v1.1 channels expressed in HEK293 or tsA-201 cells have revealed that many of the DS-associated missense mutations result in an non-functional sodium channel [8,9,35,36], and this loss-of-function of the channel may be associated with DS. One study revealed that expressed

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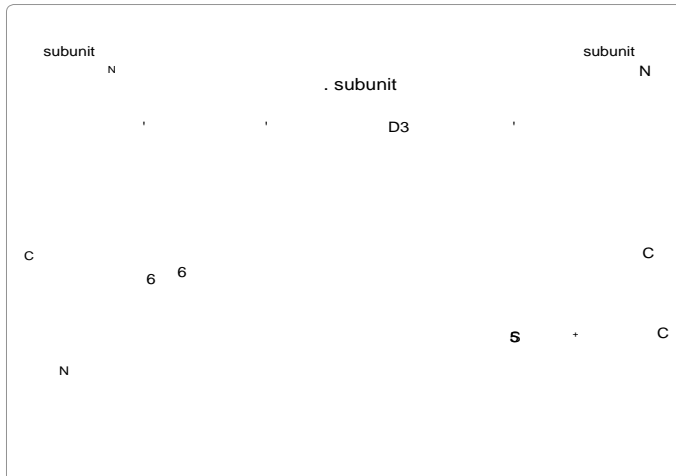


Figure 1: Na_v1.1 architecture and the location of the patient's mutation. Na_v1.1 is composed of four subunits (S1-S4) and linker regions (L1-L4). The patient's mutation (R1645*) is located in the D4/S4 region (white star). The mutation terminates at the R1645 residue, leading to a truncated protein.

heterozygous knock-out/knock-in mice were also prone to premature death [10,11].

Conditional SCN1A knock-out, which was achieved by the Cre-mediated heterozygous deletion of exonic regions, helped elucidate the brain region responsible for some of the major clinical features of DS [41]. Specifically, Dlx1/2-enhancer-driven Cre deleted Scn1a in the mouse forebrain GABAergic interneurons [42]. These mice exhibited spontaneous seizures, temperature-dependent seizure susceptibility, premature death, and autistic traits [43], as was observed in mice with global SCN1A deletion. Kalume, et al. made an extremely interesting observation regarding the mechanisms of sudden unexpected death during tonic-clonic seizures [44]: the mice that died had increased seizure frequency and ictal bradycardia, which could be ameliorated by atropine, suggesting that an increase in parasympathetic activity occurs. SCN1A knock-out in the heart did not affect heart rate.

In the global knock-in and the conditional knock-out mice, administration of drugs that act to enhance GABAergic transmission, such as clonazepam, diazepam, or stiripentol ameliorated the seizures and behavioral impairments [43,45,46], supporting the notion that dysfunction of GABAergic interneurons is involved in the symptoms described above.

Human-Based Cellular Models for DS Developed Using Patient-Derived iPSCs

Generation of DS patient-derived iPSCs

Because it remains unclear whether mouse models faithfully reproduce the pathology occurring in the patient's brain, it is desirable to study patient's neurons directly. After the development of human iPSCs by Yamanaka et al. in 2007 [47], many neurological diseases have been modeled using patient-derived iPSCs [48-53], and pathogenic mutations have been identified in their differentiated neurons. Until recently, however, no such effort has been reported for epilepsy.

We recently generated two lines of iPSCs (D1-1 and D1-6) from a female patient with a core DS phenotype, who harbors a nonsense mutation in SCN1A (p.R1645*, Figure 1) [12]. Reprogramming factors (Sox2, Klf4, Oct3/4, and c-Myc) were retrovirally transduced into the skin fibroblasts, which were biopsied from her upper arm at the age of 29 years. The generated iPSCs displayed undifferentiated status and pluripotency, harbored the patient's mutation in their SCN1A gene, and could be efficiently and reliably differentiated into neuronal cells. Neuronal differentiation from the iPSCs was performed using a method established by Okada et al. [54] with a slight modification, in which a month of embryoid body formation is followed by 3-5 weeks of neurosphere formation. Terminal differentiation into mature neurons was achieved by adherent culture of dissociated or undissociated neurosphere cells. For control experiments, we used 201B7, an iPSC line that was developed from a healthy female [47].

Functional Vulnerabilities in Patient iPSCs-Derived GABAergic Neurons

Because iPSCs-derived neurons obtained by the method described above are highly heterogeneous with regard to their neuronal subtypes and maturities, it is critical to analyze only one specific type of neuron at a defined level of maturity in order to determine whether the neurons are actually pathologic. As a first step to overcoming these difficulties, we generated a lentiviral reporter for SCN1A expression for electrophysiological assays; this harbors one main SCN1A promoter sequence [26], followed by a 5'-untranslated exon

truncated human Na_v1.1 (hNa_v1.1) did not affect the channel function of co-expressed wild-type human hNa_v1.1, hNa_v1.2, hNa_v1.3, or hNa_v1.6 [37]. It is also true that SCN1A abnormalities in DS frequently include truncation mutations (mainly nonsense mutations) and gene deletions, while there is little evidence showing that the truncated hNa_v1.1 protein is expressed associated with nonsense mutations. Nonsense mutations of SCN1A gene could result in nonsense-mediated mRNA decay. Collectively, it is tempting to speculate that haploinsufficiency may be an underlying mechanism of DS. However, some missense mutations were found to induce gain-of-function of hNa_v1.1 by way of activating sodium currents because of impairments in fast inactivation mechanisms [9]. It seems likely that the functional basis of SCN1A abnormalities related to DS may be more complex.

Dysfunction of GABAergic Interneurons in Mouse DS Models

Yu et al. first reported a mouse DS model based on Scn1a knock-out in 2006 [10], which exhibited spontaneous seizures, temperature-dependent seizure susceptibility [38], and ataxia [39]. They examined Na_v1.1 expression in the hippocampal GABAergic interneurons, and found a reduced sodium current density and impaired action potential generation in those neurons of Scn1a and Scn1a^{fl/fl} mice compared to wild-type mice, while these were normal in the pyramidal neurons. Reduced sodium current density was also confirmed in the Purkinje neurons of these animals [39]: this reduced current density may be involved in the ataxia associated with DS. Ogiwara et al. identified a parvalbumin-positive subgroup of GABAergic interneurons, which directly regulates the excitation of pyramidal neurons, as the primary type of Na_v1.1-expressing neurons in the neocortex and hippocampus [11]; moreover, intense Na_v1.1 expression was identified in their axon initial segments. The researchers generated Scn1a knock-in mice with the R1407* mutation, which exhibited spontaneous seizures, autistic traits, and cognitive decline [40], and impaired action potential generation in their neocortical GABAergic interneurons. These SCN1A promoter sequence [26], followed by a 5'-untranslated exon

from iPSCs will facilitate the elucidation of key pathophysiological mechanisms and critical therapeutic targets in human patients with DS.

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