ORIGINAL ARTICLE

SCN9A Epileptic Encephalopathy Mutations Display a Gain-offunction Phenotype and Distinct Sensitivity to Oxcarbazepine

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Abstract Genetic mutants of voltage-gated sodium channels (VGSCs) are considered to be responsible for the increasing number of epilepsy syndromes. Previous research has indicated that mutations of one of the VGSC genes, SCN9A (Nav1.7), result in febrile seizures and Dravet syndrome in humans. Despite these recent efforts, the electrophysiological basis of SCN9A mutations remains unclear. Here, we performed a genetic screen of patients with febrile seizures and identified a novel missense mutation of SCN9A (W1150R). Electrophysiological characterization of different SCN9A mutants in HEK293T cells, the previously-reported N641Y and K655R variants, as well as the newly-found W1150R variant, revealed that the current density of the W1150R and N641Y variants was significantly larger than that of the wild-type (WT) channel. The time constants of recovery from fast inactivation of the N641Y and K655R variants were markedly

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lower than in the WT channel. The W1150R variant caused a negative shift of the G–V curve in the voltage dependence of steady-state activation. All mutants displayed persistent currents larger than the WT channel. In addition, we found that oxcarbazepine (OXC), one of the antiepileptic drugs targeting VGSCs, caused a significant shift to more negative potential for the activation and inactivation in WT and mutant channels. OXC-induced inhibition of currents was weaker in the W1150R variant than in the WT. Furthermore, with administering OXC the time constant of the N641Y variant was longer than those of the other two SCN9A mutants. In all, our results indicated that the point mutation W1150R resulted in a novel gainof-function variant. These findings indicated that SCN9A mutants contribute to an increase in seizure, and show distinct sensitivity to OXC.

Keywords Voltage-gated sodium channel · SCN9A · Epilepsy - Electrophysiological function - Oxcarbazepine - Sensitivity

Introduction

The voltage-gated sodium channel (VGSC) plays a notable role in the generation and propagation of the action potentials in neurons [[1\]](#page-12-0). It has been reported that VGSCs are genetically mutated in epileptic patients as well as animal models $[2-5]$ $[2-5]$. The VGSC subtype Nav1.7 is encoded by SCN9A, which is well known to be involved in the generation, development, and maintenance of pain responses [[6,](#page-13-0) [7\]](#page-13-0). Nav1.7 is preferentially expressed in the peripheral nervous system [[8–10\]](#page-13-0) and dynamically expressed in the central nervous system, including the cerebral cortex and hippocampus [\[11](#page-13-0)]. Furthermore, it has

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been determined that the gain-of-function mutants of SCN9A are involved in neuropathic pain, such as in inherited erythromelalgia, paroxysmal extreme pain disorder, and fibrotic neuropathy, whereas the loss-of-function mutants of SCN9A can lead to an indifference to pain [\[12–14](#page-13-0)]. One noteworthy finding showed SCN9A mutants in 21 individuals in a family suffering from febrile seizures [\[15](#page-13-0)]. A missense mutation of *SCN9A* (N641Y), a conserved amino-acid residue located at the intracellular loop between domains I and II of the VGSC protein, was detected in a pedigree with febrile seizures and regarded as a gain-of-function mutation. Mice carrying the SCN9A-N641Y mutation are more susceptible to clonic and tonic seizures induced by electrical stimulation [[16\]](#page-13-0). When SCN9A was sequenced in 92 unrelated patients with childhood seizures occurring during febrile illness, an associated missense mutation (K655R) was found [[17\]](#page-13-0). In addition, in an analysis of a cohort of 109 patients with Dravet syndrome, nine were identified with eight different SCN9A mutations, including K655R [[16\]](#page-13-0). Collectively, these data confirm that SCN9A missense mutations are disease-causing for febrile seizures and Dravet syndrome. Interestingly, several SCN9A mutants either act as modifiers in the presence of stronger mutants or cause mild seizures by themselves, some of which also harbor splice site or missense mutations in SCN1A [\[17](#page-13-0)]. Interestingly, a few of the pathogenic SCN9A mutants with or without SCN1A mutations have been identified in epileptic patients [\[18](#page-13-0), [19](#page-13-0)]. It is thus worthwhile to delve into the molecular mechanism by which SCN9A variants induce epileptic seizures.

Oxcarbazepine (OXC) is one of the novel anti-epileptic drugs used to control tonic-clonic seizures. It is generally well-tolerated and has a more predictable dose-response relationship than carbamazepine. One report indicates that OXC most likely has a greater effect than carbamazepine in reducing serum $Na⁺$ levels, particularly at higher doses [\[20](#page-13-0)]. Moreover, it has been reported that OXC inhibits abnormal neuronal firing by targeting of voltage-dependent $Na⁺$ channels, and reduces the excitatory synaptic trans-mission [[21\]](#page-13-0).

In this study, we set out to investigate the molecular mechanism of SCN9A in the generation of epilepsy. To do so, we performed a genetic screen of children with febrile seizures, and identified a novel SCN9A missense variant: W1150R. We then determined the electrophysiological characteristics of the variants W1150R, N641Y, and K655R and also tested the sensitivity of three gain-offunction SCN9A variants to OXC.

Materials and Methods

Mutation Screening

Genomic DNA was extracted from peripheral blood with kit (DP348, Tiangen, Beijing, China). The samples were assessed by Shanghai Biotechnology Corp., China. SCN9A variants were examined in children with febrile seizures by whole-exome sequencing. This study was approved by the Institutional Review Board at Putuo District Center Hospital, Shanghai (Putuo Hospital, Shanghai University of Traditional Chinese Medicine). And informed consent was given by the parent or guardian.

Site-Directed Mutagenesis of SCN9A (hNav1.7) Plasmids

Three individual point-mutations (N641Y, K655R, and W1150R) were constructed. Each amino-acid substitution was introduced into the pEZ-Lv206-hNav1.7 plasmid using a Hieff MutTM Site-Directed Mutagenesis Kit (11004ES10, Yeasen, Shanghai, China) according to the manufacturer's protocol. The constructs were verified by resequencing before transfection into HEK293T cells.

Homology Modelling

An alignment of the top 48 sequences most similar to SCN9A was conducted using PSI-BLAST (Discovery Studio 2017 R2, Neotrident, Shanghai, China). The cryo-EM structure of the electric eel Nav1.4 (PDB ID 5XSY) [\[22](#page-13-0)] served as the structural template to construct wild-type and W1150R homology models of hNav1.7, using the MODELER. MODELER selected the optimal model based on probability density function (PDF) or discrete optimized protein energy (DOPE) values. When the PDF of the total energy of a structural model is the same, the DOPE score, based on the atomic statistical potential energy, can be used as a basis for measuring the quality of the model.

Cell Transfection

HEK293T cells were grown in a humidified atmosphere of 5% $CO₂$ and 95% air at 37 °C in Dulbecco's modified Eagle's medium (Invitrogen, CA) supplemented with 10% fetal bovine serum (Invitrogen), then seeded in 24-well plates 24 h before transfection. Wild-type pEZ-Lv206 hNav1.7 plasmids or mutants were transfected into HEK293T cells together with pIRES-EGFP-h β 1 using Lipofectamine 3000 (Invitrogen) with 4 µg of plasmids and 1 μ g pIRES-EGFP-h β 1 according to the manufacturer's

instructions. Electrophysiological recordings from fluorescent cells were made 48 h after transfection.

Chemicals and Solutions

OXC from Sigma (Poole, UK) was dissolved in extracellular solution containing 1% dimethyl sulfoxide at 120 μ mol/L [[23,](#page-13-0) [24\]](#page-13-0).

Electrophysiological Recording

The patch clamp recordings were performed at room temperature using EPC-10USB (HEKA Elektronik, Germany). Data were acquired and analyzed using Patchmaster (HEKA Elektronik). Cells recognized by the marker genes Cherry (pEZ-Lv206-hNav1.7) and GFP (pIRES-EGFP $h\beta1$) were chosen for patch clamp recording. The solutions used for whole-cell voltage clamp recording were: extracellular solution (in mmol/L): 140 NaCl, 2 CaCl₂, 2 MgCl₂, 10 HEPES, and 10 D-glucose, pH 7.3 with NaOH (320 mOsm adjusted with D-glucose); and intracellular solution (in mmol/L): 140 CsF , 10 CsC , 2 MgC , 10 EGTA, 10 HEPES, pH 7.3 with CsOH, osmolality adjusted to 310 mOsm with D-glucose. The patch pipettes had resistances of 2 M Ω –5 M Ω when filled with pipette solution. Cells were held at -120 mV in all experiments. When voltage errors were used with 80% series resistance compensation, this cell can be used for data statistics.

The peak currents were determined using 100-ms pulses from -100 mV to $+75$ mV in 5-mV steps from a holding potential of -120 mV at 5-s intervals. The peak current was normalized for cell capacitance, and plotted against voltage to generate the peak current density–voltage relationship. Conductance as a function of voltage was obtained from the current–voltage relationship: $G(V)$ = $I(V)/(V - Er_{Na})$ and fitted by the Boltzmann function: $G = I/(1 + \exp[(V - V_{1/2})/K])$ to determine the voltage midpoint $(V_{1/2})$ and slope factor (K) . For steady-state inactivation, cells were held at -140 mV and the test potential was from -140 mV to 20 mV for 600 ms at 10-mV increments. A second pulse to -10 mV for 50 ms was used to assess channel availability. The normalized current was plotted against voltage, and steady-state inactivation curves were also fitted with the Boltzmann equation as above to determine the voltage midpoint $(V_{1/2})$ and slope factor K. To generate fast inactivation curves, cells were stepped to inactivating potentials from $- 140$ mV to 20 mV for 60 ms followed by a 50-ms step $to - 10$ mV as the second pulse. The fast inactivation peak current was normalized by maximum current amplitude, and fitted by Boltzmann function as above to determine the voltage midpoint $(V_{1/2})$ and slope factor K. For recovery from inactivation, cells were held at -120 mV and depolarized to a test potential of 0 mV for 50 ms to inactivate $Na⁺$ channels. Recovery was determined at times between 2 ms and 40 ms with a test potential of $- 140$ mV. A 50-ms pulse to $- 10$ mV was subsequently applied to assess the extent of channel recovery. Peak current was normalized by maximum current amplitude and fitted with a single exponential function: $III_{\text{max}} = A$ $[1 - \exp(-t/\tau_{\text{rec}})]$ to determine the time constant τ .

For experiments including the testing of OXC, electrophysiological protocols under control, drug-free conditions were obtained before bath application of OXC (120 µmol/ L, 5 min).

Statistical Analysis

Data were analyzed with OriginPro 8.5 (OriginLab, CA), Excel 2016 (Microsoft, WA) and Prism 6 (GraphPad software, San Diego, CA). Data are presented as the mean \pm standard error of the mean (SEM). Student's *t*-test or one-way ANOVA was used to assess the statistical significance of differences. When $P < 0.05$, differences were accepted as significant.

Results

Identification of an Identical De Novo Variant in SCN9A (hNav1. 7) from a Patient with Febrile Seizures

We identified a novel variant $c3488T > C$ [p.(W1150R)] in a patient with febrile seizures. The patient presented at age 2 with complex focal seizures with secondary generalization. The patient's first seizure (generalized tonic-clonic seizure for 5 min) developed with fever (38.6 \degree C). The EEG showed high-potential spike activity, paroxysmal release, and δ frequency power enhancement. At age 3, seizures occurred 4 times with fever (38 $^{\circ}$ C–39.5 $^{\circ}$ C), the longest lasting 10 min. The patient had no pain or malnutrition. Growth and mental development were the same as his peers. His grandfather had a history of febrile seizures but there was no additional family history of epilepsy.

We determined that the location of amino-acid W1150 was in the domain II/III cytoplasmic linker of Nav1.7 (Fig. [1A](#page-3-0)). A previous study already reported that two mutants (N641Y and K655R) are located in the domain I/II cytoplasmic linker of Nav1.7 [\[16](#page-13-0)] (Fig. [1](#page-3-0)A). Therefore, we constructed three plasmids: SCN9A-N641Y, SCN9A-K655R, and SCN9A-W1150R (Fig. [1](#page-3-0)B).

Fig. 1 Location and sequencing of the SCN9A variants. A Predicted transmembrane topology of SCN9A depicting the location of the variants. The S4 segments are voltage sensors and marked with plus

Activation Properties of hNav1.7 Variants

Homology modeling revealed that the hNav1.7 mutation W1150R altered the α -helix of the S1 segment in domain III (Fig. [2](#page-4-0)). Representative currents of hNav1.7 and variants co-expressed with $h\beta1$ subunits in HEK293T cells are illustrated in Fig. [3A](#page-5-0). The average peak current

signs. B DNA sequencing identified the mutations in the constructed pEZ-Lv206-hNav1.7 plasmid. The mutation sites are marked by a red squares.

density–voltage relationships were measured from cells transiently expressing mutants or hNav1.7 (Fig. [3B](#page-5-0)). We measured the peak current densities of the three variants and found that those of the W1150R and N641Y variants were significantly larger than that of the WT channel (WT, $- 109.5 \pm 10.4$ pA/pF, $n = 11$; N641Y, $- 183.4 \pm 16.9$ $pA/pF, n = 16, P < 0.01; W1150R, - 159.1 \pm 15.1 \text{ pA/pF},$

Fig. 2 W1150R mutation affects the α -helix of the S1 segment in domain III. A, B Schematics of the backbone structure of the wild-type and mutated domains. C–E Stick diagrams of the S1 segment of domain III of the wild-type and W1150R mutant. Black, W1150; magenta, W1150R.

 $n = 8, P < 0.05$; Table [1](#page-6-0)). However, the current density of the K655R variant did not significantly differ from WT channels (K655R, $- 134.4 \pm 12.2$ $- 134.4 \pm 12.2$ $- 134.4 \pm 12.2$ pA/pF, $n = 10$; Table 1). Using statistical analysis, we also found a large hyperpolarizing shift of the G–V curve for the voltage-dependence of steady-state activation that occurred in the W1150R variant $(V_{1/2}$ $(V_{1/2}$ $(V_{1/2}$ by -4.3 -4.3 mV; $n = 12, P < 0.05$; Fig. 3C, D, Table 1). On the contrary, the N641Y and K655R variants presented a marked depolarizing shift of the G–V curve (Fig. [3](#page-5-0)C, D). The

 $V_{1/2}$ values for the N641Y and K655R variants were $- 15.0 \pm 0.6$ mV and $- 16.0 \pm 1.8$ mV, respectively (Table [1\)](#page-6-0). There was no difference in the slope factor (K) for any of the mutants when compared with the control group (Fig. [3E](#page-5-0), Table [1\)](#page-6-0). The transition from the open to the inactivated state was delayed in the W1150R variant at depolarizing voltages ranging $+20$ mV and $+70$ mV (Fig. [3F](#page-5-0)), but in the K655R variant the transition was delayed between $+20$ mV and $+40$ mV. As for the

Fig. 3 Steady-state activation of SCN9A variants and hNav1.7. A Average $Na⁺$ current traces recorded from HEK293T cells coexpressing pEZ-Lv206-hNav1.7 and pIRES-EGFP-h β 1 plasmids. B Average current density–voltage relationship. Peak currents were normalized to cell capacitance. C Voltage-dependence of steady-state activation of WT and variants. Curves are Boltzmann fits of the data. **D** Scatter plots of voltage at half-maximal steady-state activation $(V₁)$

2) for WT and variants. E Scatter plots of the slope factor of activation (K). **F** Average fast time constants (τ) from single exponential fits to macroscopic current decays as a function of voltage. G Magnitude of persistent current as a percentage of the peak current at -10 mV. Data are the mean \pm SEM. *P < 0.05, **P < 0.01, ***P < 0.001. Black, WT; red, N641Y; blue, K655R; magenta, W1150R.

N641Y variant, the open time was unchanged. The persistent current generated by the three variants was greater than that of the WT channel, measured as a percentage of the peak current (N641Y = $2.9\% \pm 0.2\%$, $n = 16$, $P < 0.01$; K665R = 3.0% \pm 0.5%, $n = 9$, $P < 0.05$; W1150R = 3.2% \pm 0.4%, n = 13, P < 0.01; $WT = 1.8\% \pm 0.3\%, n = 15; Fig. 3G.$

Characterization of the Inactivation of hNav1.7 Variants

To assess the voltage-dependence of steady-state inactivation and fast inactivation, cells expressing the WT and variants were tested. Compared to WT channels, there was no significant difference in any of the mutants regarding the half-maximal voltage-dependence of steady-state inactivation (WT: $V_{1/2} = -67.0 \pm 0.5$ mV, $n = 16$; N641Y: $V_{1/2} = -64.3 \pm 1.3 \text{ mV}, \quad n = 20; \quad \text{K655R:} \quad V_{1/2}$ $=$ - 66.1 \pm 0.8 mV, $n = 18$; W1150R: $V_{1/2} =$

*P $\lt 0.05$, **P $\lt 0.01$, ***P $\lt 0.001$, unpaired Student's t-test.

* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, unpaired Student's t-test.

 $- 65.4 \pm 1.1$ $- 65.4 \pm 1.1$ $- 65.4 \pm 1.1$ mV, $n = 14$; Fig. 4A, B, Table 1). Notably, only the slope factor of the N641Y variant was increased $(n = 20, P < 0.05;$ Fig. 4C, Table [1](#page-6-0)). There were no statistical differences in the average fits for fast inactivation for the variants compared to the WT channels (WT: $V_{1/2}$ $2 = -34.8 \pm 0.7 \text{ mV}, K = 8.2 \pm 0.4, n = 24; N641 \text{Y}: V_{1/2}$ $2 = -33.0 \pm 1.0 \text{ mV}, K = 7.2 \pm 0.4, n = 20; K655R: V_{1/2}$ $n_2 = -33.7 \pm 1.0$ mV, $K = 8.1 \pm 0.5$, $n = 26$; W1150R:

 $V_{1/2} = -33.5 \pm 1.3$ mV, $K = 7.6 \pm 0.7$, $n = 17$; Fig. 4D–F, Table [1\)](#page-6-0).

Recovery Properties of hNav1.7 Variants

We also examined the kinetic correlations between the recovery and inactivation of the WT and variants. The time constant of recovery from inactivation for the W1150R variant (2.1 \pm 0.2 ms, n = 12) was similar to that of the

Fig. 4 Inactivation and recovery from inactivation of SCN9A variants and hNav1.7. A Voltage-dependence of steady-state inactivation of WT and variants. Curves are Boltzmann fits of the data. B Scatter plots of voltage at half-maximal steady-state inactivation $(V_{1/2})$ for WT and variants. C Scatter plots of the slope factor of steady-state inactivation (K) . **D** Voltage-dependence of fast inactivation of WT and variants. Curves are Boltzmann fits. E Scatter plots of $V_{1/2}$ for

WT and variants. F Scatter plots of K. G Voltage dependence of recovery from inactivation of WT and variants. Curves are single exponential fits of the data. H Scatter plots of the time constant of recovery from inactivation of WT and variants. Data are the mean \pm SEM. $*P < 0.05$, $*P < 0.01$. Black, WT; red, N641Y; blue, K655R; magenta, W1150R.

WT channel $(1.8 \pm 0.2 \text{ ms}, n = 10)$. The values for the other variants were significantly lower (N641Y: 1.3 ± 0.1 ms, $n = 8$, $P < 0.05$; K655R: 1.4 ± 0.1 ms, $n = 17, P < 0.05$ $n = 17, P < 0.05$ $n = 17, P < 0.05$) (Fig. [4](#page-7-0)G, H and Table 1).

Influence of Temperature on the Activation of hNav1.7 and the W1150R Variant

We determined the effects of temperature on the activation of hNav1.7 and the W1150R variant. The $V_{1/2}$ for the WT channel did not differ from the room temperature group [WT (25 °C): $V_{1/2} = -19.36 \pm 1.567$ mV, $n = 15$; WT (38 °C): $V_{1/2} = -21.42 \pm 1.072$ mV, $n = 19$; Fig. 5A, B]. The W1150R variant had a large hyperpolarizing shift of the G–V curve for the voltage-dependence of steadystate activation when the temperature was raised $(V_{1/2}$ by $- 4.7$ mV; $n = 7$, $P < 0.05$; Fig. 5C, D).

Effects of OXC on the Activation of hNav1.7 Variants

Representative currents from steady-state activation and those after treatment with OXC are shown in Fig. [6A](#page-9-0). At 120 µmol/L, tonic block by OXC was significantly greater for the K655R (66.55% \pm 3.4%; n = 7) than for the WT currents $(55.23\% \pm 3.4\%, n = 12, P < 0.05)$ (Fig. [6B](#page-9-0)). That of the N641Y variant $(56.26\% \pm 3.5\%, n = 10)$ was similar to the WT channel. However, the tonic block by OXC was significantly weaker for the W1150R $(41.38\% \pm 3.2\%; n = 10, P < 0.01)$ than for the WT currents. With the use of OXC $(120 \mu mol/L)$, a tendency of negative shift for the G–V curve of steady-state activation occurred in the WT and variants. The difference between the half-maximal voltage values before and after OXC was significant in the N641Y variant compared to the others $(V_{1/2}$ by -7.6 mV, $P < 0.001$) (Fig. [6C](#page-9-0)–F). The slope (K) was constant for all variants (Table [2\)](#page-6-0). There was an apparent shortening in the time from the open to the inactivation state in the N641Y variant at depolarizing voltages ranging $+20$ mV and $+40$ mV (Fig. [7](#page-10-0)B), but this occurred in the K655R variant only at $+20$ mV (Fig. [7C](#page-10-0)), while the open time for the W1150R variant was unchanged (Fig. [7](#page-10-0)D).

Effects of OXC on the Inactivation of hNav1.7 Variants

As for the steady-state inactivation, the $V_{1/2}$ of the N641Y, K665R, and W1150R variants was negatively shifted by OXC (by -6.4 mV, $n = 14$, $P < 0.01$; by $- 3.4$ mV, $n = 11, P < 0.001;$ by $- 8.6$ mV, $n = 10, P < 0.001;$ respectively; Fig. [8](#page-11-0)A–D and Table [2](#page-6-0)). Treatment with OXC (120 μ mol/L) also induced a hyperpolarizing shift in the voltage-dependence of the fast inactivation in the variants (N641Y $V_{1/2}$ by -9.3 mV, $n = 9$, $P < 0.001$; K655R $V_{1/2}$ by -4.5 mV, $n = 13, P < 0.01$; W1150R $V_{1/2}$

Fig. 5 Influence of temperature on the steady-state activation of hNav1.7 and the W1150R variant. A, C Voltage-dependence of steady-state activation at 25 °C and 38 °C for hNav1.7 (A) and the W1150R variant (C). Curves are Boltzmann fits. B Scatter plots of voltage at half-maximal steady-state activation $(V_{1/2})$ for the WT at 25 °C and 38 °C (25 °C: $- 19.36 \pm 1.567$, $n = 15$; $38 °C$: $- 21.42 \pm 1.072$. $n = 19$). **D** Scatter plots of $V_{1/2}$ for W1150R at 25 $^{\circ}$ C and 38 $^{\circ}$ C $(25 °C: - 22.57 \pm 1.568,$ $n = 9$; 38 °C: $- 27.24 \pm 1.376$, $n = 7$). Data are the mean \pm SEM. $*P < 0.05$; black, 25 °C; red, 38 °C.

Fig. 6 Oxcarbazepine (OXC) inhibited $Na⁺$ channel currents of hNav1.7 and SCN9A variants and modulates the steady-state activation. A Average $Na⁺$ current traces recorded from HEK293T cells coexpressing pEZ-Lv206-hNav1.7 and pIRES-EGFP-h β 1 plasmids and treated with OXC. B Scatter plots showing the normalized macroscopic current amplitude remaining after blockade by OXC (120 μ mol/L). **C–F** Left, shifts in the voltage-dependence of

steady-state activation for WT (C), N641Y (D), K655R (E), and W1150R (\bf{F}) following treatment with OXC (120 μ mol/L). Curves are Boltzmann fits. Right, scatter plots of voltage at half-maximal steady-state inactivation $(V_{1/2})$. Data are the mean \pm SEM. $*P < 0.05,$ $**P < 0.01,$ $***P < 0.001$. Black, no drug treatment; red, treated with OXC.

by $- 12.8$ mV, $n = 9$, $P < 0.001$; Fig. F, G, H, respectively). After treatment with OXC, the voltage sensitivity (slope factor, K) was unchanged for both steady-state inactivation and fast inactivation (Table [2\)](#page-6-0).

Effects of OXC on the Recovery of hNav1.7 Variants

The time constant of recovery underlying each of the hNav1.7 variants was increased in the presence of 120 μ mol/L OXC, (WT by 0.8 ms, $n = 17$, $P < 0.01$; N641Y by 1.5 ms, $n = 8$, $P < 0.001$; K655R by 0.4 ms, $n = 16, P < 0.01$; W1150R by 0.8 ms, $n = 11, P < 0.05$; Fig. [9](#page-12-0)A–D and Table [2](#page-6-0)). The percentage recovery in the WT and variants decreased in the presence of 120μ mol/L OXC from 0.90 ± 0.006 for Control $(n = 8)$ to 0.73 ± 0.007 for WT (n = 7, P < 0.05), 0.69 \pm 0.04 for N641Y ($n = 7$, $P < 0.0001$), 0.77 ± 0.02 for K655R $(n = 12, P < 0.01)$, and 0.63 ± 0.06 for W1150R $(n = 8,$ $P < 0.01$; Fig. [9](#page-12-0)E).

Fig. 7 Oxcarbazepine (OXC) modulates the fast time constants of hNav1.7 and SCN9A variants. A–D Average fast time constants of WT hNav1.7 channels (A), average fast time constants of p.(N641Y) mutant hNav1.7 channels (B), average fast time constant of p.(K655R) mutant hNav1.7 channels (C), and average fast time constant of p.(W1150R) mutant hNav1.7 channels (D) with 120 μ mol/L OXC versus membrane potential. Data are the mean \pm SEM. $*P< 0.05$.

Discussion

To date, among the myriad epilepsy-associated $Na⁺$ channel mutations described, Nav1.7 mutants have been detected in patients suffering from generalized epilepsy, temporal lobe epilepsy, febrile seizures plus, and febrile seizures [\[15](#page-13-0), [16,](#page-13-0) [18](#page-13-0), [25](#page-13-0)]. In this study, the novel SCN9A mutant W1150R was identified in a patient with febrile seizures. Electrophysiological characterization of W1150R suggested that the mutant is a gain-of-function variant that notably alters the kinetic properties of hNav1.7. The presence of W1150R not only leads to a significant increase in current density, but also shortens the channel activation time and markedly shifts the G–V curve to negative potentials. Close attention was paid to the voltagedependent inactivation parameters of W1150R, which were constant. This implied that the window currents of the W1150R variant were increased. Increments of the window currents have been shown to reduce the action potential threshold and cause hyperexcitation [[26,](#page-13-0) [27](#page-13-0)]. In addition, the W1150R variant could enhance $Na⁺$ currents by increasing persistent currents as well as significantly prolonging the open time of hNav1.7. Several studies have supported the notion that persistent $Na⁺$ currents also drive intrinsic neuronal excitability [[28,](#page-13-0) [29\]](#page-13-0). Several epilepsyassociated Nav1.1 mutations have been found to enhance persistent currents [[30–32\]](#page-13-0). Transgenic mice expressing

mutant Nav1.2 channels that generate increased persistent currents display a severe epileptic phenotype [[33\]](#page-13-0). Our results allow us to speculate that the generalized epilepsy induced by gain-of-function mutations in VGSC genes could be related to the facilitation of channel activation of as well as the enhancement of peak and persistent $Na⁺$ currents.

The other hNav1.7 variants found in febrile seizure patients, N641Y and K655R, are also regarded as gain-offunction variants $[16, 17]$ $[16, 17]$ $[16, 17]$ $[16, 17]$ $[16, 17]$. The phenotype of these two variants in steady-state activation differs from that of W1150R. In the N641Y and K655R variants, the G-V curve of activation was shifted towards depolarization, and the time constant of recovery was significantly reduced. However, none of the three variants affected the inactivation. It has been shown that many mutant $Na⁺$ channels associated with epilepsy exhibit delayed inactivation as well as increased persistent $Na⁺$ currents [\[30–32](#page-13-0)]. As is generally known, a larger persistent current accentuates subthreshold depolarizations and facilitates the generation of the action potential, so we compared this property between the WT and variants, and ultimately found that the variants displayed larger persistent currents than WT channels. The above data suggested that hyperexcitability might be associated with an increased persistent current and rapid recovery of the inactivated channel to the resting

E Normalized Current
Population *** V_{12} (mV) -50 $\mathbf{0}$. **WT** WT OXC 0.0 -60 **WT-OTC** $\overline{.20}$ $\overline{0}$ $\overline{20}$ $\boldsymbol{\psi}$ F Normalized Current
P. B. C. S.
P. A. C. S. *** -20 $V_{1/2}$ (mV) -60 $N641Y$ **N641Y OXC** 0.0 -80 Neat^{Y XOTC} **N6474** $-140 - 120 - 100 - 80 - 60 - 40$ Voltage (mV) G 1. Normalized Gurrent
C. C. C. $V_{1/2}$ (mV) -50 **K655R** 0.0 • K655R OXC -60 **Hesta** Kessexotc $-140 - 120 - 100 - 80$ 0 - 60 - 40 -
Voltage (mV) -20 'n $\overline{20}$ 1.2 H 1.0 $V_{1,0}$ (mV) 0.2 **W1150R W1150R OXC** 0.0 **M115R** $-80 - 60 - 40$
Voltage (mV) $-140 - 120 - 100$ -20 ō $\overline{20}$ W1150R1

neuronal firing and reduce excitatory synaptic transmission

 $***P < 0.001$. Black, no drug treatment; red, with OXC.

state inactivation $(V_{1/2})$. **E–H** Left, shift in the voltage dependence of fast inactivation for WT (E), N641Y (F), K655R (G), and W1150R (H) after treatment with 120 μ mol/L OXC. Curves are Boltzmann fits. Right, scatter plots of $V_{1/2}$. Data are the mean \pm SEM. ** $P < 0.01$,

Fig. 8 Oxcarbazepine (OXC) modulated the inactivation of hNav1.7 and SCN9A variants. A–D Left, shift in the voltage-dependence of steady-state inactivation in the WT (A), N641Y (B), K655R (C), and W1150R (D) after treatment with 120 µmol/L OXC. Curves are Boltzmann fits. Right, scatter plots of voltage at half-maximal steady-

state, thereby increasing the probability that the open state of $Na⁺$ channels was configured for longer periods.

The pharmacological data in this study revealed that treatment of both the N641Y and K655R variants with 120 µmol/L OXC resulted in a marked reduction in $Na⁺$ currents and a shortening of the opening time. This may correspond with the capacity of OXC to inhibit abnormal

Fig. 9 Oxcarbazepine (OXC) modulated recovery from inactivation in hNav1.7 and SCN9A variants. A–D Shifts in the voltagedependence of recovery from inactivation in the WT (A), N641Y (B), K655R (C), and W1150R (D) after treatment with 120 μ mol/L

with some Nav channel mutations are not sensitive to OXC.

In summary, we have identified a novel SCN9A mutant (W1150R) in a patient with febrile seizures. Examination of the gain-of-function hNav1.7 mutants, N641Y, K655R, and W1150R led us to the conclusion that two of the variants are sensitive, while the W1150R variant is insensitive to OXC.

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OXC (curves are single exponential fits) and scatter plots of the time constant of recovery from inactivation. E Percentage recovery of ion channels treated with 120 µmol/L OXC. Data are the mean \pm SEM. $*P < 0.05, **P < 0.01, **P < 0.001.$

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Conflict of interest The authors declare that they have no conflict of interest.

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