Direct Measurement of Cardiac Na⁺ Channel Conformations Reveals Molecular Pathologies of Inherited Mutations

Zoltan Varga, PhD; Wandi Zhu, BS; Angela R. Schubert, BS; Jennifer L. Pardieck, BS; Arie Krumholz, PhD; Eric J. Hsu, BS; Mark A. Zaydman, BS; Jianmin Cui, PhD; Jonathan R. Silva, PhD

Background—Dysregulation of voltage-gated cardiac Na⁺ channels (NaV1.5) by inherited mutations, disease-linked remodeling, and drugs causes arrhythmias. The molecular mechanisms whereby the NaV1.5 voltage-sensing domains (VSDs) are perturbed to pathologically or therapeutically modulate Na⁺ current (I_Na) have not been specified. Our aim was to correlate I_Na kinetics with conformational changes within the 4 (DI–DIV) VSDs to define molecular mechanisms of NaV1.5 modulation.

Method and Results—Four NaV1.5 constructs were created to track the voltage-dependent kinetics of conformational changes within each VSD, using voltage-clamp fluorometry. Each VSD displayed unique kinetics, consistent with distinct roles in determining I_Na. In particular, DIII-VSD deactivation kinetics were modulated by depolarizing pulses with durations in the intermediate time domain that modulates late I_Na. We then used the DII-VSD construct to probe the molecular pathology of 2 Brugada syndrome mutations (A735V and G752R). A735V shifted DII-VSD voltage dependence to depolarized potentials, whereas G752R significantly slowed DII-VSD kinetics. Both mutations slowed I_Na activation, although DII-VSD activation occurred at higher potentials (A735V) or at later times (G752R) than ionic current activation, indicating that the DII-VSD allosterically regulates the rate of I_Na activation and myocyte excitability.

Conclusions—Our results reveal novel mechanisms whereby the NaV1.5 VSDs regulate channel activation and inactivation. The ability to distinguish distinct molecular mechanisms of proximal Brugada syndrome mutations demonstrates the potential of these methods to reveal how inherited mutations, post-translational modifications, and antiarrhythmic drugs alter NaV1.5 at the molecular level. (Circ Arrhythm Electrophysiol. 2015;8:1228-1239. DOI: 10.1161/CIRCEP.115.003155.)

Key Words: Brugada syndrome ■ fluorometry ■ ion channels ■ mutation ■ sodium channels

Atrial and ventricular action potentials are initiated by a large membrane-depolarizing Na⁺ flux through the cardiac voltage-gated Na⁺ channel (NaV1.5). In large animals and humans, persistent NaV1.5 current is also a significant regulator of action potential duration. Because of its central role in determining the action potential, molecular-level interactions that perturb NaV1.5 channel function have a significant effect on the ability of the myocardium to initiate and sustain arrhythmias. Mutations to NaV1.5 are known to cause long QT syndrome type 3, Brugada syndrome (BrS), sick sinus syndrome, atrial fibrillation, and familial heart block. Furthermore, class I small molecule antiarrhythmics target the NaV1.5 pore with the aim of diminishing Na⁺ current to prevent arrhythmia. To date, characterization of NaV1.5 mutation pathology and drug interactions has primarily relied on measuring the ionic current response to elaborately designed voltage-pulse protocols. Here, we develop novel NaV1.5 constructs to augment these protocols by monitoring changes in conformation with fluorescence labeling, at the same time we observe the ionic current, with voltage-clamp fluorometry (VCF). By applying VCF to observe channels that carry inherited mutations, we expect to improve phenotypic precision by characterizing the molecular pathology of the disease.

The NaV1.5 α-subunit, encoded by SCN5A, is composed of 4 homologous domains (DI–DIV), each with 6 transmembrane-spanning segments (S1–S6). Within DI–DIV, S1–S4 form the voltage-sensing domains (VSDs), which respond to changes in membrane potential (V_m) to cause NaV1.5 gating. The NaV1.5 pore is formed by the S5–S6 segments. A hydrophobic triplet located in the intracellular DIII/DIV linker is required for inactivation, and its action is modulated by the C-terminus.

Previously, VCF was used to relate skeletal muscle Na⁺ channel, NaV1.4, VSD conformations to channel activation and inactivation and to probe the domain-specific interactions of toxins and local anesthetics.
WHAT IS KNOWN

- The cardiac Na+ channel initiates atrial and ventricular action potentials, and inherited mutations that cause its dysfunction lead to syndromes that predispose patients to sudden death.
- Commonly prescribed class I antiarrhythmics that are targeted to the Na+ channel can be effective for treating and diagnosing affected patients. However, the most effective drug choice for treating patients with a particular mutation is not always apparent.

WHAT THE STUDY ADDS

- We develop protocols to observe the voltage-sensing machinery that controls cardiac Na+–channel opening and closing to understand how inherited mutations pathologically alter the channel at the molecular level.
- Despite having similar ionic current phenotypes, we observed that 2 proximal Brugada syndrome mutations display different molecular characteristics. This improved phenotypic precision may eventually enable therapeutic approaches that specifically account for the molecular pathology of the arrhythmia.

In this study, we present 4 novel constructs that report on the distinctive VSD conformations of Na1.5 for the purpose of assessing molecular mechanisms of Na1.5-linked pathologies and therapies. To demonstrate the potential of the method, we probe the molecular phenotype of 2 proximal BrS mutations, A735V and G752R, which are both located on the DII-VSD. The electrocardiographic phenotypes of patients with these mutations.

Despite having similar ionic current phenotypes, we observed that 2 proximal Brugada syndrome mutations display different molecular characteristics. This improved phenotypic precision may eventually enable therapeutic approaches that specifically account for the molecular pathology of the arrhythmia.

Results

Our first aim was to create 4 Na1.5 constructs to track conformational changes within each of the Na1.5 channel VSDs. Initial attempts to record fluorescence signals were unsuccessful because of insufficient expression of human Na1.5, which is significantly reduced compared with rat Na1.4, the isoform used to acquire most existing Na-channel VCF data. Examination of differences between the 2 channels revealed that Na1.5 contains an ubiquitination motif that enhances the channel recycling rate and reduces the number of channels in the membrane; this motif is not found in Na1.4. Ablation of the ubiquitination site by the Y1977A mutation and coinjection with β-subunit RNA resulted in sufficient Na1.5 expression for the detection of useful fluorescence signals. We also introduced C373Y, increasing tetrodotoxin sensitivity and allowing ionic current blockade for the measurement of gating currents. This mutation also removes an externally accessible cysteine, preventing nonspecific labeling.

Two protocols were performed to compare our new construct with wild-type (WT). We first quantified the conductance–voltage (G–V) relationship, found by measuring peak current after a series of depolarizing pulses and dividing by driving force. The second protocol measured the voltage dependence of steady-state inactivation (SSI); peak current was measured during a short test pulse to −20 mV that followed 200-ms inactivation-inducing pulses to varying potentials. The voltage dependence of the G–V and SSI curves was not substantially affected by these mutations (P=0.951 and 0.069, respectively; Figure 1). For fluorescence tracking, cysteine mutations (specified below) in the individual domains were introduced in this Y1977A–C373Y mutant, which we named WT-LFS (large fluorescence signal). The mutants produced for VSD tracking in this background will be accordingly referred to as DI-LFS, DII-LFS, DIII-LFS, and DIV-LFS. Cysteines were introduced at several positions from L212 to T220 and R222. V215C (DI-LFS) was the only mutant to express well and produce a usable fluorescence signal (Figure 2). The Na1.5 VSDs play an essential role in determining gating, and we expected the MTS-TMRA labeling in conjunction with the introduced cysteine to affect gating to some extent. We observed a negative shift (ΔV1/2=−16.8 mV) in the G–V and a slight positive shift (ΔV1/2=+8 mV) in the SSI curves compared with the

Materials and Methods

Voltage-Clamp Fluorometry

cRNAs for human Na1.5 α- and β-subunits were injected into Xenopus laevis oocytes for cut-open oocyte recordings at 19°C. The internal solution was 105 mmol/L of NMG-Mes, 10 mmol/L of Na-Mes, 20 mmol/L of HEPES, and 2 mmol/L of EGTA, pH 7.4, and the external solution was composed of 25 mmol/L of NMG-Mes, 90 mmol/L of Na-Mes, 20 mmol/L of HEPES, and 2 mmol/L of Ca-Mes, pH 7.4. For gating currents, 10 µmol/L of tetrodotoxin was used, and Na-Mes was replaced by NMG-Mes. For fluorescence recordings, oocytes were labeled with 10 µmol/L of methanethiosulfonate-carboxytetramethylrhodamine (MTS-TMRA). Data were collected on a custom rig (Methods section in the Data Supplement). Animal procedures were performed according to institutional guidelines.

Data Analysis

For photobleaching correction, baseline fluorescence recorded over time without voltage pulsing was subtracted from traces recorded during the application of the voltage protocol. Fluorescence magnitude is expressed as ΔF/ΔF0. ΔF is the signal amplitude change and F0 is the baseline fluorescence.

Steady-state voltage dependence was quantified by Boltzmann function fitting: y=1/(1+exp[(V−V1/2)/k]), V1/2 was calculated from the time constants of single exponential fits (τ). Statistical comparisons were done using paired or independent-sample t tests or 1-way ANOVA with post hoc tests for pairwise comparison. P<0.05 was considered significant. The ± symbols in the text and error bars in the figures represent the 95% confidence interval with the number of trials [n] in brackets.
1230 Circ Arrhythm Electrophysiol October 2015

background WT-LFS construct, implying that the labeled V215C channel opens at more negative potentials and inactivates at more positive potentials than WT-LFS. Comparing labeled and unlabeled DI-LFS showed that the G–V shift is a consequence of adding the MTS-TAMRA label (Figure I in the Data Supplement). We also used gating currents to assess whether charge movement across the transmembrane electric field was affected by labeling (Figure II in the Data Supplement). If the probe significantly affected charge transfer, we would expect to observe a change in the voltage dependence of the gating current integral, the gating charge. For the 4 constructs, the charge–voltage (Q–V) relationship was shifted over a range of 5 to 11 mV in comparison with WT-LFS (Figure I in the Data Supplement; Table), suggesting that charge displacement was modestly affected by cysteine-conjugated fluorophore replacement of the WT residue.

Simultaneously, recording changes in fluorescence magnitude during these protocols allowed us to correlate DI-VSD conformations with channel gating. We refer to the fluorescence that was recorded during the G–V protocol as the fluorescence–voltage relationship (F–V curve) and the fluorescence from the SSI protocols as the SSI F–V curve. The F–V curves reflect the voltage dependence of the conformations in the DI-VSD that are reported by MTS-TAMRA. For the DI-VSD, the midpoint of the F–V curve was 27.2-mV negative of the G–V curve, indicating that DI-VSD movement occurs at much more negative potentials than pore opening. On the contrary, the SSI and SSI F–V curves had similar midpoints, showing that inactivation and DI-VSD movement occur in the same voltage range. However, in contrast to DIV, the DI-VSD SSI F–V and SSI slopes differed substantially (k=−15.4 [5] versus −6.4 [8] mV, respectively; P<0.001), suggesting that the 2 events are not tightly coupled.

The fluorescence kinetics recorded during the F–V curve reflect the voltage-dependent rates of VSD activation and deactivation. Because current and VSD activation kinetics are described by different functions, we measured the time between 10% and 90% of the peak current and calculated t10%–90% for fluorescence (Methods section). DI-VSD rise time was slower (t10%–90%=0.82±0.23 ms at +30 mV) than ionic current activation (t10%–90%=0.24±0.04 ms), but the events overlapped because of the sigmoidal delay in ionic current activation (Figure III in the Data Supplement). At elevated potentials (>+20 mV), a slow component in the DI-VSD fluorescence signal became apparent with an opposite sign relative to the original deflection. Although significant numbers

Figure 1. Ionic and gating currents from the wild-type large fluorescence signal (WT-LFS) construct. Currents from WT-LFS and WT channels were recorded in the cut-open oocyte configuration. The means±95% confidence interval for groups of 6 to 22 cells is reported. A, Top, Ionic currents. From −100 mV, a 50-ms step to −120 mV preceded 100-ms depolarizing pulses from −140 to +40 mV in 10-mV steps, which were followed by a 50-ms step to −120 mV before returning to holding potential. Membrane capacitance and leak were removed using P/−8 leak subtraction. For clarity, only the first 40 ms of traces corresponding to −130 to +30 mV in 20-mV steps are shown. Bottom, Voltage dependence of steady-state activation and steady-state inactivation (SSI) curves for the WT-LFS (G–V, black circles; SSI, black squares) and the WT channels (G–V, gray up triangle; SSI, gray down triangle). G–V curves were constructed from I–V relationships recorded from cells depolarized in 10- or 20-mV increments from −120 mV. Na+ reversal potential was determined for each cell individually. For the SSI curve, cells were held at potentials ranging from −150 to +20 mV for 200 ms, and the available fraction was assessed by a −20-mV test pulse. Boltzmann-fit parameters are provided in the Table. B, Top, Gating currents from WT-LFS channels were recorded during 20-ms depolarizing steps ranging from −150 to +50 mV in 20-mV steps. Capacitance and leak were removed using P/4 leak subtraction with a subsweep holding level of +40 mV. Bottom, Gating currents were integrated for 10 ms after the voltage change.
of channels will not make this slow transition to a new state during a single action potential, channels may accumulate in this state at rapid heart rates.

Because fast inactivation is known to hinder the recovery of the gating charges on repolarization (immobilization), we performed experiments to measure the deactivation rate of the DI-VSD after depolarizing pulses of varying length, which inactivated the channels to different extents. The deactivation kinetics measured at −120 mV did not change as a function of pulse duration (τ_{10%–90%,C}=0.99±0.22 ms after a 2-ms pulse and 0.99±0.13 ms after a 200-ms pulse [4]; P=0.948). This result suggests that DI-VSD deactivation is not influenced by Na,1.5 open-state inactivation, which had not occurred during the 2-ms pulse and is nearly complete after 200 ms.

We tracked the DII-VSD with S805C (DII-LFS), which yielded large and robust signals. The voltage-dependent steady-state parameters (G–V and SSI curves) were minimally affected in comparison with WT-LFS; there was no shift in the G–V curve and a +7.4-mV shift in the SSI curve (Figure 3). Measurement of the F–V curve revealed that it was 12.5-mV negative of the G–V curve, showing that the DII-VSD starts to move before activation; however, it reaches saturation at higher potentials than the conductance because of its shallower slope, which indicates that the 2 events are not tightly coupled. Comparing the SSI and SSI-FV curves shows that inactivation occurs at more negative potentials than DII-VSD activation (V_{1/2}=−79.2 and −52.2 mV, respectively) and that the inactivation slope is much steeper than DII-VSD activation.

Figure 2. V215C (DI-large fluorescence signal [LFS]) ionic currents and fluorescence. Na+ currents and fluorescence were recorded from human Na,1.5 channels carrying the LFS-S215C mutations with cut-open oocyte voltage-clamp fluorometry (Materials and Methods section). The mean±95% confidence interval for groups of 4 to 14 cells is reported. A, Top, Ionic currents (above) and fluorescence signals (below). From −100 mV, a 50-ms step to −120 mV preceded 20-ms-long depolarizing pulses ranging from −150 to +30 mV in 20-mV steps. These steps were then followed by a 50-ms step to −120 mV before returning to the holding potential. Membrane capacitance and leak were removed using P/−8 leak subtraction. For clarity, only traces corresponding to −150, −90, −30, and +30 mV are shown. Bottom, G–V curve (black circles) and steady-state inactivation (SSI; black squares) and the corresponding fluorescence signals (orange circles and squares, respectively). All curves were obtained by Figure 1 protocols. The fluorescence amplitude for the F–V and SSI-FV curves was determined by taking the mean of the signal for at least 3 ms at the greatest displacement of the signal. For the SSI F–V curve, ΔF was calculated as the difference between the signal amplitude measured at the conditioning potential and −20 mV. Boltzmann-fit parameters are provided in the Table. Dotted lines represent WT-LFS G–V and SSI curves for comparison. B, Top, Tail currents and fluorescence measured at −120 mV after depolarizing steps to +50 mV for 2 (black) or 200 ms (orange). Inactivation does not occur during the shorter pulse resulting in a large tail current. Bottom, τ_{10%–90%,C} values calculated from deactivation time constants of the fluorescence signal from exponential fits after the step back to −120 mV, from depolarizing steps to 0 or +50 mV for 1- to 200-ms durations.
elliptic current, DII-VSD activation precedes ionic current activation at holding potentials which completely abolish the conductance by inactivation (V: −50 mV), the DII-VSD is still far more negative than that of the G−V curve was 32.2 mV more negative than that of the G−V, whereas the SSI and SSI F−V curves overlapped, further supporting strong correlation between DIV-VSD activation and closed-state inactivation that is primarily measured by the SSI curve. In addition, slowing of fast inactivation caused by the introduction of the cysteine mutation is also readily apparent in the ionic current curves of the DIV-VSD construct were shifted relative to WT-LFS by +5.3 and +12.4 mV, respectively (Figure 5). Comparison of the fluorescence and ionic current shows that the midpoint of the F−V curve was 32.2 mV more negative than that of the G−V, but 2 to 3× faster than that of DIII. Surprisingly, DIV-VSD deactivation did not slow with increasing pulse duration (τ:571±4.04 ms after a 2-ms pulse and 6.63±3.91 ms after 200-ms pulse [4]; P=0.411). Given the prominent role of DIV in inactivation, the lack of slowing in DIV-VSD recovery with longer pulses is highly unexpected and is in clear contrast with Na1.4 results, suggesting different interactions between the DIII- and DIV-VSDs and inactivation.

### Table. Parameters of Boltzmann Fits to G−V, F−V, SSI, SSI F−V, and Q−V curves

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Errors represent 95% confidence intervals and numbers in brackets indicate the number of cells measured. SSI indicates steady-state inactivation; and WT-LFS, wild-type large fluorescence signal, construct.
Our next aim was to assess the molecular pathology of 2 proximal DII-VSD BrS mutations, A735V and G752R (Figure 6). We introduced each into the DII-LFS construct. The $F$–$V$ and SSI $F$–$V$ curves of A735V were dramatically positive-shifted relative to DII-LFS (by +49.1 mV and +58.5 mV, respectively) and also relative to the $G$–$V$ and SSI curves of the channel itself (by +19.5 mV and +89.1 mV, respectively). In addition, the voltage sensitivity of the DII-VSD was severely reduced; both had shallow slope factors (35.4 mV and −39.5 mV, respectively). DII-VSD activation kinetics were also slightly slowed by the mutation at +40 mV based on the $t_{10\%-90\%}$ values (DII-LFS: 0.99±0.19 ms [8] and DII-LFS-A735V: 1.49±0.36 ms [5]; $P=0.005$), but even more strikingly, the DII-VSD activation rate of the mutant conserved its voltage dependence but was slower than DII-LFS at potentials ≤10 mV ($t_{10\%-90\%}=1.48±0.17$ ms [5] versus 0.71±0.47 ms [3], respectively, at −20 mV; $P=0.002$). Despite the severely right-shifted $F$–$V$ of A735V, the mutant $Q$–$V$ ($V_{1/2}=−75.6±8.3$ mV [5]) was not significantly different from that of DII-LFS (−80.0±7.6 mV [4]; $P=0.241$) or WT-LFS (−69.1±4.2 mV [7]; $P=0.058$).

In contrast, G752R caused minor $F$–$V$ and SSI $F$–$V$ shifts (by +1.0 mV and −9.8 mV, respectively, compared with DII-LFS) and displayed similar slope factors but resulted in a severe slowing of the DII-VSD activation. In response to a depolarizing step, the rate of DII-VSD activation was about 7-fold slower in the mutant than in the DII-LFS channel (1.42±0.19 ms at −20 mV and 0.99±0.19 ms at +40 mV [8]; $P=0.002$). To the contrary, ionic current activation of the mutant conserved its voltage dependence but was slower than DII-LFS at potentials ≤10 mV ($t_{10\%-90\%}=0.99±0.19$ ms [8] and 6.96±1.21 ms [8] at +40 mV, respectively; $P<0.001$). The $Q$–$V$ curve was right-shifted by ≤20 mV with respect to DII-LFS. However, extending the interval over which charge was integrated from 10 to 20 ms, to account for G752R-induced slowing, shifted the curve leftward and closer to DII-LFS. Significant slowing of activation kinetics was also observed in the ionic current of G752R. In
the −40 to +30 mV voltage range, the activation rate was 1.7 to 2.9× slower than that of the DII-LFS as measured by the $t_{10\%-90\%}$ times (1.51±0.15 ms [7] and 0.71±0.47 ms [3], respectively, at −20 mV; P<0.001; Figure IV in the Data Supplement).

To ensure that the mechanisms we observed in oocytes are still operative across cell lines, we expressed both mutants in HEK293T cells. A comparison (Figure V in the Data Supplement) shows that as in oocytes, current activation measured by the $t_{10\%-90\%}$ is slower in both BrS mutants compared with DII-LFS (at −20 mV, DII-LFS: 0.27±0.09 ms [4], A735V: 0.81±0.32 ms [5], G752R: 0.66±0.07 ms [4]; P=0.002).

**Discussion**

Our results represent the first measurements of human Na_+ 1.5 VSD conformations and show that each VSD has unique kinetics, consistent with specific gating roles. Specifically, the 4 VSDs activate at different membrane potentials that span a range >50 mV. DIII activates at the most hyperpolarized potentials ($V_{1/2} = −106.0$ mV), followed by DI (−83.9 mV), DIV (−66.8), and finally DII (−51.4), all negative of the $G−V$ curve that characterizes current activation ($V_{1/2} = −39.9$ mV for WT-LFS). Furthermore, all 4 VSDs have a $t_{10\%-90\%}$ rise time that is slower than ionic current activation, which is to be expected if ionic current activation is caused by the combined motions of several VSDs that can be modeled as a cubed gate (eg, m^3 in Hodgkin–Huxley type models), allowing for a more rapid activation after a delay.

Although our results support the hypothesis of concerted action of several VSDs in activating Na_+ channels, our mutation results contrast to classical models that require tight coupling of the gates to pore opening. Comparing DII-VSD activation voltage dependence in A735V with its $G−V$ relationship (Figure 6A)
reveals that the channel fully opens at 0 mV, although the DII-VSD is not fully activated even at +80 mV. This phenomenon is observed in DII-LFS as well, indicating that this property is intrinsic to NaV1.5, but the effect is greatly enhanced in A735V. Thus, DII-VSD activation facilitates channel opening through an allosteric mechanism where the lack of VSD activation simply slows activation but does not prevent it. This mechanism may be evolutionarily beneficial because it allows for moderate alteration of VSD kinetics by mutations without preventing Na$^+$ channel activation and myocyte excitability.

Origin of $\Delta F$

Our detected changes in MTS-TAMRA fluorescence emission are likely due to photoinduced electron transfer, which is a quenching nonradiative electron transfer between 2 molecules that are within 10 Å, in close van der Waals contact.$^{23}$ Many different residues may quench the fluorophore, which implies that our fluorescence signal is highly dependent on the surrounding residues that interact with the fluorophore as it moves. This dependence introduces the possibility that the fluorescence changes we observe do not necessarily reflect the movement of the charged S4 segments across the membrane.

Our $Q-V$ curves that are calculated from gating currents directly quantify charge transfer within all 4 domains
across the membrane field. Thus, we expect that if we are tracking charge transfer, then the valence-weighted average midpoint of the $F-V$ curves will match the $Q-V$ curves (Figure 7; Table). The WT-LFS $Q-V$ is accurately reconstructed by the valence-weighted $F-V$ curves (Figure 7A). Moreover, the confounding left shift in the A735V $Q-V$ relative to G752R is also predicted by this analysis (Figure 7B) and results from much less charge being assigned to the DII $F-V$ because of its reduced slope, which lessens its right-shifting contribution. With the G752R construct, we observe less charge transferred at some of the lower potentials. This slight difference is likely due to the substantial slowing of charge movement at these potentials, which sharply reduces the gating current and precludes its detection. Alternatively, G752R may be slowing the activation of the other 3 domains, causing a right-shifted $Q-V$. Previous work in Na$\nu_1.4$ shows
that a DII-VSD activation shift modestly affects the activation of the DI, DIII, and DIV VSDs. Future efforts to probe Na\textsubscript{\textastisk},1.5 cooperativity will be needed to test whether this is the case for A735V and G752R.

A simple 2-state model of the VSD would predict that the SSI $F-V$ is simply a mirror image of the $F-V$ and that they should cross at 0.5. This is the case for the DI- and DII-VSDs but not for the DIII- and DIV-VSDs, which showed a lower crossing. Because the SSI $F-V$ uses a 200-ms pulse, whereas the $F-V$ is measured after several milliseconds, the difference is likely due to multiple activated or resting states of the VSD. This is not surprising, as multiple DIII-VSD resting states have been posited to model lidocaine interaction and we also infer multiple states from the pulse duration protocol. For the DIV-VSD, this crossing was in the range of experimental variability, but it may be linked to DIV-VSD interaction with inactivation.

**Comparison With Previous Results**

VCF has been used to study Na\textsubscript{\textastisk},1.4, and many of the results have been extrapolated across the superfamily of Na\textsubscript{\textastisk}, channels. Although we observe many similarities, there are several distinct Na\textsubscript{\textastisk},1.5 features. In rNa\textsubscript{\textastisk},1.4, the VSD activation midpoints all fell within a 20-mV range. In contrast, midpoints of the $F-V$ curves for hNa\textsubscript{\textastisk},1.5 spanned a range of $\approx 50$ mV. In particular, DIII was activated at hyperpolarized potentials, and DII activation was substantially depolarized relative to the $Q-V$ (by 30 mV). For the DII-VSD, this depolarizing shift may be because of loose coupling between the DII-VSD and channel activation, which was not observed in Na\textsubscript{\textastisk},1.4.

Further differences are seen when comparing the connection between channel inactivation and VSD activation. Classical studies of Na\textsubscript{\textastisk}, gating charge movement found that, after prolonged depolarization, a fraction of the gating charge is immobilized: that is, it returns with much slower kinetics on repolarization than the majority of the charge.\textsuperscript{26} In human Na\textsubscript{\textastisk},1.4, this immobilized fraction was associated with DIII and DIV.\textsuperscript{8} Consistently, deactivation of hNa\textsubscript{\textastisk},1.5 DI-VSD and DII-VSD was independent of the length of the depolarizing pulse. Conversely, return of the hNa\textsubscript{\textastisk},1.5 DIII-VSD was significantly slowed by long depolarizations, whereas the DIV-VSD deactivation rate was unaffected, in clear contrast to Na\textsubscript{\textastisk},1.4. However, this observation is in agreement with previous reports showing that charge immobilization of the Na\textsubscript{\textastisk},1.5 DIV-VSD is independent of inactivation and that the inactivation particle can only modulate gating charge recovery of DIII but not DIV.\textsuperscript{27} Thus, our data reconcile these 2 previously discrepant results by showing that the hNa\textsubscript{\textastisk},1.5 VSDs interact with inactivation uniquely.

Many have previously probed the functional contributions of each VSD to Na\textsubscript{\textastisk},1.5 gating, and our data show the timing of these contributions. For example, outward stabilization of the DI-S4 strongly reduced peak Na\textsubscript{\textastisk},1.5 current (45\%) without affecting rapid channel kinetics.\textsuperscript{28} In our data, we observed a slow DI-VSD transition at elevated potentials that may be linked to this peak reduction through slow inactivation (Figure 2). In contrast, DII-VSD outward stabilization does affect rapid gating kinetics, shifting the $G-V$ leftward along with SSI.\textsuperscript{28} Our results show that this DII-VSD regulation of channel activation is through an allosteric connection, which facilitates channel opening when the DII-VSD is activated. Similar work has also probed the consequences of DIII and DIV-VSD outward stabilization,\textsuperscript{29} both of which alter channel availability without affecting activation. Although the link between the 4 VSDs and inactivation is consistent with our results, it remains to be seen whether a slowing of DI, DIII, or DIV may also affect channel activation as observed in DII.

**Relevance**

For the inherited BrS mutations, A735V and G752R, we observed 2 different molecular pathologies (Figure 6). A735V...
clearly shifts the voltage dependence, whereas at positive potentials, DII-VSD activation kinetics are nearly as rapid as WT. In contrast, DII-VSD voltage dependence is preserved with G752R, but it arrives at its steady state much more slowly. For both mutants, the consequence for the ionic current is slower activation. Thus, our results show that dramatically different molecular pathologies can give rise to similar ionic current phenotypes. Still, molecular-level differences are likely to have significant consequences for the interaction of the channel with antiarrhythmic therapies.

From a theoretical perspective, the noncanonical Na\textsubscript{v}1.5 activation mechanism revealed by the G752R and A735V mutations suggests a specific Markov state diagram where the VSDs are not yet activated. Recent work on L-type Ca\textsuperscript{2+} channels revealed opening is possible from closed states where the VSDs are not in their resting conformation. This model would be more suitable for describing Na\textsubscript{v}1.5 gating.

### Future Directions

As demonstrated by our ability to observe the molecular pathology of 2 BrS mutations, we expect that we will be able to better understand mechanisms whereby some of the >150 Na\textsubscript{v}1.5 inherited mutations cause disease. In addition, Na\textsubscript{v}1.5 is known to interact with many accessory proteins, and it is tightly controlled by post-translational modification. By observing how these modulatory proteins and modifications affect the VSDs, we expect to unravel molecular mechanisms whereby the cell regulates hNa\textsubscript{v}1.5 gating to modulate cardiac myocyte excitability.

### Acknowledgments

We thank Jennifer N.A. Silva, MD, and James Ballard for many helpful discussions and advice.

### Sources of Funding

This work was supported by Burroughs Welcome Fund Career Award at the Scientific Interface 1010299 (J.R. Silva), National Institutes of Health (NIH) training grants T32-HL007275 (J.R. Silva) and R01-HL70397 and R01-NS060706 (J. Cui), and American Heart Association fellowship 11PRE5720009 and NIH T32-HL007873 (J. Cui), and American Heart Institutes of Health (NIH) training grants T32-HL007275 (J.R. Silva) and R01-HL70393 and R01-NS060706 (J. Cui), and American Heart Association fellowship 11PRE5720009 and NIH T32-HL007873 (J.R. Silva) and NIH T32-HL007275 (J. Cui), and American Heart Associations of molecular mechanisms. Trends Cardiovasc Med. 2002;12:629–645.

### Disclosures

None.

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Direct Measurement of Cardiac Na⁺ Channel Conformations Reveals Molecular Pathologies of Inherited Mutations
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Circ Arrhythm Electrophysiol. 2015;8:1228-1239; originally published online August 17, 2015; doi: 10.1161/CIRCEP.115.003155

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SUPPLEMENTAL MATERIAL

Supplemental Methods

Molecular Biology
All mutagenesis was performed using the overlap extension polymerase chain reaction (PCR) with Phusion Hot Start Flex Kit (New England Biolabs) and primers from Sigma-Aldrich. PCR products were ligated into the parent plasmid using T4 DNA ligase (New England Biolabs) and were chemically transformed into Turbo Competent cells (New England Biolabs). Multiple clones were selected and plasmids were isolated using the NucleoSpin Plasmid miniprep kit (Macherey-Nagel). Samples were then sequenced to select a single clone for Midiprep (NucleoBond Xtra Midi, Macherey-Nagel). Each construct was then linearized and purified with the NucleoSpin Gel and PCR Clean-up kit (Macherey-Nagel). Finally, capped mRNA was synthesized (mMessage mMACHINE T7 Transcription Kit, Life Technologies).

Xenopus Laevis
Oocyte harvest was performed on Xenopus Laevis (Nasco) no more than four times (~25 frogs). During the oocyte harvest procedure, distress was minimized by anesthetizing frogs in water containing 0.2% tricaine (3-aminobenzoic acid ethyl ester, methane sulfonate salt). After oocyte harvest, the wound was sutured while the frog is still anesthetized, according to our protocols that were approved by the Institutional Animal Care and Use Committee and in accordance with NIH guidelines.

Cut-open oocyte recording
cRNAs for the human β1 subunit (UniProtKB/Swiss-Prot accession no. Q07699.1) and α-subunit NaV1.5 (accession no. Q14524.1) were produced from the pBSTA and pMAX vectors (respectively) and injected at a 2:1 molar ratio (50 ng per cell total) into Xenopus laevis oocytes. Oocytes were incubated at 18°C for 2–7 d in solution with (mM) 93 NaCl, 5 KCl, 1.8 CaCl2, 1 MgCl2, 5 HEPES, and 2.5 Na-pyruvate, and 1% penicillin-streptomycin, pH 7.4. Cut-open oocyte recordings1,2 were performed using an amplifier (CA-1B; Dagan Corporation) coupled to an A/D converter (Digidata 1440; Molecular Devices) with Clampex and Clampfit software (v10; Molecular Devices) for acquisition and analysis. Temperature was maintained at 19°C with a controller (HCC-100A; Dagan Corporation). The internal solution was (mM): 105 NMG-Mes, 10 Na-Mes, 20 HEPES, and 2 EGTA, pH 7.4. The external solution was composed of (mM): 25 NMG-Mes, 90 Na-Mes, 20 HEPES, and 2 Ca-Mes2+, pH 7.4. For gating currents, Na-Mes was replaced by NMG-Mes in both the external and internal solutions and the external solution contained 10 μM TTX.

Data was collected with standard I-V protocols by simultaneous recording of the ionic current and the fluorescence signal from the labeled domain to construct the voltage dependence of steady-state activation (G-V) and voltage dependence of VS movement (F-V) functions. Cells were depolarized in 10 or 20 mV increments from a holding potential of -100 mV. Depolarizing pulses were preceded by a 100-ms-long prepulse and 50-ms-long postpulse to -120 mV. Capacitance compensation and P-8 leak subtraction were applied prior to recording ionic currents. To obtain the voltage-dependence of steady-state inactivation (SSI) and the corresponding VS movement (SSI F-V) curves cells were held at the conditioning potential for 200 ms and the available channel fraction was assessed by a depolarizing pulse to -20 mV. For gating currents P/4 subtraction was used with an interpulse holding potential of +40 mV.

VCF measurements
Oocytes were labeled with 10 μM methanethiosulfonate-carboxytetramethylrhodamine (MTS-TAMRA; Santa Cruz Biotechnology) in a depolarizing solution (mM: 110 KCl, 1.5 MgCl2, 0.8 CaCl2, 0.2 EDTA and 10 HEPES, pH 7.1) on ice for 20 min. MTS-TAMRA stock solution was 10 mM in DMSO and stored at ~20°C. Illumination was provided by a green, high-powered LED (Luminus, PT-121) controlled through a driver
(Lumina Power, LDPC-30-6-24VDC) by the acquisition software to minimize photobleaching of the probe. The light was then focused into a liquid light guide with a 45°, 5mm compound parabolic concentrator (Edmund Optics) and the guide was coupled to the microscope via a collimating adapter (EXFO). A 40x water-immersion objective with a numerical aperture of 0.8 (CFI Plan Fluor, Nikon) was used. Light measurements were made with a photodiode (PIN-040A; United Detector Technology) mounted on an XY axis manipulator (Thorlabs Inc.) at the microscope epifluorescence port. The photodiode was attached to the integrating headstage of a patch-clamp amplifier (Axopatch-200A; Molecular Devices) for low noise amplification of the photocurrent. The fluorescence emission was focused onto the photodiode active area using an achromatic doublet (Thorlabs Inc.) with a focal distance of 25 mm.

Data analysis
For the analysis of fluorescence data, baseline fluorescence traces were recorded with no change of voltage during the illumination period. To correct for photobleaching, this baseline trace was filtered and subtracted from the fluorescence traces recorded during the application of the voltage protocol. The magnitude of fluorescence signals is expressed as $\Delta F / F_0$, where $\Delta F$ is the change in the signal amplitude in response to the voltage change and $F_0$ is the baseline fluorescence.

Steady-state G-V, SSI, F-V and SSI F-V curves were obtained by fitting the data points with a Boltzmann-function: $y = 1 / (1 + \exp[-(V-V_{1/2})/k])$, where $V_{1/2}$ is the half-activation voltage and $k$ is the slope factor. For direct comparison of current and VSD kinetics we used $t_{10-90\%}$ due to the different functions they follow. $t_{10-90\%}$ for current activation kinetics was determined by the time duration between the time points when the current reached 10 and 90 % of the peak value. For fluorescence signals with low signal to noise ratio $t_{10-90\%}$ determination was inaccurate, therefore for all fluorescence signals we calculated $t_{10-90\%c}$ from the time constants of single exponential fits ($\tau$) to the signal by $t_{10-90\%c} = 2.197\tau$.

Valence-weighted F-V curves were calculated as $F(V)_w = (F(V)_1 \times z_1 + F(V)_2 \times z_2 + F(V)_3 \times z_3 + F(V)_4 \times z_4) / (z_1 + z_2 + z_3 + z_4)$, where $F(V)_i$ represents the $F(V)$ function of the $i$th domain and $z_i$ the valence of $F(V)_i$ determined from the Boltzmann-fit $y = 1 / (1 + \exp[-z \times (V-V_{1/2})/kT])$, where $V_{1/2}$ is the half-activation voltage and $k$ is the Boltzmann-constant and $T$ is temperature.$^a$

Statistical significance was attributed to $p<.05$ as determined by a two-tailed Student’s t-test. For the comparison of multiple groups one-way ANOVA was applied and in the case of a significant difference it was followed by post-hoc Holm-Sidak pairwise comparisons among all groups or versus control. Errors in text and error bars in figures represent 95% confidence interval with number of trials [n] in brackets.

References
Figure S1. G-V and SSI functions of the unlabeled fluorescence constructs

G-V and SSI functions were obtained using the protocols described in the text from unlabeled LFS constructs (circles). Points represent mean ± 95CI from groups of 3 to 6 cells. The dotted line shows the WT-LFS data, while the dashed lines are curves from TAMRA-MTS labeled constructs. For DIV-LFS the SSI curve did not saturate at negative potentials (filled circles), but after DTT treatment (empty circles) approached the labeled channel.
Figure S2. Comparison of integrated gating charge movement for WT-LFS and fluorescence constructs.

Voltage-dependence of integrated gating charge movement for WT-LFS, DI-LFS, DII-LFS, DIII-LFS and DIV-LFS channels. Gating currents were recorded during 20-ms depolarizing steps ranging from -150 to +50 mV in 20-mV steps. Capacitance and leak were removed using P/4 leak subtraction with a sub-sweep holding level of +40 mV. Gating currents were integrated for 10 ms following the voltage change. See Table 1 in manuscript for parameters. Each point represents the mean ± 95CI from 4 to 7 cells.
Figure S3. Comparison of ionic current and fluorescence kinetics in the four domains.

Na⁺ currents and fluorescence signals were recorded from DI-LFS, DII-LFS, DIII-LFS and DIV-LFS channels to compare the kinetics of activation. Traces were recorded during a voltage step to +30 mV from -120 mV. The first 10 ms duration is shown.
Figure S4. Comparison of ionic current activation kinetics of DII-LFS and the BrS mutants.

Activation kinetics were measured as \( t_{10-90\%} \) rise time following a step to the indicated potentials from a prepulse of -120 mV for DII-LFS, DII-LFS-A735V and DII-LFS-G752R. Each point represents the mean ± 95CI from groups of 3 to 7 cells.
Figure S5: Steady-state inactivation, activation, and rise times for BrS mutants compared to wild-type expressed in HEK293T cells.

(A) Activation kinetics were measured as t_{10-90\%} rise time following a step to the indicated potentials from a prepulse of -120 mV for WT [n=4], A735V [n=3], and G752R [n=4].

(B) Voltage-dependence of steady-state activation and steady-state inactivation curves for the WT, A735V, and G752R (purple, green, and red respectively). G-V curves were constructed from I-V relationships recorded from cells depolarized in 10 or 20 mV increments from a prepulse potential of -120 mV. Na⁺ reversal potential was determined for each cell individually. For the SSI curves, cells were held at the conditioning potential ranging from -120 to +20 mV for 50 ms and the available channel fraction was assessed by a depolarizing pulse to -20 mV. Each point represents the mean ± 95CI from 4 to 11 cells.