Loss of Function of hNa$_{\text{1.5}}$ by a ZASP1 Mutation Associated With Intraventricular Conduction Disturbances in Left Ventricular Noncompaction

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**Background**—Defects of cytoarchitectural proteins can cause left ventricular noncompaction, which is often associated with conduction system diseases. We have previously identified a p.D117N mutation in the LIM domain-binding protein 3—encoding Z-band alternatively spliced PDZ motif gene (ZASP) in a patient with left ventricular noncompaction and conduction disturbances. We sought to investigate the role of p.D117N mutation in the LBD3 NM_001080114.1 isoform (ZASP1-D117N) for the regulation of cardiac sodium channel (Na$_{\text{1.5}}$) that plays an important role in the cardiac conduction system.

**Methods and Results**—Effects of ZASP1-wild-type and ZASP1-D117N on Na$_{\text{1.5}}$ were studied in human embryonic kidney-293 cells and neonatal rat cardiomyocytes. Patch-clamp study demonstrated that ZASP1-D117N significantly attenuated $I_{\text{Na}}$ by 27% in human embryonic kidney-293 cells and by 32% in neonatal rat cardiomyocytes. In addition, ZASP1-D117N rightward shifted the voltage-dependent activation and inactivation in both systems. In silico simulation using Luo-Rudy phase 1 model demonstrated that altered Na$_{\text{1.5}}$ function can reduce cardiac conduction velocity by 28% compared with control. Pull-down assays showed that both wild-type and ZASP1-D117N can complex with Na$_{\text{1.5}}$ and telethonin/T-Cap, which required intact PDZ domains. Immunohistochemical staining in neonatal rat cardiomyocytes demonstrates that ZASP1-D117N did not significantly disturb the Z-line structure. Disruption of cytoskeletal networks with 5-iodonaphthalene-1-sulfonyl homopiperazine and cytochalasin D abolished the effects of ZASP1-D117N on Na$_{\text{1.5}}$.

**Conclusions**—ZASP1 can form protein complex with telethonin/T-Cap and Na$_{\text{1.5}}$. The left ventricular noncompaction-specific ZASP1 mutation can cause loss of function of Na$_{\text{1.5}}$, without significant alteration of the cytoskeletal protein complex. Our study suggests that electric remodeling can occur in left ventricular noncompaction subject because of a direct effect of mutant ZASP on Na$_{\text{1.5}}$. (Circ Arrhythm Electrophysiol. 2012;5:1017-1026.)

**Key Words:** Z-band alternatively spliced PDZ motif gene ■ sodium channel ■ cardiac conduction disturbance ■ left ventricular noncompaction

Left ventricular noncompaction (LVNC) is associated with heart failure and arrhythmias, such as atrioventricular block and intraventricular conduction disturbance. Recently, we have demonstrated that genetic defects of the LIM domain-binding protein 3—encoding Z-band alternatively spliced PDZ-motif protein (ZASP) are associated with LVNC.1 In the study, we identified ZASP1-D117N mutation in 2 white men who suffered from systolic dysfunction, dilated left ventricle with hypertrabeculated myocardium, and intraventricular conduction disturbance. Both patients showed sporadic heterozygote mutation. One of the patients had a family history of sudden cardiac death.

**Clinical Perspective on p 1026**

ZASP is one of the major components of the Z-disk proteins in cardiac muscle,2 which plays an important role in stabilizing the Z-disk structure through its PDZ-mediated...
interaction with α-actinin-2, the main component of the Z-disk actin cross-linker, and F-actin, the main cytoarchitectural protein of cardiomyocytes. Global ablation of the murine ZASP homolog cypher can disorganize both sarcomere and cytoskeleton, leading to severe cardiomyopathy and skeletal myopathy in mice and humans, termed zaspopathy, whereas the cardiac-specific ablation of cypher led to dilated cardiomyopathy and sudden cardiac death. However, the detailed underlying mechanisms of arrhythmias in zaspopathy remain unclear.

In contrast, loss of function of sodium channel (Na1.5) has been recognized as a key pathophysiological mechanism of inherited conduction diseases. In addition, recent studies proposed a novel concept that the defects of nonion channel proteins or channel-interacting proteins can affect the function of various ion channels, leading to secondary channelopathies.

Along these lines of evidence, we hypothesized that mutant ZASP in LVNC patients might affect Na1.5. The effects of ZASP1-D117N on the function of Na1.5 and the anatomic remodeling of cytoarchitecture were studied in mammalian expression systems and neonatal rat cardiomyocytes (NRCMs). The amplitude and voltage dependency of activation and inactivation of Na1.5 were affected by ZASP1-D117N, which can lead to conduction disturbances confirmed by a computer simulation. These findings uncover some key elements of the mechanisms leading to conduction disturbances in zaspopathy.

**Materials and Methods**

**Human Embryonic Kidney-293 Cell Preparation and Transient Expression of Wild-type and Mutant ZASP1**

The detailed methods are described in Expanded Methods in the online-only Data Supplement. Briefly, human embryonic kidney-293 (HEK-293) cells stably expressing hNa1.5 were transfected with the plasmid pcDNA3.1–CT-green fluorescent protein-TOPO containing wild-type (wt) or mutant ZASP1 cDNA.

**NRCM Isolation and Transient Expression of wt and Mutant ZASP1**

This research protocol was approved by the Institutional Animal Care and Use Committee at Texas Heart Institute and Indiana University. The NRCMs were isolated according to the procedure described previously (see Expanded Methods in the online-only Data Supplement).

**Patch Clamp**

Whole-cell configuration of the voltage-clamp technique was used to record \( I_{Na} \) and \( I_{Na}^{\text{m}} \) as previously described (see Expanded Methods in the online-only Data Supplement).

**Computer Simulation**

Computer simulations of conduction were performed in a 3-cm-long cable of coupled myocytes described by the Luo-Rudy phase 1 model. The voltage is governed by the following partial differential equation:

\[
\frac{\partial V}{\partial t} = \frac{I_{\text{in}}}{C_m} + D \frac{\partial^2 V}{\partial t^2}
\]

where \( C_m = 1 \mu F/cm^2 \), and \( D=0.001 \) cm\(^2\)/ms is the diffusion constant. This value of the diffusion constant corresponds to a lumped myoplasmic and gap junctional intercellular conductance of 0.92 \( \mu S/\mu m \). The differential equations were integrated with a finite difference method, with a spatial step of 100 \( \mu m \) and a time step of 0.01 ms. The maximum sodium channel conductance was set as \( G_{Na} = 16 \) mS/cm\(^2\), which gives rise to a conduction velocity (CV) of 57.4 cm/s.

**Immunohistochemistry**

Immunohistochemical staining was performed by the standard technique as described in Expanded Methods in the online-only Data Supplement.

**In Vitro Interaction Pull-Down Assay**

Interactions between ZASP1 and Na1.5 were studied with His-tagged pull-down assays (ProFound pull-down PolyHis Protein-Protein Interaction Kit; Pierce, IL; see details in Expanded Methods in the online-only Data Supplement).

**Statistics**

Comparison of the continuous variables between 2 groups (ZASP1-wt versus ZASP1-D117N) was performed using Mann-Whitney-Wilcoxon test. The Kruskal-Wallis test was conducted to compare continuous variables among 3 groups, with post hoc Mann-Whitney-Wilcoxon test to compare differences between any 2 groups. All comparisons were performed to test 2-tailed methods, and \( P<0.05 \) was considered statistically significant. Statistical analyses were performed using SPSS PASW Statistics 17 software (IBM, Chicago, IL). Data in the text and figures are presented as median (25th percentile; 75th percentile) or mean±SD unless otherwise stated.

**Results**

**ZASP1-D117N Causes Loss of Function of hNa1.5 in HEK-293 Cells**

To study the effects of wt and mutant ZASP1 on hNa1.5 function, HEK-293 cells stably expressing hNa1.5 were transiently transfected with green fluorescent protein-tagged ZASP1-wt or ZASP1-D117N plasmids (5 µg). Figure 1A represents superimposed macroscopic hNa1.5 current \( (I_{Na}) \) traces at various depolarization levels obtained from the cells expressing ZASP1-wt or ZASP1-D117N. The peak \( I_{Na} \) densities were significantly reduced in the cells transfected with ZASP1-D117N compared with ZASP1-wt. Compared with ZASP1-wt, ZASP1-D117N shifted the onset and peak voltage of the I-V curve toward positive by 10 and 15 mV, respectively (Figure 1B).

To study the voltage dependency of steady-state activation and inactivation, the peak conductance and peak currents induced by a prepulse protocol were plotted against the membrane potentials and fitted with the Boltzman equation. ZASP1-D117N was found to rightward shift the activation curve by 7 mV and rightward shift the inactivation curve by 5 mV compared with ZASP1-wt (Figure 1C). The slope factors (k) in the steady-state activation were also affected by ZASP1-D117N. Despite the smaller shift of inactivation curve, the larger shift of activation curve might increase the voltage threshold required to activate \( I_{Na}^{\text{m}} \), contributing to the decrease in CV.

Recovery time course from fast inactivation was examined by a double-pulse protocol. ZASP1-D117N was found to accelerate the fast component of recovery time compared with ZASP1-wt (Figure 1D). Figure 1E represents the development of slow inactivation. The time course was comparable between the 2 groups. In addition, direct transition from...
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The effects of ZASP1-wt and ZASP1-D117N on hNa1.5 in HEK-293 cells. A, Superimposed whole-cell current traces induced by a step-pulse protocol (20 ms between −120 and 80 mV) from a holding potential of −140 mV. B, I-V relationships. C, Voltage dependence of peak conductance and steady-state fast inactivation. Conductance $G(V)$ was calculated by the equation $G(V) = I(V - E_{rev})$, where $I$ is the peak current, $E_{rev}$ is the measured reversal potential, and $V$ is the membrane potential. The normalized peak conductance was plotted as a function of membrane potentials. Steady-state inactivation was estimated by prepulse protocols (500 ms) from a holding potential of −140 mV. The normalized peak currents were plotted as a function of membrane potentials. Steady-state activation and inactivation were fitted with the Boltzmann equation $y = \frac{1}{1 + \exp \left( \frac{V - V_h}{k} \right)}$, where $y$ represents variables; $V_h$, midpoint; $k$, slope factor; and $V_{m}$, membrane potential. Data were represented as mean±SD. D, Recovery from the fast inactivation estimated by a double-pulse protocol shown in inset. The recovery time course was fitted with a double exponential function $I(t)/I_{max} = C - A_f \times \exp(−t/\tau_f) - A_s \times \exp(−t/\tau_s)$, where $t$ is the recovery time, $A_f$ and $A_s$ are the fraction of fast and slow components, and $\tau_f$ and $\tau_s$ are the time constants of fast and slow components of recovery. E, Time course for the development of slow inactivation. The pulse protocol is shown as inset. Voltage was stepped from a holding potential of −90 to −30 mV for various times, stepped to −90 mV for 20 ms to allow recovery from fast inactivation, and then stepped to −30 mV (20 ms). To generate the curves, the current amplitude during the test pulse (second pulse) was normalized as a fraction of the current amplitude during the first pulse and plotted against the duration of control pulse. The curve was fit with a double exponential equation. F, Closed-state inactivation. The membrane potential was held at −100 mV for various durations ($\Delta t$) from a holding potential of −140 mV before the test pulse (20 ms at −20 mV). The normalized currents by the maximal currents ($t = 1 \text{ ms}$) were plotted against $\Delta t$. Data are presented as mean±SD.

Table 1. Na$_{\text{v}}$1.5 Parameters

<table>
<thead>
<tr>
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<th>HEK-293 Cells</th>
<th>NRCMs</th>
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<tr>
<td></td>
<td>wt (n)</td>
<td>D117N (n)</td>
<td>wt (n)</td>
</tr>
<tr>
<td>Peak current density, pA/pF</td>
<td>20</td>
<td>−265.1 (−306.4 to −181.8)</td>
<td>19</td>
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<tr>
<td>Activation</td>
<td>23</td>
<td>−45.4 (−52.2 to −41.3)</td>
<td>18</td>
</tr>
<tr>
<td>$V_h$, mV</td>
<td>7.26 (5.9 to 8.4)</td>
<td>6.55 (5.8 to 8.1)*</td>
<td>7.3 (6.4 to 7.7)</td>
</tr>
<tr>
<td>Fast inactivation</td>
<td>16</td>
<td>−97.0 (−103.0 to −95.4)</td>
<td>19</td>
</tr>
<tr>
<td>$k$</td>
<td>6.1 (5.8 to 6.5)</td>
<td>7.2 (6.4 to 7.8)</td>
<td>6.9 (6.1 to 7.4)</td>
</tr>
</tbody>
</table>

NRCM indicates neonatal rat cardiomyocytes; n, the number of patches; $V_h$, midpoint voltage of maximal activation/inactivation; $k$, slope factor.

*P<0.05; †P<0.01 vs ZASP1-wt.

The effects of ZASP1-D117N on the late $I_{Na}$ were also studied in HEK-293 cells. ZASP1-D117N did not significantly affect the 30-μmol/L tetrodotoxin-sensitive late $I_{Na}$ induced by a long depolarization pulse (online-only Data Supplement Figure I).

closed state to inactivation state without channel opening (closed-state inactivation) was studied. Interestingly, the time course of closed-state inactivation was accelerated by ZASP1-D117N compared with ZASP1-wt (Figure 1F). Tables 1 and 2 summarize the parameters of $I_{Na}$ studied in HEK-293 cells.
D117N plasmids on ied the effects of different ratios of ZASP1-wt and ZASP1-
slow inactivation \( \tau \), ms 8.00.1 (7.61.4–8.38.8) 12.02.6 (11.45.5–13.47.0)

\[ A_f, \% = 0.3 (0.2–0.3) \]
\[ A_s, \% = 0.9 (0.8–0.9) \]

\[ \tau_{\text{state-inactivation}} = 14 \]
\[ \tau_{\text{slow inactivation}} = 800.1 (761.4–838.8) \]
\[ 1202.6 (1145.5–1347.0) \]

n indicates the number of patches; \( \tau_{f} \) and \( \tau_{s} \), the time constants of fast and slow components of recovery; \( A_f \) and \( A_s \), the fraction of fast and slow components.

\[ *P<0.05 \text{ vs ZASP1-wt.} \]

Because our patients were heterozygote, \(^1\) we also studied the effects of different ratios of ZASP1-wt and ZASP1-D117N plasmids on \( I_{\text{Na}} \). Although transfection with 5 \( \mu \)g of ZASP1-wt and 1 \( \mu \)g of ZASP1-D117N plasmids did not significantly reduce \( I_{\text{Na}} \), compared with 5 \( \mu \)g of ZASP1-wt, the transfection with 3 \( \mu \)g of ZASP1-wt and 3 \( \mu \)g of ZASP1-D117N, which might mimic the heterozygotic situation, significantly decreased \( I_{\text{Na}} \) and rightward shifted the peak voltage (online-only Data Supplement Figure II).

Effects of ZASP1-D117N on Delayed Rectifier Potassium Channels

We also studied whether ZASP1-D117N can affect 2 major components of delayed rectifier potassium channels (slow component, \( I_{\text{Ks}} \) and rapid component, \( I_{\text{Kr}} \)). ZASP1-D117N did not significantly affect \( I_{\text{Ks}} \) and \( I_{\text{Kr}} \) in mammalian cell lines (online-only Data Supplement Figure III). These results indicate that ZASP1-D117N specifically alters the \( I_{\text{Na}} \) functions.

Expression of ZASP1 and Cytoarchitectural Proteins in HEK-293 Cells

The expression of mRNAs from genes encoding various cytoarchitectural proteins in HEK-293 cells suggests that this cell line may express cardiomyocyte-like proteins. \(^14\) The expression of various cytoskeletal proteins was studied using proteins extracted from HEK-293 cells stably expressing Flag-tagged hNa\(_1.5\) and transiently expressing V5-tagged ZASP1-wt or ZASP1-D117N. Figure 2 demonstrates that exogenous ZASP1-wt and ZASP1-D117N (V5-tagged), as well as endogenous ZASP, \( \alpha \)-actinin-2, dystrophin (DMD), syntrophin \( \alpha_1 \), T-Cap, and \( \beta \)-actin, were expressed in HEK-293 cells.

Protein Interaction Between Na\(_1.5\) and ZASP1-Telethonin/T-Cap Complex

To study the protein-protein interaction between hNa\(_1.5\) and ZASP1-wt or ZASP1-D117N, pull-down assays were performed (Figure 3). First, 3 batches of *Escherichia coli* were transformed with the plasmids containing SCN5A, V5/His-tagged ZASP1-wt, or V5/His-tagged ZASP1-D117N. The protein expression of Na\(_1.5\) and ZASP was confirmed with Western blot using anti-pan sodium channel and anti-V5 antibodies (panel A, left blot). Second, the proteins extracted from the HEK-293 cells stably expressing hNa\(_1.5\) were incubated with V5/His-tagged ZASP1-wt or ZASP1-D117N produced in *E. coli* transformed with the corresponding plasmids. The protein mixture was immunoprecipitated with the beads coated with anti-His antibody. The precipitants were analyzed with Western blot using anti-pan sodium channel antibody, anti–T-Cap antibody, and anti-V5 antibody. The results showed that both ZASP1-wt and ZASP1-D117N can form a protein complex with hNa\(_1.5\) and T-Cap (panel A, mid blot). Third, the same protocol was performed using the NRCM lysates. Panel A, right blot shows that both ZASP1-wt and ZASP1-D117N can form a protein complex with rat Na\(_1.5\) and T-Cap.

Because ZASP1 possesses N-terminal PDZ domain that is important for protein-protein interaction, we examined whether the PDZ domain is essential for the formation of protein complex. A pull-down assay using a ZASP1 segment (ZM) that lacks the PDZ domain was performed. The proteins extracted from the stable HEK-293 cells were incubated with V5/His-tagged ZM-wt or ZM-D117N produced in *E. coli*. The protein mixture was immunoprecipitated with anti-His antibody, and the precipitants were analyzed with Western blot. Figure 3B shows that neither Na\(_1.5\) nor T-Cap was detected in the immunoprecipitants, indicating that the PDZ domain is critically involved in the formation of protein complex among ZASP1, Na\(_1.5\), and T-Cap.

ZASP1-D117N Alters Na\(_1.5\) Functions in NRCMs

The interaction and functional modification of \( I_{\text{Na}} \) by ZASP in HEK-293 cells may substantially differ from those in cardiomyocytes. Therefore, we studied the effects of ZASP1-wt and ZASP1-D117N on \( I_{\text{Na}} \) in NRCMs. The isolated NRCMs were transfected with green fluorescent protein-tagged ZASP1-wt or ZASP1-D117N using electroporation. Figure 4A represents superimposed macroscopic \( I_{\text{Na}} \) traces obtained from the NRCMs transfected with ZASP1-wt or ZASP1-D117N. Similar to the observation in HEK-293 cells, ZASP1-D117N decreased the \( I_{\text{Na}} \) densities and rightward shifted the onset and peak voltage of I-V relationships by 15 mV compared with ZASP1-wt (Figure 4B). ZASP1-D117N was found to rightward shift the voltage dependency of steady-state activation and inactivation by 11.8 and 8.4 mV, respectively (Figure 4C). The slope factors in the steady-state activation and inactivation were not significantly affected by ZASP1-D117N (Figure 4C). These data indicate that ZASP1-D117N can cause loss of function of cardiac sodium channel in NRCMs similar to the effects on human Na\(_1.5\) in mammalian cell lines. Table 1 summarizes the \( I_{\text{Na}} \) parameters in NRCMs.

Localization of ZASP1 and Cytoarchitectural Proteins in NRCMs

Next, we studied the localization of ZASP-wt and ZASP-D117N in NRCMs. NRCMs were transfected with green fluorescent protein-tagged ZASP1-wt or ZASP1-D117N. The cells were cultured for 24 to 48 hours, then fixed and stained with antibodies against various cytoarchitectural proteins.
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demonstrates that the voltage dependency of steady-state activation and inactivation was not affected by ZASP1-D117N after ML-7 treatment. Similar results were obtained in the cells treated with Cyto-D (Figure 6D–6F). Table 3 summarizes the parameters with ML-7 and Cyto-D treatments.

**Decline of Na+ Conductance by ZASP1-D117N Modulates CV and Conduction Failure**

An important question is whether these modifications of Na1.5 by ZASP-D117N can cause conduction disturbances in actual human hearts. It has been believed that cardiac conduction in ventricles depends on the magnitude of the available Na+ conductance, which in turn depends on the voltage dependence of channel activation and inactivation. Computer simulations were performed with the Luo-Rudy phase 1 model using the gating kinetic parameters of the sodium channel provided in Table 1 (HEK-293 cells). The results demonstrated that the alteration of Na+ channels mediated by ZASP1-D117N would have a distinct effect in depolarized tissue compared with that by ZASP1-wt. Figure 7 shows the influence of sodium channel conductance and kinetics on CV. At control, CV was 57.4 cm/s. At 30% reduction of GNa to 11.2 mS/cm2, CV was reduced by ≈12% to 50.5 cm/s. A right shift of 10 mV in both the activation and inactivation curves resulted in a 16% reduction to 48.1 cm/s. The combined effect of both changes applied at the same time results in a reduction of 27% in CV to 41.8 cm/s.

**Discussion**

In this study, we demonstrated several underlying mechanisms by which ZASP1-D117N, a ZASP mutation identified in patients suffering from dilated cardiomyopathy/LVNC, may cause intraventricular conduction disturbance: (1) ZASP1-D117N can cause loss of function of Na1.5 in human cell lines, as well as in neonatal cardiomyocytes; (2) in silico simulation using the Luo-Rudy model shows that the extent of functional disturbances of Na1.5 caused by ZASP-D117N is sufficient enough to delay cardiac conduction in human hearts; (3) the interaction between ZASP1 and Na1.5 requires a preservation of Z-disk protein complex; and (4) the modification of Na1.5 by ZASP1-D117N occurs without significant disruption of Z-line structures in cardiomyocytes.

**How Does ZASP1 Interact With Na1.5?**

In cardiomyocytes, various cytoarchitectural proteins interact with each other to form structural networks: (1) ZASP1 binds...
to ACNT2; (2) F-actin fibers are anchored to the Z-line via ACNT2; (3) DMD binds to F-actin, and (4) syntrophin α1 forms a complex with DMD (dystrophin-associated protein complex). It has been reported that these proteins can alter the function and localization of \( \text{Na}^+_{1.5} \). For example, dystrophin-associated protein complex can directly interact with the 3 last residues of \( \text{Na}^+_{1.5} \) (Ser-Ile-Val) that constitutes a PDZ-binding motif and plays a role in anchoring \( \text{Na}^+_{1.5} \) to the lateral membranes. Ablation of dystrophin can attenuate cardiac conduction because of a reduction in \( I_{\text{Na}} \).
ZASP Mutation Alters Cardiac Sodium Channel

Telethonin/T-Cap, a member of Z-disk protein complex, can interact with Na\textsubscript{v}1.5, and a mutation of T-Cap can alter the function of Na\textsubscript{v}1.5.\textsuperscript{19} Recently, SAP97 was found to interact with Ser-Ile-Val motif of Nav1.5 and contribute to the localization of Nav1.5 in intercalated disks.\textsuperscript{20} However, no data have been previously reported with regard to an interaction among ZASP1, telethonin/T-Cap, and Nav1.5.

Our study demonstrates that: (1) both wt and mutant ZASP1 can form a protein complex with Nav1.5 and telethonin/T-Cap (Figure 3A); (2) ZASP1-D117N does not alter the association with Nav1.5 and telethonin/T-Cap (Figure 3A); (3) the PDZ domain is necessary to form the protein complex among ZASP1, Nav1.5, and telethonin/T-Cap (Figure 3B); and (4) Z-line structures were not significantly disrupted by ZASP1-D117N in cardiomyocytes (Figure 5). Therefore, we speculated that the stability of Z-line structure network is important for interaction between ZASP1 and Nav1.5 and that ZASP1-D117N might alter the function of Nav1.5 by affecting local protein conformational change. In fact, when we disbanded the linkage between ZASP and the cytoskeleton with ML-7 and Cyto-D, the modulation of Nav1.5 by ZASP1-D117N was abolished. However, our study also showed that the treatment

**Table 3. Effect of ML-7 and Cytochalasin D on Nav1.5 Parameters**

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<tr>
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<th>ML-7</th>
<th>Cytochalasin D</th>
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<tbody>
<tr>
<td></td>
<td>wt (n=15)</td>
<td>D117N (n=10)</td>
</tr>
<tr>
<td>Peak current density, pA/pF</td>
<td>(-231.6 (-288.4 to -193.9))</td>
<td>(-230.8 (-282.3 to -159.1))</td>
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<tr>
<td>Activation</td>
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<tr>
<td>V\textsubscript{a}, mV</td>
<td>(-36.2 (-38.7 to -35.2))</td>
<td>(-42.2 (-47.2 to -39.4))</td>
</tr>
<tr>
<td>k</td>
<td>7.5 (5.7 to 8.3)</td>
<td>7.4 (6.8 to 7.8)</td>
</tr>
<tr>
<td>Fast inactivation</td>
<td></td>
<td></td>
</tr>
<tr>
<td>V\textsubscript{h}, mV</td>
<td>(-99.9 (-104.6 to -96.4))</td>
<td>(-95.0 (-101.7 to -91.2))</td>
</tr>
<tr>
<td>k</td>
<td>6.8 (6.3 to 7.2)</td>
<td>6.2 (5.6 to 7.1)</td>
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n indicates the number of patches; V\textsubscript{h}, midpoint voltage of maximal activation/inactivation; k, slope factor.
of NRCMs with ML-7 and Cyto-D did not alter \( I_{\text{Na}} \) in the cells transfected with ZASP1-wt. This suggests that ML-7 and Cyto-D may affect unknown signal transduction pathways by which ZASP1-D117N can cause modification of Na\(_{\text{v}}\) 1.5.

Another speculative underlying mechanism is that a local conformational change of Z-line complex by ZASP1-D117N may alter the mechanical stress between F-actin and DMD/syntrophin α1 complex, which may ultimately lead to modification of Na\(_{\text{v}}\) 1.5 function. Although we do not have a direct evidence of this mechanism, a similar concept has been proposed by a recent study using atomic force microscope that directly demonstrated a critical role of telethonin/T-Cap molecule in the regulation of mechanical tension of cytoskeletal networks.\(^{21}\)

**Localization of Na\(_{\text{v}}\) 1.5 via ZASP/Telethonin Complex**

Although Na\(_{\text{v}}\) 1.5 preferentially localizes at the intercalated disk via SAP97 and lateral membranes via dystrophin-associated protein complex (2 pools), localization at the T-tubular system has also been recognized.\(^{22-24}\) It seems that Na\(_{\text{v}}\) 1.5 upon posttranslational modification remains attached to the cytoskeleton probably linked to multiprotein complexes and stored in subcellular compartments. Recent study showed that Na\(_{\text{v}}\) 1.5 localizes at the cardiomyocyte membrane along the sarcomeric Z-lines via α-actinin-2, thus connecting Na\(_{\text{v}}\) 1.5 to actin filaments.\(^{25}\) ZASP/telethonin may contribute to localizing Na\(_{\text{v}}\) 1.5 to the T-tubular membrane at the Z-line. Therefore, it is unlikely that the ZASP1-Na\(_{\text{v}}\) 1.5-telethonin/T-Cap protein complex represents a new pool, but rather it brings further evidence of multiprotein complex associated with α-actinin-2.

**Electrical Remodeling May Precede Anatomic Remodeling**

Our study suggests that electric remodeling may precede anatomic remodeling in LVNC associated with ZASP: the loss of function of Na\(_{\text{v}}\) 1.5 by the mutated ZASP1 can occur without significant disruption of cytoarchitectural networks. This is particularly important in a clinical situation because patients who carry ZASP1-D117N may develop arrhythmias even before manifesting heart failure symptoms. Although the conduction disturbances observed in our patients might be caused by degeneration or fibrosis of conduction system as a consequence of anatomic remodeling, it is reasonable to speculate that the loss of function of Na\(_{\text{v}}\) 1.5 by ZASP1-D117N might exaggerate the conduction delay even if it is caused by anatomic remodeling.

Interestingly, we have previously reported a similar observation in a cardiac-specific transgenic mouse model of dilated cardiomyopathy caused by p.S196L mutation in ZASP4, another ZASP isoform highly expressed in human hearts. In mice expressing ZASP4-S196L, cardiac conduction defects and atrioventricular block were observed at 3 months of age before myocardial structural remodeling, and ventricular dysfunction occurred at 10 months of age.\(^{26}\) In this model, we observed attenuation of L-type Ca\(^{2+}\) currents and rightward shift of voltage dependency of Na\(_{\text{v}}\) 1.5, which was different from electric remodeling by ZASP1-D117N.

Because we do not have multiple biopsy samples of patients’ cardiac muscles at different time points because of ethical reasons and a transgenic mouse model of ZASP1-D117N was embryonic lethal (data not shown), we cannot infer whether ZASP1-D117N, also, follows the same pattern of ZASP4-S196L.

**Can the Biophysical Modification of Na\(_{\text{v}}\) 1.5 by ZASP1-D117N Cause Conduction Blocks?**

Our computer simulation demonstrated that the biophysical modification of \( I_{\text{Na}} \) by ZASP1-D117N can reduce CV by 27%. However, because the actual CV in our patients was unknown, whether such decrease in CV can cause intraventricular conduction delay remains undetermined in this study. Recently, Smits et al\(^{27}\) reported that an SCN5A mutation E161K identified in a patient who suffered from overlap disease of Brugada syndrome and conduction block can decrease the peak \( I_{\text{Na}} \) and rightward shift the voltage dependency of steady-state activation, resulting in the reduction of CV in ventricle from 65 to 50 cm/s. This suggests that a 27% reduction in CV may be sufficient to cause conduction disturbances, although further clinical electrophysiological studies are warranted.

**Figure 7. Changes in conduction velocity (CV) in a cable of Luo-Rudy 1 model cells because of changes in the sodium properties.**

**A** Measured CV as a function of \( G_{\text{Na}} \) and \( \Delta V_{\text{act/inact}} \) (the shift in activation and inactivation curves).

**B** Standard steady-state activation and inactivation curves (solid lines) and the activation and inactivation curves shifted by +10 mV (dashed lines).

**C** Change in CV from the situation with standard parameter values (control) because of a reduction in the maximum sodium channel conductance to 11.2 mS/cm\(^2\) (low \( G_{\text{Na}} \)), a shift by 10 mV in the positive direction of the sodium channel activation and inactivation curves (shifted curves), and both of these changes (both).
Conclusions
We conclude that ZASP1-D117N, a mutation previously identified in patients with cardiomyopathy, might contribute to conduction system diseases associated with the structural cardiac disease. These data confirm our previous hypothesis and provide novel insights into the relationship between cytoskeletal proteins and ion channels. Although further studies elucidating the detailed dynamics of wt and mutant ZASP in human arrhythmias and heart failure are warranted, we believe that our data contribute to understanding the mechanisms of arrhythmias in this LVNC subject and provide a new framework for therapeutic interventions in patients suffering from arrhythmias associated with cardiomyopathy.

Study Limitation
Our system uses overexpression of ZASP1-D117N in isolated cells rather than using a genetically engineered mouse model. However, our rationale originated from the observation that the mRNA level of ZASP is increased in human idiopathic dilated cardiomyopathy, thus we tested whether the overexpression of ZASP in NRCMs might recapitulate the cytoarchitectural environment in cardiomyocytes. In addition, although we have identified some components interacting with Na⁺1.5 in a complex, other sodium channel components, such as SCN1B, SCN2B, SCN3B, and SCN4B or currently unknown proteins, could also be involved in the localization and regulation of Na⁺1.5. Therefore, it is likely that Na⁺1.5 complex is much more multifaceted, and further investigation to elucidate these intrinsic connections is warranted.

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Disclosures
None.

References


**CLINICAL PERSPECTIVE**

The mechanistic links between genetic cardiomyopathies and arrhythmias are not fully defined. Some patients die suddenly before symptomatic heart failure develops. Mutations in the Z-band alternatively spliced PDZ motif gene that encodes a Z-disk protein have been identified in patients with dilated cardiomyopathy, left ventricular noncompaction, and various cardiac arrhythmias. In the current study, we demonstrate that a Z-band alternatively spliced PDZ motif gene mutation previously identified in left ventricular noncompaction patients can cause loss of function of the cardiac sodium channel. Z-band alternatively spliced PDZ motif gene forms a protein complex with telethonin, a member of Z-disk proteins, and Na_1.5. The proper function of this complex, including its interaction with actin fibers, may play an important role in the regulation of cardiac ion channels. This suggests a mechanism by which a mutation that disrupts a structural protein causes electrophysiological remodeling that may contribute to arrhythmias as an early manifestation of these cardiomyopathies.
Loss of Function of hNa\textsubscript{v,1.5} by a ZASP1 Mutation Associated With Intraventricular Conduction Disturbances in Left Ventricular Noncompaction

Yutao Xi, Tomohiko Ai, Enno De Lange, Zhaohui Li, Geru Wu, Luca Brunelli, W. Buck Kyle, Isik Turker, Jie Cheng, Michael J. Ackerman, Akinori Kimura, James N. Weiss, Zhilin Qu, Jeffrey J. Kim, Georgine Faulkner and Matteo Vatta

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Expanded Methods

Cell preparation and transient expression of wt and mutant ZASP1

Wt and mutant ZASP1 were generated as previous described. Cell preparation and transient transfection were performed as previously described. Sarcomere disturbances were carried out by the incubation of HEK-293 cells for 30 minutes in the medium containing 30 μM ML-7 (Sigma-Aldrich, MO) or Cytochalasin D (Cyto-D, Sigma-Aldrich, MO). The effects of wt and mutant ZASP1 on $I_K$ were studied in CHO cells which stably expressed KCNQ1 and KCNE1, or KCNH2 and KCNE2 with transient expression of ZASP1-wt or ZASP1-D117N.

Neonatal rat cardiomyocyte (NRCM) isolation and transient expression of wt and mutant ZASP1

All procedures were approved by the Institutional Animal Care and Use Committee at the Texas Heart Institute. The neonatal rat cardiomyocytes were isolated according to the procedure as previously described. Briefly, neonates (<3 days after birth) were deeply anesthetized with pentobarbiturate (i.p.). The hearts were excised quickly and rinsed in ice-cold PBS (Dulbecco’s phosphate-buffered saline, Invitrogen, Carlsbad, CA). The ventricles were transferred to a dry Petri dish and minced with a scalpel blade. The minced hearts were digested in a warm collagenase II and procaine. The digested cells were resuspended in adhesion medium: DMEM (ATCC, Manassas, VA) supplemented with 10% FBS and 2 mM glutamate. The cells were
placed on a 100 mm Petri dish and incubated for 1-1.5 hours at 37°C with 5% CO₂. After
fibroblasts were settled and stick to the bottom of the dish, the supernatants were collected.
Cardiomyocytes (1-2 millions) were aliquot into a 1.5 ml Eppendorf tube and centrifuged. The
cells were resuspended in a transfection buffer (VPE-1002, Amaxa, Gaithersburg, MD) with 10
µg plasmid pcDNA3.1-CT-GFP-TOPO containing either ZASP1-wt or ZASP1-D117N cDNA
and transferred into cuvettes. The transfection (nucleofection) was performed with an
electroporator according to the company’s protocol (Nucleofector-I Amaxa, Gaithersburg, MD).
The cells were incubated for 24 hours at 37°C with 5% CO₂. The cells showing green
fluorescence were selected to recode sodium currents ($I_{Na}$).

**Patch-clamp**

Experiments were carried out at ambient temperature unless otherwise stated. For $I_{Na}$
recording, the pipette solution contained (in mM): 5 NaF, 115 CsF, 20 CsCl, 10 EGTA and 10
HEPES (pH 7.35 with CsOH), and the bath solution contained (in mM): 145 NaCl, 1.0 MgCl₂,
10 tetraethylammonium (TEA) chloride, 5 CsCl, 10 HEPES, and 10 glucose (pH 7.35 with
NaOH). Whole-cell currents amplitude and gating kinetics were analyzed with Clampfit (Axon
Instruments, Sunnyvale, CA) and Igor software (WaveMetrics, Lake Oswego, OR).

**Immunohistochemistry**

Following antibodies were used: (1) mouse monoclonal anti-telethonin/T-Cap (1:100,
Sigma-Aldrich); (2) mouse monoclonal anti-ACTN2 (1:200); (3) rabbit polyclonal anti-
dystrophin (DMD, 1:200); and (4) rabbit polyclonal anti- α₁-syntrophin (SNTA1, 1:200). F-actin
was labeled with fluorescent phalloidin (1:500, Invitrogen). The nucleus was labeled with To-pro
633 nm (Invitrogen).

**In vitro interaction pull-down assay**

To produce ZASP and Na₁.5, E. coli were transformed with pcDNA 3.1/V5-His containing
ZASP1-wt or ZASP1-D117N, and SCN5A. The purified ZASP1-wt (His) or ZASP1-D117N (His)
was incubated with preys: the purified Na₁.5 from HEK-293 cells, and the lysate from NRCMs.
The eluted proteins were separated by SDS–PAGE, and stained with anti-pan voltage-gated
sodium channel (1:100), anti-telethonin (1:100), and anti-α-actinin antibodies (1:100). The
pcDNA3.1/V5-His-TOPO/lacZ (Invitrogen, Carlsbad, CA) was used for negative controls.
Supplemental Experiments

Supplemental Figure S-I. Effects of ZASP1-wt and ZAP1-D117N on the late $I_{\text{Na}}$.

(A) Representative traces of late $I_{\text{Na}}$ ($I_{\text{Na,L}}$) obtained from the cells stably expressing Nav1.5 transfected with ZASP-wt or ZASP-D117N. $I_{\text{Na,L}}$ was induced with a long depolarization pulse (-30 mV for 1000 ms from a holding potential of -80 mV). (B) Bar graph demonstrates the normalized amplitudes of $I_{\text{Na,L}}$ obtained from the cells transfected with ZASP1-wt or ZASP1-D117N. $I_{\text{Na,L}}$ were measured at 200 to 220 ms of the test pulse, and normalized by the peak $I_{\text{Na}}$. The numbers in the parenthesis depict the number of cells studied. The error bars represent SD.
Supplemental Figure S-II. Effects of different ratios of ZASP1-wt and ZASP1-D117N plasmids on Nav1.5. (A) The I-V relationships of peak $I_{Na}$ obtained from the cells transfected with various combinations of ZASP1-wt and ZASP1-D117N plasmids: 1 µg/5 µg; 3 µg/3 µg; 5 µg/1 µg. (B) The bar graphs of peak $I_{Na}$ for each condition. The numbers in the parenthesis depict the number of cells studied. The error bars represent SD. *$p<0.05$ vs. 5 µg/1 µg.
Effects of ZASP1-D117N on delayed rectifier potassium channels

Since abnormal repolarization may also cause cardiac conduction disturbances, we sought to investigate whether ZASP1-D117N can affect the function of two major components of delayed rectifier potassium channels (the slow component, $I_{Ks}$ and the rapid component, $I_{Kr}$). The experiments were conducted in the CHO cells stably-transfected with KCNQ1 with KCNE1 or KCNH2 with KCNE2, which mimics $I_{Ks}$ and $I_{Ks}$, respectively. Supplemental Figure S-III showed that the steady-state peak $I_{Ks}$ (Panel A) and $I_{Kr}$ (Panel C) were not significantly affected by ZASP1-D117N. The I-V relationships of the steady-state $I_{Ks}$ (Panel B) and $I_{Kr}$ (Panel D) were almost identical between the cells expressing ZASP1-D117N and ZASP1-wt. These results indicate that ZASP1-D117N specifically altered the Na,v1.5 functions. Supplemental Table S-I summarizes the parameters.
Supplemental Figure S-III. The effect of ZASP1-wt and ZASP1-D117N on slow delayed rectify potassium currents ($I_{\text{Ks}}$) and rapid delayed rectifier current ($I_{\text{Kr}}$). (A) Representative current traces of $I_{\text{Ks}}$. (B) Current-voltage (I-V) relationship of $I_{\text{Ks}}$ activation. The current amplitude was measured at the end of five second pulse between -60 mV and 60 mV from a holding potential of -80 mV. (C) Representative current traces of $I_{\text{Kr}}$. (D) I-V relationship of $I_{\text{Kr}}$ activation. The current amplitude was measured at the end of second pulse between -60mV and 60 mV from a holding potential of -80 mV.

Table S-I. Parameters of $K^+$ channels

<table>
<thead>
<tr>
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<th>$I_{\text{Ks}}$</th>
<th></th>
<th>$I_{\text{Kr}}$</th>
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<tbody>
<tr>
<td></td>
<td>WT (n=15)</td>
<td>D117N (n=11)</td>
<td>WT (n=10)</td>
</tr>
<tr>
<td>Peak current density (pA/pF)</td>
<td>40.6 [36.5; 47.2] @ 60mV</td>
<td>35.2 [33.8; 41.3] @ 60mV</td>
<td>2.4 [1.0; 3.3] @ 0mV</td>
</tr>
<tr>
<td>Tail current density at (pA/pF)</td>
<td>-15.0 [-24.0; -11.7] @ -40mV</td>
<td>-12.1 [-35.9; -6.7] @ -40mV</td>
<td>2.7 [0.4; 4.2] @ -40mV</td>
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Data are presented as median [25th percentile; 75th percentile].