

Voltage-gated sodium channel (Na_V) protein dissection creates a set of functional pore-only proteins

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Many voltage-gated ion channel (VGIC) superfamily members contain six-transmembrane segments in which the first four form a voltage-sensing domain (VSD) and the last two form the pore domain (PD). Studies of potassium channels from the VGIC superfamily together with identification of voltage-sensor only proteins have suggested that the VSD and the PD can fold independently. Whether such transmembrane modularity is common to other VGIC superfamily members has remained untested. Here we show, using protein dissection, that the *Silicibacter pomeroyi* voltage-gated sodium channel (Na_VSp1) PD forms a stand-alone, ion selective pore (Na_VSp1p) that is tetrameric, α -helical, and that forms functional, sodium-selective channels when reconstituted into lipid bilayers. Mutation of the Na_VSp1p selectivity filter from LESWSM to LDDWSD, a change similar to that previously shown to alter ion selectivity of the bacterial sodium channel Na_VBh1 (NaChBac), creates a calcium-selective pore-only channel, Ca_VSp1p. We further show that production of PDs can be generalized by making pore-only proteins from two other extremophile Na_Vs: one from the hydrocarbon degrader *Alcanivorax borkumensis* (Na_VAb1p), and one from the arsenite oxidizer *Alkalilimnicola ehrlichei* (Na_VAe1p). Together, our data establish a family of active pore-only ion channels that should be excellent model systems for study of the factors that govern both sodium and calcium selectivity and permeability. Further, our findings suggest that similar dissection approaches may be applicable to a wide range of VGICs and, thus, serve as a means to simplify and accelerate biophysical, structural, and drug development efforts.

Voltage-gated sodium channels (Na_Vs) are large polytopic membrane proteins involved in action potential generation in excitable cells and belong to an ion channel superfamily that includes voltage-gated calcium channels (Ca_Vs), voltage-gated potassium channels (K_Vs), and transient receptor potential (TRP) channels (1, 2). Within the voltage-gated ion channel (VGIC) superfamily, Na_Vs and Ca_Vs are close relatives (1–3) that share a topology of 24 transmembrane segments organized in four homologous six-transmembrane repeats. These two families are also thought to share some common structure in the ion selectivity filter despite having markedly different ion permeation properties (4). Both are central to human neuromuscular, cardiovascular, and neural physiology. Consequently, they are targets for a host of pharmaceuticals used to treat a diverse set of disorders and remain active targets for drug development (5–7). Recently, single subunit, six-transmembrane segment Na_Vs have been identified in a large number of bacteria from diverse environments (8, 9). These channels show clear similarities to eukaryotic Na_Vs and Ca_Vs (2, 9, 10), suggesting that the prokaryotic channels may have been ancestors of the more complex vertebrate channels.

Despite the central importance of Na_Vs, nothing is known about the high-resolution structure of the Na_V transmembrane portions. Present knowledge is limited to low-resolution electron

microscopy studies (19 Å) that have suggested some general features of Na_Vs purified from eel electric organs (11) but that lack the resolution for detailed mechanistic insight. Study of bacterial Na_Vs provides a simplified system for understanding basic aspects of both Na_V and Ca_V function and holds promise as a template for guiding small molecule modulator development (6). Although there have been ongoing efforts to produce bacterial Na_V samples that can be used for biochemical and structural studies (12–14), these have yet to achieve the multi-milli-gram amounts required for extensive structural studies.

Here, we show that a protein dissection approach produces folded, electrophysiologically active pore domains (PDs) from a set of bacterial Na_Vs. These PDs are well-behaved, biochemically tractable, stand-alone pores that can be produced in multi-milli-gram amounts. Application of a battery of biochemical and biophysical characterizations demonstrates that the PD-only proteins self-assemble as tetramers having α -helical structure and form functional channels when incorporated into lipid bilayers. We further show that introduction of aspartic acid residues at key selectivity filter positions in the *Silicibacter pomeroyi* PD-only channel Na_VSp1p creates a channel, Ca_VSp1p, in which ion selectivity is changed from sodium to calcium. Taken together, our data demonstrate that the Na_V pore-only proteins are active and biochemically accessible ion channels. Because of their favorable biochemical properties, these Na_V PDs should provide excellent model systems for the structural study of the factors that govern sodium selectivity and permeability. Further, the dissection strategy eliminates the potential complications that arise from voltage-sensing domain (VSD) conformational heterogeneity and should be a generally applicable means to simplify studies of the PDs of other VGIC superfamily members.

Results

Creation of a Pore-Only Na_V. We previously identified an Na_V from the marine sulfur-reducing bacterium *S. pomeroyi* (Na_VSp1), which is functional when expressed in mammalian cells (8), as a protein that could be highly expressed (approximately 20 mg L⁻¹) in *Escherichia coli* membranes (15). Despite the high expression level, size-exclusion chromatography analysis of purified, detergent-solubilized Na_VSp1 revealed a broad elution profile indicative of a polydisperse sample that was not well suited to further

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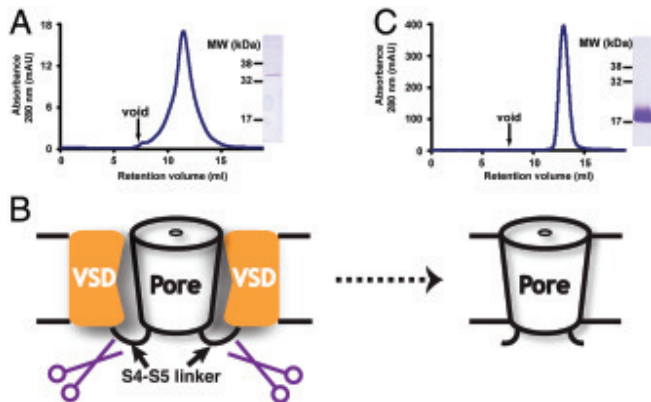


Fig. 1. Creation of a pore-only Na_V . (A) Superdex 200 size-exclusion chromatography of $\text{Na}_V\text{Sp1}$ in 200 mM NaCl, 0.3 mM DDM, 20 mM HEPES, pH 8.0. (Inset) Fifteen percent SDS-PAGE of the peak fraction. (B) Cartoon depicting the strategy for creating a pore-only channel. Two of the four VSDs are shown along with the S4-S5 linker. Scissors indicate the dissection point (Left). (C) Superdex 200 size-exclusion chromatography of $\text{Na}_V\text{Sp1p}$ in 200 mM NaCl, 0.3 mM DDM, 20 mM Hepes pH 8.0. (Inset) Fifteen percent SDS-PAGE of the peak fraction.

characterization (Fig. 1A). Thus, we sought alternative strategies to produce biochemically tractable Na_V samples.

Three lines of evidence have suggested that VGIC members are composed of two domains that can fold independently, the VSD and PD (16–18): comparison of potassium channel gene families (19), structural and chimera studies of potassium channels (16, 20–25), and identification of both pore-only (26) and voltage-sensor-only proteins (27–29). In further support of this idea, the independence of potassium channel PDs have been demonstrated by the functional reconstitution of a PD-only potassium channel from *Listeria monocytogenes* following genetic deletion of the VSD (30). We were inspired by these potassium channel examples and reasoned that the poor size-exclusion chromatography behavior of $\text{Na}_V\text{Sp1}$ was most likely caused by VSD conformational heterogeneity. Therefore, we decided to execute a protein dissection strategy that would remove the likely problematic region, the VSD, and create a pore-only sodium channel, $\text{Na}_V\text{Sp1p}$, by cutting the protein in the S4–S5 linker region that connects the VSD to the PD (Fig. 1B and Fig. S14). In line with our expectations, the pore-only construct $\text{Na}_V\text{Sp1p}$ was expressed in the membrane fraction of *E. coli* to very high levels as a hexahistidine tag, maltose binding protein fusion ($>25 \text{ mg L}^{-1}$), and yielded material that displayed greatly improved size-exclusion behavior relative to full-length $\text{Na}_V\text{Sp1}$

following removal of the affinity tags and purification (Fig. 1A and C). These properties made $\text{Na}_V\text{Sp1p}$ very suitable for further biochemical and biophysical characterization.

Biophysical Characterization Demonstrates That $\text{Na}_V\text{Sp1p}$ Is Folded and Forms Tetramers. Structurally characterized VGIC members have high α -helical content (16, 24, 31, 32). To examine $\text{Na}_V\text{Sp1p}$ secondary structure, we used circular dichroism (CD) and measured spectra in two different detergents, n-dodecyl- β -D-maltopyranoside (DDM) and n-decyl- β -D-maltopyranoside (DM). In both, $\text{Na}_V\text{Sp1p}$ showed the characteristic hallmark double minima of helical proteins (Fig. 2A) (33). These spectral signatures are similar to those reported for purified, detergent-solubilized full-length $\text{Na}_V\text{Bh1}$ (NaChBac) (12, 13), electric eel Na_V (34), and the pore-only potassium channel KcsA (35, 36) and indicate that $\text{Na}_V\text{Sp1p}$ has the high α -helical content characteristic of the VGIC superfamily. Thermal denaturation experiments monitored by CD indicate that $\text{Na}_V\text{Sp1p}$ undergoes a cooperative loss of secondary structure (Fig. 2B) that is characteristic of a folded protein and that resembles that seen in the full-length electric eel Na_V (34). Moreover, $\text{Na}_V\text{Sp1p}$ has different degrees of stability in DDM and DM (apparent melting temperatures, T_m s, of 44°C and 52°C , respectively) and the thermal transition in DDM can be made largely reversible (90% recovery of the signal at 222 nm) by the inclusion of 8% glycerol (Fig. S1B). Together, these spectral and thermal denaturation properties suggest that $\text{Na}_V\text{Sp1p}$ is a well-folded, α -helical protein that has similar secondary structure to other members of the VGIC superfamily.

Prior studies of purified full-length $\text{Na}_V\text{Bh1}$ indicate that bacterial Na_V s are tetramers (14). We expected that this property should be maintained in $\text{Na}_V\text{Sp1p}$ and used two independent methods to probe $\text{Na}_V\text{Sp1p}$ oligomerization (Table 1): glutaraldehyde (GTA) chemical cross-linking (37, 38) and size-exclusion chromatography coupled with triple detector analysis (SEC-TDA) (39). SDS-PAGE analysis of GTA cross-linked $\text{Na}_V\text{Sp1p}$ solubilized in DDM revealed the presence of three cross-linked products that corresponded to dimers, trimers, and tetramers, but did not indicate higher-order species (Fig. 2C and Table 1). Altering the conditions to favor more extensively cross-linked species showed a reduction of lower-order cross-linked species and enhancement of the tetrameric species, thereby indicating that $\text{Na}_V\text{Sp1p}$ assembles into a complex containing four subunits. This behavior was recapitulated in DM (Fig. S1C).

We further examined the association state of $\text{Na}_V\text{Sp1p}$ by SEC-TDA. This methodology, in which changes in refractive index, ultraviolet absorption, and static angle light scattering are

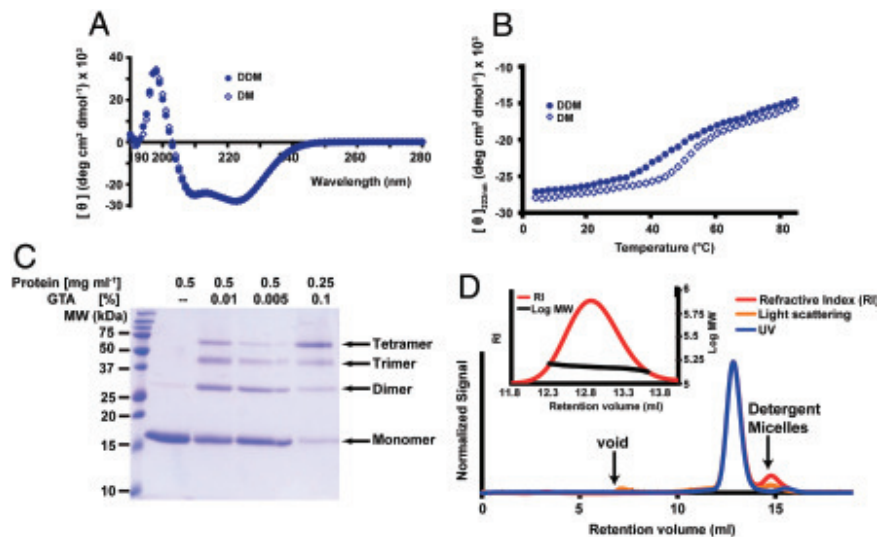


Fig. 2. Biophysical characterization of $\text{Na}_V\text{Sp1p}$. (A) CD spectra for $\text{Na}_V\text{Sp1p}$ at 4°C in 150 mM NaCl, 10 mM Na-phosphate pH 7.4, and either 0.3 mM DDM or 2.7 mM DM. (B) Thermal denaturation of $\text{Na}_V\text{Sp1p}$ in the same buffers as A, monitored by CD at 222 nm. (C) SDS-PAGE analysis for GTA cross-linked $\text{Na}_V\text{Sp1p}$ in DDM. Protein concentrations, GTA concentrations, and oligomeric species are indicated. (D) $\text{Na}_V\text{Sp1p}$ exemplar SEC-TDA in 200 mM NaCl, 0.3 mM DDM, 20 mM Hepes, pH 8.0. Void and empty micelle positions are indicated. (Inset) Molecular weight distribution across the main peak.

Table 1. Oligomeric states of pore-only proteins

	GTA cross-linking		SEC-TDA				
	Number of subunits	Number of subunits	Mass, kDa	Mw/Mn	Mw	Monomer mass, kDa	n
Na _V Sp1p	4 (DDM)	4.2 ± 0.1 (DDM)	67.3 ± 1.9	1.057	168.2 ± 0.6	15.87	4
Na _V Ab1p	4 (DDM)	4.3 ± 0.1 (DDM)	72.6 ± 2.3	1.004	145.6 ± 2.1	17.27	5
Na _V Ae1p	4 (DDM)	4.1 ± 0.2 (DDM)	70.8 ± 3.1	1.015	154.1 ± 4.4	17.45	5
Ca _V Sp1p	4 (DM)	4.3 ± 0.1 (DM)	68.8 ± 1.2	1.011	130.1 ± 1.4	15.87	4

measured, allows determination of the absolute molecular weight of the protein component of the protein-detergent micelle (39, 40) and has been recently applied to determine the association states of a variety of membrane proteins in different detergents (41–43). SEC-TDA of Na_VSp1p (Fig. 2D) indicates that the protein complex is a monodisperse entity that contains four monomers (Table 1). The excellent agreement between these experiments and the GTA experiments provides strong evidence that Na_VSp1p is a tetramer.

Functional Characterization of Reconstituted Na_VSp1p. Although the biochemical evidence provided strong indications that Na_VSp1p is a folded, tetrameric protein, it was essential to determine whether Na_VSp1p retained any functional ion channel properties. Therefore, we reconstituted purified Na_VSp1p into 1,2-diphytanoyl-sn-glycero-3-phosphocholine (DPhPC) giant unilamellar vesicles (GUVs) created by electroformation (44, 45) and assayed the properties of the reconstituted channels using planar patch clamp technology (46, 47). Measurement of the reversal potential of bilayers containing hundreds of channels under asymmetric NaCl conditions yielded $E_{rev} = 53.69 \pm 8.05$ mV ($n = 6$) (Fig. S2) in good agreement with the expected Nernst potential for sodium, 58.5 mV, and indicated that Na_VSp1p is a cation-selective channel. Following bilayer formation, varying the holding potential between –80 mV and +100 mV revealed channel activity displaying spontaneous openings ($n = 7$, where n is the number of bilayers with activity formed over the glass aperture) (Fig. 3A). As expected from the absence of the VSD, Na_VSp1p activity lacked a strong voltage dependence (Fig. 3B and Fig. S3). Importantly, application of mibefradil, a Ca_V blocker that

blocks bacterial Na_Vs (9, 13), inhibited the activity of the purified, reconstituted Na_VSp1p (Fig. 3C and D) and provided evidence that the ion channel activity was the result of a reconstituted sodium channel.

To characterize the biophysical properties of the Na_VSp1p channel further, we measured its ion selectivity properties. Comparison of the selectivity for sodium, potassium, and calcium ions by measuring the reversal potentials in a set of asymmetric ion conditions indicated that Na_VSp1p has a preference for permeant ions of $\text{Na}^+:\text{K}^+:\text{Ca}^{2+} = 1:0.22:0.08$ (Fig. 3B and E and Table 2). The measured preference for sodium over calcium ($P_{\text{Ca}}/P_{\text{Na}} = 0.08$) is in good agreement with the reported value for the related bacterial channel Na_VBh1 ($P_{\text{Ca}}/P_{\text{Na}} = 0.15$) (10), which bears strong similarity to Na_VSp1p in the selectivity filter (Fig. 4A and Fig. S1A). These selectivity properties, together with the sensitivity to mibefradil, indicate that the core functions of the PD, ion selectivity and conduction, remain intact and provide strong evidence that the folded, tetrameric Na_VSp1p forms a functional, stand-alone ion selective channel.

Selectivity Filter Mutations Convert Na_VSp1p into a Calcium-Selective Channel, Ca_VSp1p. It has long been thought that the selectivity filters of Na_Vs and Ca_Vs are related (4). In accord with this view, bacterial Na_Vs bear sequence similarity to both Na_Vs and Ca_Vs (9). Further, prior studies of bacterial Na_V selectivity filter elements have shown that a triple aspartate mutation in the Na_VBh1 (NaChBac) selectivity filter amino acid sequence, LESWAS → LDDWAD, creates a channel Ca_VBh1 (CaChBac_m) that is calcium-selective rather than sodium-selective (10). We incorporated the same triple aspartate change into the analogous Na_VSp1p selectivity filter positions to create a mutant channel “Ca_VSp1p” (Fig. 4A). Characterization of purified Ca_VSp1p by CD, GTA cross-linking, and SEC-TDA (Fig. 4B–D and Table 1) showed that Ca_VSp1p had physical properties that were identical to Na_VSp1p. Importantly, incorporation of Ca_VSp1p into DPhPC GUVs and subsequent electrophysiological recording by planar patch clamp revealed that Ca_VSp1p forms functional channels (Fig. 4E and F). In stark contrast to Na_VSp1p, Ca_VSp1p channels were calcium-selective (Fig. 4G and Table 2) and displayed an approximately 30-fold increase in single channel conductance in calcium compared to Na_VSp1p (335.3 ± 6.2 pS versus 31.1 ± 1.4 pS, for Ca_VSp1p and Na_VSp1p, respectively, Table 2) and approximately 39-fold change in $P_{\text{Ca}}/P_{\text{Na}}$ (3.13 ± 0.16 versus 0.08 ± 0.01 for Ca_VSp1p and Na_VSp1p, respectively, Table 2).

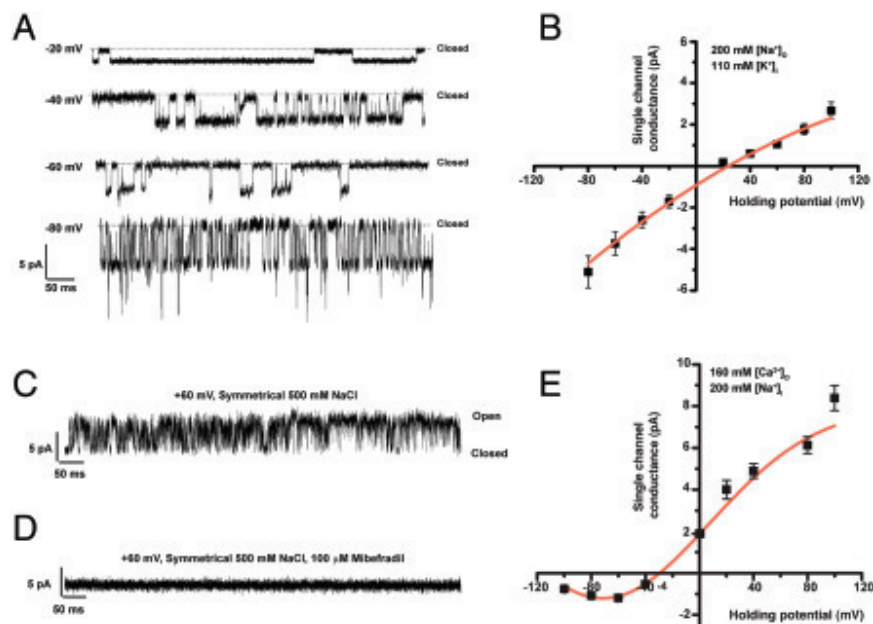


Fig. 3. Electrophysiological characterization of reconstituted Na_VSp1p. (A) Representative traces recorded from a planar lipid bilayer containing single Na_VSp1p channels at the indicated holding potentials using 110 mM KCl, 10 mM Hepes, pH 7.0 and 200 mM NaCl, 10 mM Hepes, pH 7.0 internal and external solutions, respectively. Closed channel current level is indicated. (B) Single channel *I*–*V* relationships for Na_VSp1p channels in 110 mM KCl internal, [K⁺]_i, and NaCl 200 mM external, [Na⁺]_o, solutions. (C and D) Bilayer recordings of Na_VSp1p at +60 mV in symmetrical 500 mM NaCl before (C) and after (D) addition of 100 μM mibefradil. (E) Single channel *I*–*V* relationships for Na_VSp1p channels in 200 mM NaCl internal, [Na⁺]_i and 160 mM CaCl₂ external, [Ca²⁺]_o, solutions. *I*–*V* curves in B and E are derived from single channel recordings of multiple bilayers.

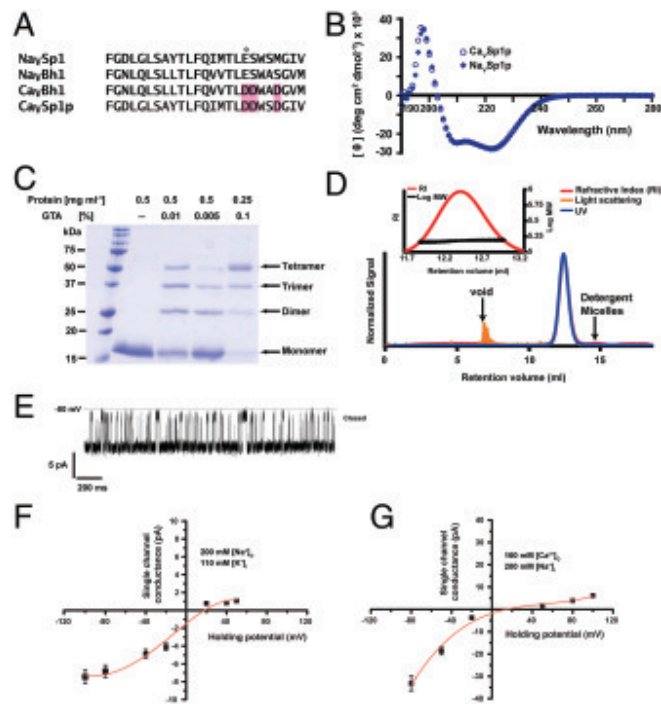


Fig. 4. Characterization of a calcium-selective NavSp1p mutant. (A) Pore region sequence comparison. Residues changed to alter CavBh1 and CavSp1p ion selectivity are highlighted. (B) Comparison of CavSp1p (open circles) and NavSp1p (blue circles) CD spectra at 4 °C in 150 mM NaCl, 2.7 mM DM, 10 mM naphosphate, pH 7.4. (C) SDS-PAGE analysis for GTA cross-linked CavSp1p in DM. Protein concentrations, GTA concentrations, and oligomeric species are indicated. (D) CavSp1p exemplar SEC-TDA in 200 mM NaCl, 2.7 mM DM, 20 mM Hepes, pH 8.0. Void and empty micelle positions are indicated. (Inset) Molecular weight distribution across the main peak. (E) Representative trace at -80 mV holding potential from a planar lipid bilayer containing CavSp1p using 200 mM NaCl, 10 mM Hepes, pH 7.0; and 110 mM KCl, 10 mM Hepes, pH 7.0 external and internal solutions, respectively. Closed channel current level is indicated. (F) Single channel *I*-*V* relationships for CavSp1p in the solutions from E indicated as [K⁺]_i internal and [Na⁺]_o external. Solid line was obtained by a nonlinear fit. (G) Single channel current-voltage relationships for CavSp1p channels measured using 200 mM NaCl internal, [Na⁺]_i and 160 mM CaCl₂ external, [Ca²⁺]_o solutions. Solid line was obtained by a nonlinear fit.

These data are consistent with the previous studies of CavBh1 (10) and show definitively that the measured single channel currents must arise from the reconstituted channels.

Generation of Pore-Only Proteins from Other Extremophile Navs. To test whether the ability to make folded PDs could be generalized to other Navs, we investigated the application of the dissection approach to three related extremophile bacterial Navs. To examine a diverse set, we picked Navs that have sequence identities of approximately 50% or less with NavSp1p. These included the well-characterized *Bacillus halodurans* NavBh1 (NaChBac) (9) (40% identical to NavSp1p), an Nav from the hydrocarbon

Table 2. Ion conduction and selectivity properties for NavSp1p and LDDWSD mutant CavSp1p

Pore sequence	Ion	Conductance, pS	G _x /G _{Na+}	P _x /P _{Na+}
NavSp1p FQIMTLESWSMGIV	Na ⁺	31.1 ± 1.4	1	1
	K ⁺	18.4 ± 2.1	0.59	0.22 ± 0.01
	Ca ²⁺	10.7 ± 1.7	0.34	0.08 ± 0.01
CavSp1p FQIMTLDWSDGIV	Na ⁺	74.4 ± 4.2	1	1
	K ⁺	30.3 ± 2.9	0.41	0.25 ± 0.01
	Ca ²⁺	335.3 ± 6.2	4.51	3.13 ± 0.16

n = 7 except for CavSp1p P_K⁻/P_{Na}⁺ where *n* = 5. Values are mean ± SD. Ratios were measured using 200 mM NaCl, 110 mM KCl, and 160 mM CaCl₂.

degrading bacterium *Alcanivorax borkumensis* (51% identical to NavSp1p), and the Nav from the arsenite oxidizing bacterium *Alkalilimnicola ehrlichei* (48% identical to NavSp1p), (Fig. 5 A and B and Fig. S1A). Attempts to purify NavBh1p were unsuccessful. However, we were able to express, purify, and characterize pore-only proteins from NavAb1 and NavAe1. Both showed CD spectra that were very similar to that of NavSp1p (Fig. 6 A and B). Additionally, GTA cross-linking (Fig. 6 C and D) and SEC-TDA analysis (Fig. 6 E and F) indicated that NavAb1p and NavAe1p form tetramers. Further, reconstitution of NavAb1p into GUVs and measurement by planar patch clamp methodology revealed the activity of single channels lacking a strong voltage dependence (Fig. 6 G and H and Fig. S3) and having a single channel conductance very similar to that of NavSp1p, 37.3 ± 1.5 pS. Interestingly, NavAb1p has different behavior than NavSp1p and displays a lower open probability (e.g., Po at +80 mV of 0.5 versus 0.25 for NavSp1p and NavAb1p, respectively, Fig. S3) but substantially longer channel openings. These differences must arise from divergent elements in the PDs that affect the intrinsic properties of the PD. Similar functional studies with NavAe1p did not yield clear single channel activity and were not analyzed further. Taken together, the similarity of the biophysical properties of NavAb1p and NavAe1p to NavSp1p demonstrate that NavAb1p and NavAe1p are well-folded, stand-alone pore domains. These results show that the protein dissection approach to create PD-only proteins can be generalized and should be applicable to a range of VGICs.

Discussion

Developing a detailed understanding of the structural principles that underlie VGIC superfamily transmembrane architecture is an important goal that has a direct bearing on elaboration of channel gating and ion permeation mechanisms, design of ion channels having unique function, drug development, and understanding channel evolution. Within the VGIC superfamily, a number of lines of evidence have suggested that the transmembrane segments of K_v channels are arranged in distinct domains comprising the VSD and PD. This possibility was first noted from comparison of K_v channels, which have six-transmembrane segments that include a VSD, and inward rectifiers, which contain only a two-transmembrane pore-forming unit, as both contain common pore elements (19). A variety of structural and chimera studies of different potassium channels have further supported this intramembrane domain segregation idea (16, 20–25). Most notably, independent X-ray and NMR structures of the VSD from the *Aeropyrum pernix* voltage-gated potassium channel KvAP show that the VSD can fold separately from the pore domain (23, 25); however, this folding appears to be subject to strong context-dependent effects (23, 48). Additional evidence for potassium channel transmembrane modularity comes from the recent purification and reconstitution of a PD-only potassium channel from *Listeria monocytogenes* following genetic removal of the VSD (30). Besides these potassium channel studies, the idea

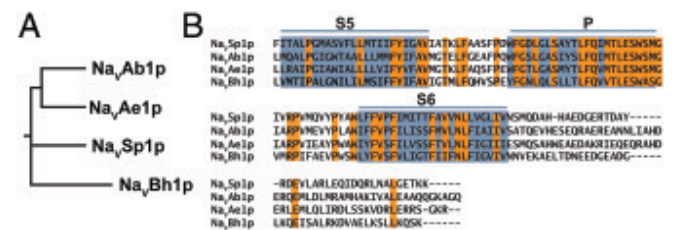


Fig. 5. Sequence relationships of bacterial Navs. (A) Phylogenetic tree of the pore regions of from *A. borkumensis* (NavAb1p), *A. ehrlichei* (NavAe1p), *S. pomeroyi* (NavSp1p), and *B. halodurans* (NavBh1p). (B) Sequence alignment of NavAb1p, NavAe1p, NavSp1p, and NavBh1p. Absolutely conserved residues are shown in orange. Blue shading and lines indicate the predicted transmembrane segments S5 and S6 and the pore region, P.

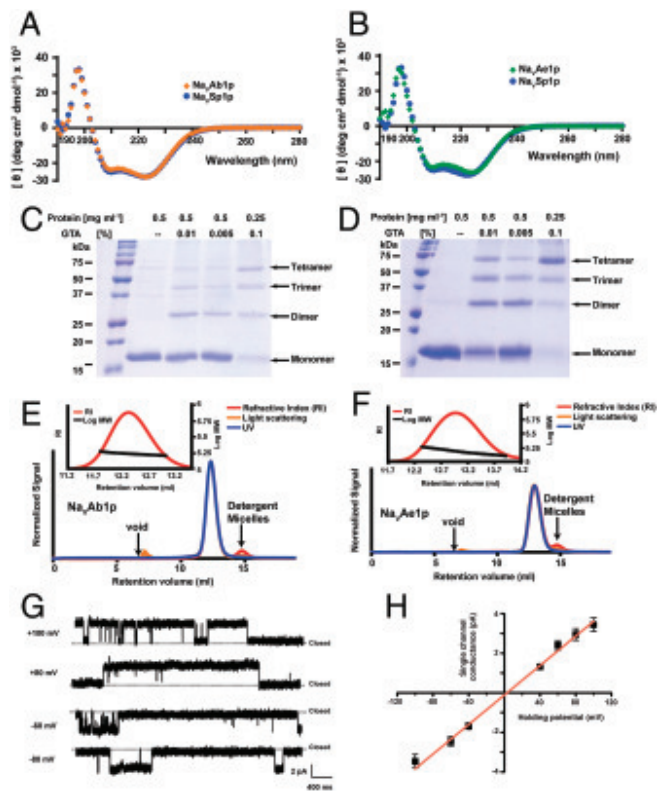


Fig. 6. $\text{Na}_V\text{Ab1p}$ and $\text{Na}_V\text{Ae1p}$ characterization. Comparison of CD spectra of **A**, $\text{Na}_V\text{Ab1p}$ (orange diamonds) and **B**, $\text{Na}_V\text{Ae1p}$ (green diamonds) with $\text{Na}_V\text{Sp1p}$ (blue circles) at 4 °C in 150 mM NaCl, 0.3 mM DDM, 10 mM naphosphate, pH 7.4; 15% SDS-PAGE analysis for GTA cross-linked (**C**) $\text{Na}_V\text{Ab1p}$ and (**D**) $\text{Na}_V\text{Ae1p}$ in DDM. Protein concentrations, GTA concentrations, and oligomeric species are indicated; exemplar SEC-TDA of (**E**) $\text{Na}_V\text{Ab1p}$ and (**F**) $\text{Na}_V\text{Ae1p}$ in 200 mM NaCl, 0.3 mM DDM, 20 mM Hepes, pH 8.0. Void and empty detergent micelles positions are indicated. (*Inset*) Molecular weight distribution across the main peak. (**G**) Representative traces recorded from a planar lipid bilayer containing $\text{Na}_V\text{Ab1p}$ at different holding potentials as indicated using symmetrical 200 mM NaCl, 10 mM Hepes, pH 7.0. (**H**) $\text{Na}_V\text{Ab1p}$ single channel current–voltage relationships. Main conductance was calculated from the slope of the linear regression and was 37.3 ± 1.5 pS.

that the VSD can fold and function independently from the PD (17, 18) has been further advanced by the identification of a family of voltage-sensor-only proteins (27–29). Nevertheless, despite this accumulating evidence, whether this principle of modular transmembrane structural arrangement exists in other members of the VGIC family has remained untested. Further, to date, no naturally occurring PD-only channels from the Na_V , Ca_V , or TRP branches of the VGIC superfamily have been reported.

Our data demonstrate that transmembrane structural modularity is present in members of the Na_V family. We show that it is possible to generate pore-domain-only proteins from three different extremophile Na_V s by genetic excision of the VSD: *S. pomeroyi*, $\text{Na}_V\text{Sp1p}$, *A. borkumensis*, $\text{Na}_V\text{Ab1p}$, and *A. ehrlichii*, $\text{Na}_V\text{Ae1p}$. In all cases, the PDs can be expressed in the *E. coli* membrane fraction in amounts that facilitate purification and characterization (approximately 25 mg L^{-1}). Further, all three PDs form stable, tetrameric complexes in at least one mild detergent, either DDM or DM. Importantly, both $\text{Na}_V\text{Sp1p}$ and $\text{Na}_V\text{Ab1p}$ form functional ion channels when reconstituted into lipid bilayers. Critically, electrophysiological studies of purified $\text{Na}_V\text{Sp1p}$ reconstituted into lipid bilayers demonstrate that $\text{Na}_V\text{Sp1p}$ retains the principal properties of a bacterial sodium channel. $\text{Na}_V\text{Sp1p}$ forms ion channels having a selectivity sequence of $\text{Na}^+:\text{K}^+:\text{Ca}^{2+} = 1:0.22:0.08$ (Table 2) and is sensitive to block by a known bacterial Na_V pore blocker, mibefradil (9, 13) (Fig. 3 C and D). Taken together, these data strongly

indicate that the pore-only proteins are folded properly and retain the core functions of the pore domain, which are to act as functional ion channels that maintain ion selectivity.

Functional studies of a number of bacterial Na_V s have shown them to be sodium-selective (8–10). Yet, in line with the close evolutionary relationship of Na_V s and Ca_V s (1–4), the bacterial Na_V selectivity filter sequences also bear some sequence similarity to those of Ca_V s (9, 10, 49). Incorporation of a triple aspartate change in the $\text{Na}_V\text{Bh1p}$ (NaChBac) selectivity filter sequence, $\text{LESWAS} \rightarrow \text{LDDWAD}$, turns $\text{Na}_V\text{Bh1p}$ from a sodium-selective channel into a calcium-selective channel, $\text{Ca}_V\text{Bh1}$ (CaChBac_m) (10). Our data show that incorporation of the analogous aspartate triple mutant into the $\text{Na}_V\text{Sp1p}$ selectivity filter creates a calcium-selective channel, $\text{Ca}_V\text{Sp1p}$ (Fig. 4G and Table 2). Similar to $\text{Ca}_V\text{Bh1}$ (CaChBac_m) (10) $\text{Ca}_V\text{Sp1p}$ not only prefers calcium over sodium but also retains a preference for sodium over potassium (Table 2). The creation of the calcium-selective channel $\text{Ca}_V\text{Sp1p}$ together with the three pore-only Na_V s we describe establishes a set of biochemically tractable proteins that should allow the exploration of the atomic basis for both sodium and calcium selectivity.

The complexity and transmembrane nature of VGIC superfamily members remains a barrier to understanding their function from a high-resolution structural standpoint. The demonstration that it is generally feasible to create folded and functional PDs from a variety of extremophile Na_V s, including channels that are either sodium- or calcium-selective, opens the possibility that this strategy may lead to the crystallization and structure determination of both sodium- and calcium-selective pores. Further, the biochemical tractability of the PD-only proteins may permit them to be used as platforms for screening and characterization of previously undescribed peptide or small molecule pore blockers.

The PDs display an apparent general conformational and functional robustness that contrasts with the context-dependent folding and conformational heterogeneity of the VSD. Such robustness is consistent with the high stereochemical demands required to make a channel that is selective for particular permeant ions. The independent folding of PDs as demonstrated here for Na_V s and by Montal and colleagues for K_V s (50) suggests that similar strategies may be applicable for other members of the VGIC superfamily. Such efforts may facilitate attempts to obtain structural information about the pore regions of homomeric members of the VGIC that presently lack structural data such as TRP channels.

Taken together with the previous work on potassium channels (16, 20–26) and voltage-sensor only proteins (27–29), our results provide support for the general independent nature of the PD and VSD within the VGIC superfamily. This concept is also supported by recent studies from McCusker et al. that reported the creation of an $\text{Na}_V\text{Sp1}$ pore-only protein (51) similar to the one described here. This modular division is consistent with the hypothesis that the architecture of the transmembrane parts of the VGIC reflects an evolutionary path where various types of sensor domains were fused to a core, pore-forming module to generate a diversity of gating responses (19).

Materials and Methods

Molecular Biology and Protein Purification. Please see *SI Text* for a detailed description of the molecular biology and purification methods used to make the described Na_V PDs.

Circular Dichroism Spectroscopy. CD spectra were recorded on an Aviv 215 circular dichroism spectrometer using a 1-mm path-length quartz cell at 4 °C. Melting temperature, T_m , was determined as the inflection point of first derivative of the data.

Cross-Linking. Purified pore proteins, 10 μg or 5 μg , were combined with 0.01% and 0.005% or 0.1% glutaraldehyde (Aldrich), respectively, in a final volume of 20 μL and incubated for 10 min at 37 °C. Reactions were quenched

with a final concentration of 100 mM Tris pH 8.0 at room temperature and boiled for 10 min in a reducing SDS-sample buffer prior to analysis by 15% SDS-PAGE and Coomassie brilliant blue R-250.

Size-Exclusion Chromatography–Tridector Analysis. Simultaneous detection of UV, refractive index, and right angle light scattering signals from SEC of pore-only domains was performed using a Viscotek 302 Tetra Detector Array (TDA, Malvern/Viscotek) in line with a Superdex 200 10/300 GL (GE Healthcare) column.

Functional Characterization of Reconstituted Pore-Only Proteins. Lipid bilayer experiments performed using a planar patch clamp system (Port-a-Patch, Nanion Technologies GmbH) on Na_vSp1p, Na_vAe1p, or Na_vAb1p were incorporated into GUVs using procedures described previously (44, 45). To determine Na⁺, K⁺, and Ca²⁺ permeabilities, the reversal potential was measured in asymmetric conditions where the internal solution contained 10 mM Na-Hepes, 200 mM NaCl, pH 7.0 (adjusted with NaOH) and the external solution contained 10 mM Hepes, 160 mM CaCl₂, pH 7.0 (adjusted with HCl) or 10 mM Hepes, 110 mM KCl, pH 7.0 (adjusted with KOH). The perme-

ability ratio of ions was estimated according to the following equation: $P_{Na^+}/P_x = a_s[\exp(E_{rev}F/RT)]\{[\exp(E_{rev}F/RT) + 1]/(4a_{se})\}$ (10). R , T , F , and E_{rev} are the gas constant, absolute temperature, Faraday constant, and reversal potential, respectively; “x” represents K⁺ or Ca²⁺. Activity coefficients for Na⁺, K⁺, and Ca²⁺ were estimated as follows: $a_s = \gamma_s[X_s]$, where activity, a_s , is the effective concentration of an ion in solution, s is related to the nominal concentration $[X_s]$ by the activity coefficient, γ_s . γ_s was calculated from the Debye–Hückel equation: $\log \gamma_s = -0.51 * z_s \sqrt{\mu} / (1 + 3.8\alpha_s \sqrt{\mu})$, where μ is the ionic strength of the solution, z_s is the charge on the ion, and α_s is the effective diameter of the hydrated ion in nanometers.

Detailed procedures can be found in *SI Text*.

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