Peregrination of the selectivity filter delineates the pore of the human voltage-gated proton channel hHv1

Deri Morgan,1 Boris Musset,1 Kethika Kulleperuma,2,3 Susan M.E. Smith,4 Sindhu Rajan,5 Vladimir V. Cherny,1 Régis Pomès,2,3 and Thomas E. DeCoursey1

1Department of Molecular Biophysics and Physiology, Rush University, Chicago, IL 60612
2Molecular Structure and Function, Hospital for Sick Children, Toronto, Ontario M5G 1X8, Canada
3Department of Biochemistry, University of Toronto, Toronto, Ontario M5S 1A1, Canada
4Department of Biology and Physics, Kennesaw State University, Kennesaw, GA 30144
5Department of Medicine, University of Chicago, Chicago, IL 60637

Extraordinary selectivity is crucial to all proton-conducting molecules, including the human voltage-gated proton channel (hHv1), because the proton concentration is >106 times lower than that of other cations. Here we use “selectivity filter scanning” to elucidate the molecular requirements for proton-specific conduction in hHv1. Asp112 in the middle of the S1 transmembrane helix, is an essential part of the selectivity filter in wild-type (WT) channels. After neutralizing Asp112 by mutating it to Ala (D112A), we introduced Asp at each position along S1 from 108 to 118, searching for “second site suppressor” activity. Surprisingly, most mutants lacked even the anion conduction exhibited by D112A. Proton-specific conduction was restored only with Asp or Glu at position 116. The D112V/V116D channel strikingly resembled WT in selectivity, kinetics, and ΔpH-dependent gating. The S4 segment of this mutant has similar accessibility to WT in open channels, because R211H/D112V/V116D was inhibited by internally applied Zn2+. Asp at position 109 allowed anion permeation in combination with D112A but did not rescue function in the nonconducting D112V mutant, indicating that selectivity is established externally to the constriction at F150. The three positions that permitted conduction all line the pore in our homology model, clearly delineating the conduction pathway. Evidently, a carboxyl group must face the pore directly to enable conduction. Molecular dynamics simulations indicate reorganization of hydrogen bond networks in the external vestibule in D112V/V116D. At both positions where it produces proton selectivity, Asp frequently engages in salt linkage with one or more Arg residues from S4. Surprisingly, mean hydration profiles were similar in proton-selective, anion-permeable, and nonconducting constructs. That the selectivity filter functions in a new location helps to define local environmental features required to produce proton-selective conduction.

INTRODUCTION

Voltage-gated proton channels (Hv1s) enable phagocytes to kill pathogens (Henderson et al., 1988; DeCoursey et al., 2003; Morgan et al., 2009; DeCoursey, 2010; Demaurex, 2012), basophils to secrete histamine (Musset et al., 2008b), and airway epithelia to control surface pH (Fischer, 2012), as well as enable sperm motility (Musset et al., 2012) and capacitation (Lishko et al., 2010), and B lymphocyte signaling (Capasso et al., 2010), and may exacerbate breast cancer metastasis (Wang et al., 2012) and ischemic brain damage (Wu et al., 2012). All of these functions are predicated on the proton selectivity of Hv1. The low concentration of H+ in biological fluids means that extraordinary selectivity is necessary even to ensure that H+ is the main conducted species. In fact, proton selectivity in Hv1 appears to be perfect (Musset et al., 2011; DeCoursey, 2013).

An acidic group in the middle of the S1 transmembrane segment is critical to the proton specificity of Hv1 and is provided by Asp112 in human Hv1 (hHv1; Musset et al., 2011) and Asp551 in Hv1 from a dinoflagellate, Karlodinium veneficum (Smith et al., 2011). Despite only 15% amino acid identity of the proteins, the conservative Asp→Glu mutation preserved proton specificity, whereas Ser, Ala, or His substitution for Asp at this position resulted in anion permeability in both species, strongly suggesting that the selectivity mechanism is widely conserved evolutionarily. The presence of an Asp facing the pore is not sufficient, however, because Asp155 can be neutralized without compromising proton selectivity, and does not preserve selectivity when Asp112 is neutralized (Musset et al., 2011). Other molecular elements that may be required are not known. Our homology model indicates that the second of three Arg residues in

D. Morgan and B. Musset contributed equally to this paper.

Correspondence to Thomas E. DeCoursey: tdecoursey@rush.edu

Abbreviations used in this paper: EC, extracellular; hHv1, human voltage-gated proton channel; Hv1, voltage-gated proton channel; IC, intracellular; MD, molecular dynamics.

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the S4 segment, Arg208, forms a salt bridge with Asp112, and that the resulting charge compensation is important for proton selectivity (Kulleperuma et al., 2013). To refine further the molecular requirements of the selectivity filter, we explore here the extent to which the critical Asp can be moved along the S1 segment. We find that an excellent proton channel is produced when Asp is shifted from position 112 to position 116. The mutant channel is proton specific, exhibits ΔpH-dependent gating characteristic of all H1,1s, and surprisingly, neutral amino acid substituents at this location produce anion permeability. Molecular dynamics (MD) simulations indicate that Asp116 forms a salt bridge with Arg205 and/or permeability. Molecular dynamics (MD) simulations in

MATERIALS AND METHODS

Gene expression

Site-directed mutants were created using the Stratagene QuickChange (Agilent Technologies) procedure according to the manufacturer’s instructions. Transfection was done as described previously (Kulleperuma et al., 2013). Both HEK-293 cells and COS-7 cells were used as expression systems, the latter more frequently. In a previous study, we systematically compared the properties of hH1 when expressed in these two cell lines and found no difference (Musset et al., 2008a). Although currents that decayed at large positive voltages (presumed to be volume-regulated anion currents) were sometimes seen at the start of experiments, these disappeared over time. Occasional cells displayed a few unidentified single-channel currents superimposed on the macroscopic currents. The unitary conductance of hH1,1 is just 140 fS at pH i

Electrophysiology

GFt-tagged proton channels were identified using inverted microscopes (Nikon) with fluorescence capability. Conventional patch-clamp techniques were used at 21°C or at room temperature (20–25°C) (Kulleperuma et al., 2013). Bath and pipette solutions contained 60–100 mM of buffer, 1–2 mM CaCl2 or MgCl2 (intracellular [IC] solutions were Ca2+-free), 1–2 mM EGTA, and TMAcSO4 to adjust the osmolality to ~300 mOsm, titrated with TMAOH. Buffers used were Mes at pH 5.5–6.0, HomoPIPES at pH 4.5, and PIPES at pH 7.0. For Zn2+ measurements, EGTA was omitted. Currents are shown without leak correction. Reversal potentials were corrected for measured liquid junction potentials. Unless stated otherwise, cells were held at a holding potential, Vhold, before pulses and returned to Vhold after families of pulses.

Reversal potentials were determined by two methods, depending on the relative positions of Vthreshold and Vrev. For most constructs, Vthreshold was positive to Vrev, and the latter was determined by examining tail currents (e.g., Fig. 2 B). Because hH1 currents were the only time-dependent conductance present, estimates of the amplitude and direction of current decay during deactivation were used to establish Vrev (Morgan and DeCoursey, 2007). By this procedure, time-independent leak or other extraneous conductances do not affect Vrev. For mutants in which Vthreshold was negative to Vrev, (for example, D112A/V116D in Fig. 2 C), it was possible to observe the reversal of the direction of currents activated during pulse families. Tail currents were not observed in nontransfected cells for example, Fig. 1 B illustrates the absence of tail currents in a cell with the nonconducting D112V mutant.

MD simulations

MD simulations of the WT protein, single-point mutants D112V and D112S, and double-point mutants D112V/V116D (‘VD’) and D112V/V112S (‘VS’) were performed in a hydrated lipid bilayer based on the homology model constructed and validated in a recent study (Kulleperuma et al., 2013).

12 conformations of the WT protein with pore-associated water were used as initial structures. These snapshots correspond to the endpoint of 12 different 200-ns-long unrestrained simulations in a membrane-mimetic octane slab (Kulleperuma et al., 2013). Each conformation represents one of the three configurations of the D112-R208 salt bridge: bidentate and monodentate conformations (involving two or one hydrogen bond, respectively), and open, in order of increasing separation. A preequilibrated configuration of a 1-palmitoyl-2-oleoylphosphatidylcholine (POPC) bilayer was obtained from a previous study (Kulleperuma et al., 2013). The OPLS-AA protein force field (Jorgensen et al., 1996) was mixed with the Berger lipid parameters (Berger et al., 1997) by applying the half-fe double-pairlist method (Chakrabarti et al., 2010). The TIP3P water model was used (Jorgensen et al., 1983). InflateGRO (Kandt et al., 2007) was used to embed the protein in the bilayer. The system was then hydrated, and 54 Na+ and 56 Cl- ions were added to neutralize the charge of the system and yield an approximate ionic concentration of 500 mM. The resulting simulator cell consisted of 126 POPC and ~5,900 water molecules in a box of ~6.5 × 6.5 × 8 nm3. The MD parameters used for this study are described elsewhere (Kulleperuma et al., 2013).

Each of the 12 WT systems was first energy-minimized using 50,000 steps of steepest descent, followed by an equilibration phase of 50 ns with position restraints on protein backbone and pore-associated water oxygen atoms. The production run consisted of 200-ns-long unrestrained simulations for each system. Snapshots of protein and pore-associated water molecules were selected from each of the 12 equilibrated WT protein systems at t = 100 ns to produce single- and double-point mutants. Mutations were introduced using an in-house script, followed by 1,000 steps of energy minimization. Asp112 and Val116 side chains were modified to Val, Ser, or Glu by either overwriting the WT heavy atoms or deleting some or both. Side-chain and backbone dihedral angles were checked after energy minimization. Extra ions were added to the solution as required to neutralize the system after mutations were introduced. Another 50,000 steps of energy minimization were performed before an equilibration phase consisting of an additional 25 ns with position restraints, as described above. 12 time trajectories of 200 ns differing in the initial conformation of the protein were generated for each mutant. The total production time was 12 μs. For the final analysis, eight replicas of WT and VD and seven replicas of VS, D112V, and D112S were selected after discarding replicas that displayed significant changes in secondary structure.

Snapshots saved every 20 ps during the last 100 ns of each selected production run were analyzed for each system. Molecular graphics were generated by VMD 1.8.7 (Humphrey et al., 1996), and all trajectories were analyzed using Gromacs tools and in-house codes.
Online supplemental material
Figs. S1 and S2 illustrate the structural plasticity of the channel with respect to translation of the four transmembrane helices during extended MD simulations. Table S1 provides \( V_{\text{rev}} \) data for D112V/V116D and D112V/V116D/R211H mutants in the presence of several cations or Cl\(^-\) that show both constructs to be proton selective. The online supplemental material is available at http://www.jgp.org/cgi/content/full/jgp.201311045/DC1.

**RESULTS**

We generated a series of mutants in which the Asp residue critical to proton specificity was effectively shifted up and down the S1 helix to each position from 108 to 118. In the initial series of experiments, we replaced Asp\(^{112}\) with Ala (D112A) to produce an anion-permeable channel (Mussen et al., 2011), and then introduced a second mutation with the goal of restoring proton selectivity ("second site suppression"). Additional studies were done in the D112V background, which in a sense is more rigorous, because this single mutant does not conduct at all (Mussen et al., 2011). All mutations were introduced into a Zn\(^{2+}\)-resistant background (H140A/H193A), so that spurious small native H\(_{\text{v}}\)I currents often present in COS-7 or HEK-293 cells (Mussen et al., 2011) could be identified by their sensitivity to 10 µM Zn\(^{2+}\). Distinct Zn\(^{2+}\)-insensitive currents were observed only in mutants with Asp at positions 116 or 109 (D112A/V116D, D112A/V109D).

The second site mutation V116D restores proton selectivity to nonconducting or anion-permeable mutants

Fig. 1 shows that although the single-point mutation D112V eliminates current altogether (Mussen et al., 2011), introducing Asp at position 116 restores robust proton current to the double mutant, D112V/V116D. Similarly, the D112A single mutant is anion permeable (Mussen et al., 2011), but introducing Asp at position 116 restored proton-specific current to the double mutant, D112A/V116D. The proton selectivity of both double mutants, D112A/V116D and D112V/V116D, was confirmed by the proximity of their reversal potentials, \( V_{\text{rev}} \), to the Nernst potential for H\(^{+}\), \( E_{\text{H}} \) (Fig. 2 A), over a wide pH range (pH\(_{\text{r}}\), 4.5–7.5 and pH\(_{\text{i}}\), 5.5–7.0). Fig. 2 B illustrates determination of \( V_{\text{rev}} \) from tail currents in a cell with D112V/V116D channels at pH\(_{\text{r}}\) 5.5 and 7.0, with pH\(_{\text{i}}\) 5.5. As indicated by the arrows, \( V_{\text{rev}} \) shifted from 0 to \(-77 \text{ mV} \) near \( E_{\text{H}} \) of \(-87 \text{ mV} \). The D112A/V116D mutant activated in a more negative voltage range so that inward currents were observed negative to \( E_{\text{H}} \) in families of currents. Fig. 2 C illustrates currents from pulses bracketing \( V_{\text{rev}} \) that reveal an \(~60-\text{mV} \) shift between pH\(_{\text{r}}\) 5.0 and 6.0. In addition, substituting Na\(^{+}\), Li\(^{+}\), or K\(^{+}\) for TMA\(^{+}\), or Cl\(^-\) for CH\(_{3}\)SO\(_{3}^{-}\) had no effect on \( V_{\text{rev}} \) (Table S1). In summary, shifting Asp from position 112 to 116 moves the proton selectivity filter outward by one turn of the helix.

Asp supports current only when facing the pore

Surprisingly, moving Asp to positions other than 109 or 116 eliminated voltage-gated current altogether. All mutants were tagged with GFP, and transfected cells with green “halos” indicating membrane expression were selected under fluorescence for recording. Nonconducting Asp mutants included (mutation, number of cells): positions 108 (D112A/L108D, 10), 110 (D112A/V110D, 4), 111 (D112A/L111D, 4), 113 (D112A/A113D, 5), 114 (D112A/L114D, 4), 115 (D112A/L115D, 4), 117 (D112A/L117D, 7), and 118 (D112A/A118D, 4). Positions 116, 112, and 109 (Fig. 1, cartoon) all face the “pore” in the predicted open-state structure of hH\(_{\text{v}}\)I (Kulleperuma et al., 2013). Evidently, Asp at a nonpore-facing location fails to support conductance, confirming that positions 109, 112, and 116 line the pore of H\(_{\text{v}}\)I.

As a control for the possibility that nonconducting mutants did not fold properly, we created a single mutant, A113D, in which the native Asp\(^{112}\) was preserved. If Asp at a nonpore-facing location caused the protein to misfold, A113D should not conduct. Instead, A113D displayed small voltage-gated currents that were kinetically different from WT currents but were unequivocally...
proton selective (Fig. 3). Thus, nonconducting mutants, including D112A/A113D, most likely were expressed but nonfunctional. If, despite the appearance of green protein in the membrane, some mutants misfolded, the fact remains that these proteins do not function as channels.

At position 109, Asp plays a permissive role

Introducing Asp at position 109 into the nonconducting D112V background (Musset et al., 2011) did not overcome the lack of conductance produced by the D112V single mutation (n = 8 cells). However, the D112A/V109D mutant exhibited distinct currents at pHo, 5.5 and pHi, 5.5 (Fig. 4 A), in contrast to the majority of mutants that did not conduct (D112A/L108D, D112A/V110D, D112A/L111D, D112A/A113D, D112A/L114D, D112A/L115D, D112A/L117D, and D112A/A118D). Replacing CH$_3$SO$_3^-$ with Cl$^-$ increased the outward current (Fig. 4 C), reflecting Cl$^-$ influx, and produced a large negative shift of $V_{rev}$ (Fig. 4 B vs. D), confirming Cl$^-$ permeability. The shift of $V_{rev}$ when Cl$^-$ replaced CH$_3$SO$_3^-$ was $-35.9 \pm 4.2$ mV (SEM; n = 5), in the range reported for the D112A single mutant, $-29$ mV (Musset et al., 2011). Evidently, introducing Asp at position 109 did not interfere with anion conduction seen in the D112A single mutant (Musset et al., 2011). Both the anion selectivity of D112A/V109D and the lack of conductance in D112V/V109D suggest that at position 109, Asp cannot mediate proton selectivity and has no discernible effect on the selectivity that is established elsewhere. The two positions where Asp produced proton selectivity are in the external vestibule in our model, outside the highly conserved charge transfer center delimiter Phe$_{150}$ (Tao et al., 2010).

The engineered Asp$_{116}$ proton channel functionally resembles WT

To what extent does moving the selectivity filter outward by one turn of the helix reinstate native hHV1 properties? The gating and pH dependence of the D112A/V116D and D112V/V116D mutants are illustrated in Fig. 5. The general appearance of the proton currents is unremarkable; the voltage dependence and gating kinetics are roughly similar to WT. In D112V/V116D, the time constant of tail current decay, $\tau_{tail}$, was $1.1 \pm 0.02$ s (mean $\pm$ SEM; n = 3) at $-40$ mV and pH $p$
changes in the gating of the mutant channels were not observed.

A characteristic property shared by all known HVT is tight regulation of the position of the $g_{H-V}$ relationship by the pH gradient, $\Delta p\text{H}$ (Cherny et al., 1995; Musset et al., 2011). Thus, marked changes in the gating of the mutant channels were not observed.

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Figure 3. Introducing Asp at position 113, predicted by our model to be in a non-pore-facing location, results in membrane expression of a functioning proton-selective channel. The cartoon emphasizes that Asp$^{112}$ is still present. Families of currents are shown in a COS-7 cell in whole-cell configuration at pH$_{o}$ 5.5 (A) or 7.0 (B), with pH$_{i}$ 5.5, with pulses applied from $V_{\text{hold}}$ as labeled to the indicated voltages in 10-mV increments. Cells were returned to $V_{\text{hold}}$ after pulses. (C) Proton selectivity is shown by the proximity of $V_{\text{rev}}$ to $E_{\text{H}}$ (dashed line). Insets show $V_{\text{rev}}$ determination (left) at pH$_{o}$ 5.5 and pH$_{i}$ 5.5 by reversal of current during a family of pulses in 10-mV increments ($V_{\text{hold}} = -60 \text{ mV}$) and at pH$_{o}$ 7.0 and pH$_{i}$ 5.5 (right) by tail currents. $V_{\text{rev}}$ was measured at pH$_{o}$ 4.5, 5.0, 5.5, 6.5, 7.0, and 7.5, and at pH$_{o}$ 5.5 or 6.5.

Figure 4. Moving aspartate from position 112 to 109 results in anion currents. Whole-cell currents in a COS-7 cell expressing D112A/V109D channels, all at pH$_{o}$ 5.5 and pH$_{i}$ 5.5, in symmetrical TMA$^+\text{CH}_{3}\text{SO}_{3}^-$ (A and B) or with Cl$^-$ in the bath (C and D). Pulses applied in 10-mV increments. $V_{\text{hold}}$ was $-40 \text{ mV}$ (A and B) or $-60 \text{ mV}$ (C and D). Cells were returned to $V_{\text{hold}}$ after pulses. $V_{\text{rev}}$ determination from tail currents (B and D), with pulses in 10-mV increments.
Mutations at position 116 (in D112V channels) mimic mutations at 112

That proton selectivity was restored to D112V and D112A mutants by introducing Asp at position 116 suggests that the intramolecular interactions at both positions that contribute to proton selectivity are similar. To explore the extent of equivalence of these positions, we compared effects of several other mutations at 116 with those at 112. Fig. 6 shows that robust proton-selective currents were observed when Glu replaced Asp at position 116 (in the D112V background), just as with replacement of Asp by Glu at position 112 (Musset et al., 2011). We found previously that neutral mutants of Asp112 were anion selective (Musset et al., 2011). Astoundingly, both Asn and Ser at position 116 produced anion-permeable channels in the D112V background, which itself does not conduct. Fig. 7 illustrates a current family

![Figure 5](http://rupress.org/jgp/article-pdf/142/6/625/1230304/jgp_201311045.pdf)
in a cell with D112V/V116S in symmetrical pH 5.5 
TMACH3SO3 solutions (Fig. 7 A), with Vrev near 0 mV
(Fig. 7 B). Replacing bath CH3SO3 with Cl− increased
the outward current (Fig. 7 C) and shifted Vrev strongly
negatively (Fig. 7 D): on average, by −37.0 ± 2.4 mV
(mean ± SEM; n = 7) for Asn and −35.8 ± 1.8 mV (n = 4)
for Ser. These values are similar to those obtained previ-
ously for single mutants D112N and D112S upon Cl−addition: −33.1 and −40.8 mV, respectively (Musset
et al., 2011). Thus, the introduction of Glu, Ser, or Asn
at position 116 conferred permeability onto the non-
conducting D112V mutant, in each case recapitulating
the selectivity of the corresponding single mutations at
position 112. Viewed in terms of the ability of a single–

amino acid substituent to produce anion or proton se-

lectivity, positions 112 and 116 were identical.

Zn2+ sensitivity of Arg→His mutants shows S4 position
in open channels
It seemed possible that shifting the selectivity filter out-
ward might alter the position of S4 in open channels. As
a frame of reference, R211H currents were found previ-
ously to be sensitive to internal but not external Zn2+
during depolarizing pulses, suggesting that Arg211 remains
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Selectivity filter scanning of hHV1

Thus, His at position 211 in R211H/D112V/V116D was accessible to the internal solution even in the open state, indicating similar accessibility of the S4 Arg residues in open channels with the selectivity filter at either position 112 or 116.

Introducing Asp into S2 or S3 did not support proton conduction

Given that Asp can produce proton selectivity at two locations on S1, we moved Asp to several positions in the S2 or S3 transmembrane segments, always in the non-conducting D112V background. We chose five locations in the outer vestibule (S143D, I146D, L147D, V178D, and S181D) that face the pore in our model and are located roughly between the levels of positions 112–116. Four failed to produce distinct current. D112V/S143D generated small Zn2+-insensitive currents that reversed at $-17 \pm 6.6$ mV (mean ± SEM; $n = 5$) at pHo 7.0 and pHi 5.5, well positive to $E_H$, which is $-87$ mV. In five cells, $V_{rev}$ shifted by $-24.3 \pm 1.6$ mV when CH3SO3$^-$ was replaced with Cl$^-$ at pHo 5.5 and pHi 5.5, demonstrating Cl$^-$ permeation. That Asp at position 143 (in the S2 segment) overcame the nonconduction of D112V is consistent with position 143 facing the pore, as predicted in our model, but in a location incompatible with its producing H$^+$ selectivity.

Accessibility of His$^{211}$ in R211H/D112V/V116D channels in the open state was evaluated by adding Zn$^{2+}$ or EGTA during pulses. In Fig. 8 A, shortly after the start of a pulse, 10 µM Zn$^{2+}$ was introduced (red record), producing slowly progressing block. The subsequent pulse (Fig. 8 A, blue) illustrates the full extent of inhibition. Given that the probability of being open is high during large pulses—95% at pH 5.5 and 75% at pH 6.5 (Cherny et al., 2003)—and that gating is slow, cycling of channels through closed states during the pulse seems unlikely. Because Zn$^{2+}$ must diffuse through the unstirred volume at the tip of the pipette to reach the membrane, onset of block was slow and likely dependent on pipette and patch geometry, but was observed unequivocally in four patches for long pulses. The addition of EGTA during a pulse to remove Zn$^{2+}$ resulted in rapid reversal of block (Fig. 8 B) in six patches. The application of 10 µM Zn$^{2+}$ to inside-out patches from cells expressing the control construct D112V/V116D produced comparatively minor effects on the current (Fig. 8 C), reminiscent of its effects on native Hv1 (Cherny and DeCoursey, 1999). Thus, His at position 211 in R211H/D112V/V116D was accessible to the internal solution even in the open state, indicating similar accessibility of the S4 Arg residues in open channels with the selectivity filter at either position 112 or 116.

MD simulations reveal significant differences in the electrostatic properties of mutant channels

To assess the structural impact of the filter shift, MD simulations were performed on the WT protein, single-point mutants D112V and D112S, and double mutants D112V/V116D (VD) and D112V/V112S (VS) in a hydrated lipid bilayer bathed in 500 mM NaCl, based on our homology model (Kulleperuma et al., 2013). The overall structure of the channel was preserved in the mutants. In particular, the average root-mean-square deviation between WT and mutants ranged from 2.0 Å to 3.5 Å.
Despite these overall similarities (Fig. 9), differences were evident in the local structure of the pore near the EC bottleneck (Fig. 10). In the WT (Fig. 10 A), the EC constriction usually consists of a salt bridge between Arg^{208} and Asp^{112} (or occasionally Asp^{185}), whereas the other charged residues in the EC vestibule, namely Asp^{185} and Arg^{205}, usually form a spatially distinct ion pair. Consistent with our previous simulation study (Kulleperuma et al., 2013), Asp^{112}–Arg^{208} in WT is present as an ion pair most of the time but is occasionally disrupted by water molecules, resulting in the transient appearance of a water chain. In all four mutants considered, however, the absence of a charged side chain at position 112 led to the reorganization of the ionic network in the EC vestibule. In the proton-selective VD mutant (Fig. 10 B), various arrangements of ionic networks involving between two and four charged side chains from helices S1 (Asp^{116}), S3 (Asp^{185}), and S4 (Arg^{205} and Arg^{208}) were observed. Fig. 11 illustrates the most frequent configurations adopted by Asp^{116}. Most of the time (~82%), it interacts with Arg^{205} (Fig. 11 A) or Arg^{208}.

Figure 9. Pore hydration is similar in WT and several mutant channels despite very different selectivity. Average water density within a 0.7-nm radius of the mean axis of the pore is plotted, normalized to the bulk water density for 5,000 snapshots from each replica of different systems. The membrane boundaries are indicated by dashed lines, with the external surface to the right. The nadir is near Phe^{150} in all cases. Average axial water density for: (A) WT (proton selective) and D112V (VAL, nonconducting); (B) WT and D112V/V116S (VS) and D112S (S), two anion-penetrable channels; (C) WT and D112V/V116D (VD), of which both are proton selective.
(Fig. 11 D) or both (Fig. 11 C). Similarly, in WT hHV1, Asp\textsuperscript{112} was engaged in salt linkage 90% of the time but almost exclusively with Arg\textsuperscript{208}. However, in WT hHV1, a continuous water chain was present only when the Asp\textsuperscript{112}–Arg\textsuperscript{208} salt bridge was broken, which occurred ~10% of the time (Kulleperuma et al., 2013). In contrast, water pathways were observed in all configurations of the VD mutant, reflecting the greater width of the pore at this level compared with position 112. That an aqueous pathway is not predictive of proton selectivity is not surprising given the example of aquaporin channels that conduct water at high rate but are impermeable to protons (Zeidel et al., 1994). In contrast with WT, pore hydration is not significantly modulated by the configurations of Asp\textsuperscript{116} in the VD mutant.

In particular, Arg\textsuperscript{208} was observed to form ion pairs with Asp\textsuperscript{116}, Asp\textsuperscript{185}, or neither, or both. In contrast to WT, the local hydration of the constriction at the bottom of the EC funnel does not depend on whether or not Arg\textsuperscript{208} is engaged in ion pairing (Fig. 10 B). Furthermore, our models predict the presence of water pathways in the anionic mutants D112S and VS (Fig. 10, C and D), and even in the nonconducting D112V mutant (Fig. 10 E). In all systems considered, the channel contains a narrow bottleneck ~0.5 nm in length (~0.68 < z < ~0.18 nm) between the tips of the EC and IC funnels. Although this bottleneck is lined with nonpolar residues including Val\textsuperscript{109}, Phe\textsuperscript{150}, Val\textsuperscript{178}, and Val\textsuperscript{209}, it contains a single file of two water molecules at least 75% of the time, consistent with a putative ion pathway between the EC and IC funnels.

As a first step toward characterizing the energetics of ion permeation in the channel, we computed the static-field energy for a virtual positive point charge along water pathways spanning the length of the channel. Fig. 12 A shows that D112V, D112S, and VS mutants contain an

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**Figure 10.** The EC salt-link network realigns in mutants. Representative snapshots of ionic networks in the WT and mutants, with the external end up. (A) WT protein in contact (left) and water-mediated (right) states of the D112–R208 ion pair. (B) VD mutant, with R208 participating in (left) and free from (right) the EC salt-link network. (C) VS mutant. (D) D112S mutant. (E) D112V mutant. Acidic and basic side chains in the external and internal funnel, together with side chains of residues 112, 116, F150, and R211 are shown in licorice representation together with ribbon traces of the four α-helical transmembrane regions: red, S1; yellow, S2; green, S3; blue, S4. Salt bridges are shown as orange lines. The volumetric surface of water within the pore is shown with a water radius of 0.14 nm.
electrostatic barrier opposing the movement of a cation through the EC side of the bottleneck, which is lacking in the WT. In contrast, the energetic properties of the VD double mutant depend on the local arrangement of ionic residues in the EC funnel. Specifically, a static-field barrier to cation movement is present at the EC bottleneck when Arg\(^{208}\) does not take part in any salt link (Fig. 12 A, “VD unpaired”), but this barrier is reduced by at least one half when the guanidinium group of Arg\(^{208}\) is paired with the carboxylate group of either Asp\(^{116}\) or Asp\(^{185}\), or both (Fig. 12 B, “SL,” salt linkage). In the latter cases, the static-field profile becomes comparable to that of WT. Intriguingly, the electrostatic profile seems to be relatively insensitive to the nature of the ionic pairing of Asp\(^{116}\) (illustrated in Fig. 11).

Collectively, the above results suggest that the lack of proton selectivity in D112V, D112S, and VS mutants is caused at least in part by the distribution of charged groups in the lumen, where the presence of an excess positive charge near the EC constriction would tend to favor anions over cations. This finding is consistent with the anionic selectivity of D112S and VS mutants. Conversely, the neutrality of the EC bottleneck region in WT and VD systems results in approximate cancellation of the static field, which, although it does not explain proton selectivity, is consistent with the fact that these two channels are permeable to a cation.

**DISCUSSION**

Nonconducting mutants

When the critical Asp\(^{112}\) residue was moved along the S1 segment from position 108 through 118 (with D112A), 8 of 10 mutants did not conduct, proton current was seen at 116, and anion current was seen at 109. Positions 116, 112, and 109 all face the “pore” in the predicted open-state structure of hHV1 (Kulleperuma et al., 2013). Asp at pore-facing position 143 in the S2 segment also exhibited anion current. Evidently, the Asp carboxyl group must face the pore to enable conductance of any kind, and with Asp at a nonpore-facing location, the S1 segment is not free to rotate enough for the carboxyl group to reach the pore. When Asp faces away from the pore, its pK\(_a\) likely increases substantially, making it permanently neutral. When Lys was introduced at a series of locations in the acetylcholine receptor channel, its pK\(_a\) was decreased, often drastically, when it did not face the pore directly (Cymes et al., 2005). When ionizable amino acids are inserted inside proteins by mutation, their pK\(_a\) generally shifts in the direction that promotes neutrality (Isom et al., 2008). In contrast, in native proteins, ionizable residues have evolved to establish interactions with their neighbors that favor ionization (Kim et al., 2005; Gunner et al., 2011).

The rules of the game

The selectivity of various mutants summarized in Table 1 reveals “the rules of the game” for hHV1. In the mutants studied, the presence of Asp or Glu at position 112 or 116 was necessary and sufficient to produce H\(^+\) selectivity. The identity of the amino acid at position 109 had no effect; selectivity was determined entirely by positions 112 and 116. When Val was present at both critical positions, 112 and 116, the channel failed to conduct (an effect that was not overcome by introducing Asp at 109). That Val seems to disfavor permeation may reflect its relative hydrophobicity (Kyte and Doolittle, 1982; Hessa et al., 2005). When ionizable amino acids are inserted inside proteins by mutation, their pK\(_a\) generally shifts in the direction that promotes neutrality (Isom et al., 2008). In contrast, in native proteins, ionizable residues have evolved to establish interactions with their neighbors that favor ionization (Kim et al., 2005; Gunner et al., 2011).

**Microenvironment of positions 112 and 116**

With respect to selectivity, voltage dependence, kinetics, and ΔpH dependence of gating, the filter-shifted D112V/V116D channels were quite similar to WT. In
addition, the effects of point mutations at position 116 closely resembled those at 112. Glu replacing Asp at either position preserves proton specificity. Channels with neutral residues like Ser or Asn at either position (with Val occupying the other) conduct anions. These phenomenological parallels indicate that in terms of the molecular details required to establish proton (or anion) selectivity, the two positions are virtually indistinguishable. However, the identities of individual neighbors of the critical aspartate differ substantially at the two positions. Side chains with atoms within 6 Å of Asp\(^{112}\) (WT) or Asp\(^{116}\) (in the D112V background) at least 50% of the time were identified from time-averaging of MD simulations. Intriguingly, in WT, the nearest neighbors to Asp\(^{112}\), excluding those on the S1 segment (Ala\(^{113}\), Leu\(^{111}\), Leu\(^{115}\), Val\(^{116}\), and Val\(^{109}\)), include residues on both S2 (Ile\(^{146}\), Ser\(^{143}\), and Phe\(^{150}\)) and S4 (Arg\(^{208}\)), whereas in the VD mutant, only S4 residues (Arg\(^{205}\) and Arg\(^{208}\); along with S1 residues Leu\(^{117}\), Glu\(^{119}\), Leu\(^{115}\), and Leu\(^{120}\)) are within 6 Å of Asp\(^{116}\). In the D112V/V116D

| Construct      | 109 | 112 | 116 | Selectivity | Reference         |
|----------------|-----|-----|-----|-------------|-------------------|
| WT hHv1        | Val | Asp | Val | H\(^+\)      | Many              |
| A113D          | Val | Asp | Val | H\(^+\)      | This              |
| D112E          | Val | Glu | Val | H\(^+\)      | Musset et al., 2011 |
| D112A/V116D    | Val | Ala | Asp | H\(^+\)      | This              |
| D112V/V116D    | Val | Val | Asp | H\(^+\)      | This              |
| D112V/V116E    | Val | Val | Glu | H\(^+\)      | This              |
| D112V          | Val | Val | Val | 0            | Musset et al., 2011 |
| D112V/V109D    | Asp | Val | Val | 0            | This              |
| D112A, N, S, H, K, F | Val | Ala | Val | Cl\(^-\)     | Musset et al., 2011 |
| D112A/V109D    | Asp | Val | Val | Cl\(^-\)     | This              |
| D112V/V116S    | Val | Val | Ser | Cl\(^-\)     | This              |
| D112V/V116N    | Val | Val | Asn | Cl\(^-\)     | This              |

Selectivity to H\(^+\) means \(V_{rev}\) was close to \(E_0\) at various \(\Delta\text{pH}\); 0 means no credible currents; Cl\(^-\) means \(V_{rev}\) shifted negatively when Cl\(^-\) replaced CH\(_3\)SO\(_3\)\(^-\) in the external solution. Acidic residues are bold; neutral residues other than Val are italicized.
The presence of an excess positive charge at the narrow end of the external funnel in neutral Asp$^{112}$ mutants leads to a barrier opposing cation movement but compatible with anion selectivity. In addition, the presence of an ionic network involving Arg$^{208}$ results in dynamic fluctuations of pore hydration and/or electrostatic properties that may contribute to the mechanism of proton selectivity in the WT and VD channels.

**Parallels in other molecules**

To our knowledge, hH$\text{V}_1$ is the first example of a selective ion channel whose selectivity filter can be moved by a pair of point mutations. The acetylcholine receptor channel remains nonselective among cations when its ring of Glu residues is shifted by one turn of the $\alpha$ helix (Cymes and Grosman, 2012). Several other proton-conducting pathways permit shifts of critical amino acids, although in these molecules the portable function is primarily rapid proton flux rather than proton selectivity per se. For example, in F$_{1}$F$_{0}$-type ATP synthase (Escherichia coli), proton translocation is preserved when Asp$^{61}$ is shifted to position 24 on another helix (Miller et al., 1990). Asp$^{61}$ can be replaced by Glu$^{61}$, but with diminished proton transport, suggesting that precise location of the carboxyl is critical (Fillingame, 1990). Portability of Asp shows that the precise structure of apolar neighbors of the carboxyl group is not critical (Fillingame, 1990). Another essential residue in ATP synthase is Arg$^{210}$, which is thought to lower the $pK_a$ of Asp$^{61}$ transiently to ensure proton release (Fillingame et al., 2003; von Ballmoos et al., 2009).

As in ATP synthase, an Asp$^{213}$ critical for proton translocation in nicotinamide nucleotide transhydrogenase can be replaced by Glu, but activity is decreased to 18% (Yamaguchi et al., 2002). In enzyme studies, activity that is rate-limited by proton translocation is assessed. The correlate in hH$\text{V}_1$ is single-channel conductance, which was not examined here. Our criterion is perfect proton selectivity, which is preserved when Glu replaces Asp at either position 112 or 116 in hH$\text{V}_1$. We cannot say whether Glu is equally efficient.

When Asp$^{135}$ in the proton entry channel in cytochrome $b_{5}$ ubiquinol oxidase of E. coli is neutralized, its function can be restored by shifting Asp to position 139 or 142 (Garcia-Horsman et al., 1995).

Neutralizing Asp$^{132}$, the namesake of the D channel in cytochrome $c$ oxidase from Rhodobacter sphaeroides, by mutations D132N or D132A nearly abolishes proton uptake (Fetter et al., 1995), which is restored by repositioning the Asp at N139D (Varanasi and Hosler, 2011, 2012). Intriguingly, proton uptake is also restored by removing subunit III (Adelroth and Hosler, 2006) and also in the D132N/N139T double mutant, showing that in the D channel, rapid proton uptake can be accomplished without an acidic group, although enzyme turnover remains impaired (Johansson et al., 2013). Asn$^{130}$ is thought to serve a special “gating” function in cytochrome
c oxidase that may normally limit WT H’ flux (Henry et al., 2009); Thr193 appears to optimize aqueous connectivity within the pore (Johansson et al., 2013).

Finally, His64 shuttles protons from the catalytic center of human carbonic anhydrase II, and function is preserved with His shifted to His67 (H64A/N67H), but not His62 (H64A/N62H), despite crystal structures indicating that the side chains of both His62 and His67 extend into the active-site cavity at distances from the catalytic zinc similar to His64 (Fisher et al., 2005).

These examples show that an amino acid side chain must be positioned correctly to maintain a high rate of proton transfer, but that in some cases a reasonable rate of proton transfer can be retained upon moving the side chain, especially if it is not moved too far. Given that proton transfer via titratable amino acid side chains is a way to achieve proton selectivity, proton transfer and proton selectivity may be the same process, and thus in some cases, a side chain essential for H’ selectivity may be moved without losing selectivity.

In summary, shifting Asp along the S1 segment identified three locations in hHV1 that line the pore and permit conduction: 109, 112, and 116. Asp produced proton specificity only at positions 112 and 116. When introduced at nonpore-facing positions, Asp abolished function. Glu at either position preserved selectivity, indicating leeway in side-chain length. We conclude that the minimal requirements for proton specificity of hHV1 include Asp or Glu, which must face the pore directly, and evidently must be located in the external vestibule, above the charge transfer center, Phe150. The portability of the selectivity filter indicates latitude in the requisite local environment. This observation seems consistent with the suggestion that ionizable groups that enable proton transport could have evolved by random mutation without the suggestion that ionizable groups that enable proton transfer via titratable amino acid side chains of hHV1 preserve selectivity, in- permitting conduction: 109, 112, and 116. Asp produced proton specificity only at positions 112 and 116. When introduced at nonpore-facing positions, Asp abolished function. Glu at either position preserved selectivity, indicating leeway in side-chain length. We conclude that the minimal requirements for proton specificity of hHV1 include Asp or Glu, which must face the pore directly, and evidently must be located in the external vestibule, above the charge transfer center, Phe150. The portability of the selectivity filter indicates latitude in the requisite local environment. This observation seems consistent with the suggestion that ionizable groups that enable proton transport could have evolved by random mutation without the need to simultaneously develop a specialized micro-environment for charge stabilization (Isom et al., 2008).

On the other hand, the inability of Asp to produce H+ selectivity of human carbonic anhydrase II, and function is preserved with His shifted to His67 (H64A/N67H), but not His62 (H64A/N62H), despite crystal structures indicating that the side chains of both His62 and His67 extend into the active-site cavity at distances from the catalytic zinc similar to His64 (Fisher et al., 2005).

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