



Accessibility of ENaC extracellular domain central core residues

Received for publication, January 3, 2022, and in revised form, March 16, 2022. Published, Papers in Press, March 23, 2022.
<https://doi.org/10.1016/j.jbc.2022.101860>

Lei Zhang^{1,2,3}, Xueqi Wang^{1,2,3}, Jingxin Chen¹, Thomas R. Kleyman^{1,4,5,*}, and Shaohu Sheng¹

From the ¹Departments of Medicine, University of Pittsburgh, Pittsburgh, Pennsylvania, USA; ²Department of Nephrology, Hunan Key Laboratory of Kidney Disease and Blood Purification, The Second Xiangya Hospital, Central South University, Changsha, Hunan, China; ³The Third Xiangya Hospital of Central South University, Changsha, Hunan, China; ⁴Cell Biology, and ⁵Pharmacology and Chemical Biology, University of Pittsburgh, Pittsburgh, Pennsylvania, USA

Edited by Mike Shipston

The epithelial Na⁺ channel (ENaC)/degenerin family has a similar extracellular architecture, where specific regulatory factors interact and alter channel gating behavior. The extracellular palm domain serves as a key link to the channel pore. In this study, we used cysteine-scanning mutagenesis to assess the functional effects of Cys-modifying reagents on palm domain β 10 strand residues in mouse ENaC. Of the 13 ENaC α subunit mutants with Cys substitutions examined, only mutants at sites in the proximal region of β 10 exhibited changes in channel activity in response to methanethiosulfonate reagents. Additionally, Cys substitutions at three proximal sites of β and γ subunit β 10 strands also rendered mutant channels methanethiosulfonate-responsive. Moreover, multiple Cys mutants were activated by low concentrations of thiophilic Cd²⁺. Using the Na⁺ self-inhibition response to assess ENaC gating behavior, we identified four α , two β , and two γ subunit β 10 strand mutations that changed the Na⁺ self-inhibition response. Our results suggest that the proximal regions of β 10 strands in all three subunits are accessible to small aqueous compounds and Cd²⁺ and have a role in modulating ENaC gating. These results are consistent with a structural model of mouse ENaC that predicts the presence of aqueous tunnels adjacent to the proximal part of β 10 and with previously resolved structures of a related family member where palm domain structural transitions were observed with channels in an open or closed state.

Epithelial Na⁺ channels (ENaCs) are members of the ENaC/degenerin family of ion channels that are formed by subunits with large extracellular domains that interact with factors in the external environment that regulate channel gating (1, 2). Channel subunits are similar in structure, with complex highly folded extracellular regions that connect to two transmembrane α helices that form the channel pore where the selectivity filter and gate reside and cytoplasmic N- and C-termini (3). ENaCs are heterotrimers composed of α (or δ),

β , and γ subunits. They are expressed in the apical membrane of specific cells in the aldosterone-sensitive distal nephron, where the channel has a key role in the reabsorption of filtered Na⁺ and regulation of extracellular fluid volume and blood pressure, as well as facilitating the secretion of K⁺ (1, 2, 4). They are expressed at other sites that also influence blood pressure, including lingula epithelia, monocytes, endothelium, and vascular smooth muscle (4, 5).

The resolved structures of the extracellular regions of an acid-sensing ion channel 1 (ASIC1) and ENaC have provided important insights regarding channel structure and regulation (6–10). The extracellular regions of members of this ion channel family are formed by five distinct domains, referred to as palm, β -ball, finger, thumb, and knuckle. The palm and β -ball domains are formed by β strands. The more peripheral finger, thumb, and knuckle domains are formed by α helices. ENaCs are regulated by a number of extracellular factors, including Na⁺, H⁺, Cl⁻, proteases, and shear stress (1, 2, 11–16). For example, extracellular Na⁺ inhibits ENaC by binding to a site in the finger domain of the α subunit, leading to structural transitions that are transmitted to the transmembrane domains with a reduction in channel open probability (10, 17). Channels with a δ subunit from specific species are also inhibited by extracellular Na⁺ (18). Specific proteases cleave the α and γ subunits at multiple specific sites in their finger domains, releasing imbedded inhibitory tracts and transitioning channels to higher open probability states (1, 2). While studies have implicated specific residues and extracellular domain structures in regulating ENaC gating, a clear understanding of the structural transitions that occur in association with gating is lacking.

The palm domains within ENaC subunits are composed of a series of antiparallel beta strands and provide the key link between the extracellular and transmembrane regions of the channel (9, 10). Recent studies suggest that the palm domain has an important role in regulating the gating of members of the ENaC/degenerin family of ion channels (7, 19–21), although exact mechanisms are unclear. Within the palm domain, a long β strand (β 10) resides within the trimeric symmetry axis, bordering the knuckle and thumb domains. β 10 residues that are proximal to the channel pore, together with other palm domain β strands, enclose a central vestibule

* For correspondence: Thomas R. Kleyman, kleyman@pitt.edu.
Present address for Xueqi Wang: Department of Nephrology, Beijing Friendship Hospital, Capital Medical University, Beijing 10,050, China.

ENaC palm domain

whose function is also unknown (9, 10). To explore the accessibility and potential functional roles of the mouse α subunit β 10 strand, individual residues within β 10 were systematically mutated to Cys. We also mutated specific residues in the β 10 strand of the β and γ subunits to Cys. We examined the functional response of wildtype and mutant channels to the Cys-reactive reagents sodium (2-sulfonatoethyl) methanethiosulfonate (MTSES) and [2-(trimethylammonium) ethyl] methanethiosulfonate bromide (MTSET), as well as the inhibitory response to extracellular Na^+ . We found that channels with specific Cys substitutions in the proximal aspects of the β 10 strand of the α , β , and γ subunits are modified by methanethiosulfonate (MTS) reagents, respond to Cd^{2+} , and have an altered Na^+ self-inhibition response, suggesting a role in modulating ENaC gating.

Results

A structural homology model of mouse ENaC was built using SWISS-MODEL (22), based on the resolved structure of human ENaC (PDB 6BQN (9)). Trimeric and monomeric structural models are shown in Figure 1. The proximal end of β 10 links to the thumb domain, whereas the distal end of β 10 links to the knuckle domain (Fig. 1B). The β 10 sequence is well conserved among α , β , and γ subunits of human, mouse and rat ENaC, and chicken ASIC1 (Fig. 1C).

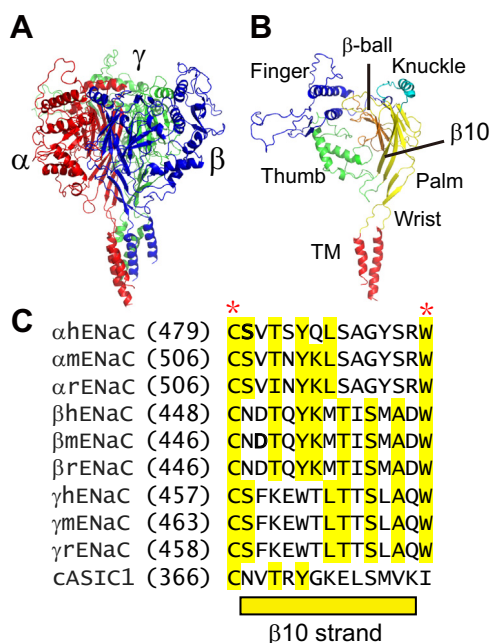


Figure 1. ENaC model and the β 10 strand. A, structural model of mouse ENaC. A structural model of mouse ENaC was generated with SWISS-MODEL, using a trimeric human ENaC structure (PDB 6BQN) and PyMOL 2.4 (75). The α , β , and γ subunits are presented in red, blue, and green, respectively. B, structural model of the α subunit. Finger, knuckle, thumb, palm, and β -ball domains are presented in blue, cyan, green, yellow, and orange, respectively. The transmembrane (TM) α helices are highlighted in red. C, sequence alignment of human, mouse, and rat ENaC α , β , and γ subunit β 10 strands and chicken ASIC1 β 10 strand. Identical residues are highlighted. The asterisks identify human α subunit residues where variants associated with a gain-of-function reside (56–58). Alignments were generated using Clustal Omega (76). ASIC, acid-sensing ion channel; ENaC, epithelial Na^+ channel.

Thirteen β 10 residues in the mouse ENaC α subunit were individually mutated to Cys. Wildtype and mutant ENaCs were expressed in *Xenopus* oocytes. Amiloride (10 μM)-sensitive Na^+ currents were monitored by two-electrode voltage clamp, and the response to extracellular MTS reagents (MTSES and MTSET) was assessed. We chose these Cys-reactive reagents as they are similar in size. While MTSES modification adds a negative charge, MTSET adds a positive charge. If a Cys-containing mutant channel responded to either reagent with a significant change in channel current, this Cys was considered as functionally accessible and important. If a Cys mutant channel did not respond to any reagent, this Cys was described as functionally inaccessible. The latter category includes channels with Cys substitutions that were not chemically modified by MTS reagents as well as channels where MTS modifications did not alter activity.

ENaCs are known to be inhibited by extracellular Na^+ , a process referred to as Na^+ self-inhibition (1). When an ENaC-expressing oocyte is bathed in a solution with a low (1 mM) $[\text{Na}^+]$ at a holding potential of -100 mV, there is negligible inward Na^+ current. A transition to a high (110 mM) $[\text{Na}^+]$ results in a rapid increase in inward Na^+ current, which reaches a peak (I_{peak}) that is followed by a fall in current, reflecting a reduction in channel open probability due to Na^+ self-inhibition (11, 12, 23). The Na^+ current eventually reaches a new steady-state level (I_{ss}), and the ratio of I_{ss} to I_{peak} reflects the magnitude of the Na^+ self-inhibition response. Based on previous studies showing that extracellular cues often regulate ENaC gating by altering Na^+ self-inhibition response (12–14, 24), we examined whether MTS reagents modified the Na^+ self-inhibition response of the Cys mutants that showed a significant change in current in response to these reagents.

Specific introduced Cys residues in the proximal part of the α subunit β 10 strand are functionally accessible to MTS reagents

All mutant ENaCs expressed sufficient amiloride-sensitive currents to permit examination of their response to externally applied MTS reagents. Similar effects of the MTS reagents were noted when examined before or after assessing the Na^+ self-inhibition response. Neither MTSES nor MTSET altered currents in oocytes expressing wildtype ENaC, in agreement with previous observations (25, 26) (Fig. 2, A and D). In contrast, three mutants responded to MTSES with significant increases in whole-cell current. Amiloride-sensitive Na^+ currents measured in the presence of MTSES (I_{MTSES}) were normalized to currents measured prior to the addition of MTSES (I). We observed significant increases in currents in oocytes expressing α T509C β and α N510C β (Figs. 2 and 3A), while a very modest but statistically significant increase in I_{MTSES}/I was observed with α K512C β (Fig. 3A). In contrast, MTSES significantly inhibited α S514C β (Figs. 2C and 3A). For other Cys mutants, responses to MTSES were similar to wildtype ENaC (Fig. 3A).

Four of the 13 α subunit β 10 mutants (α S507C, α N510C, α Y511C, and α S514C) exhibited significant reductions in amiloride-sensitive Na^+ currents after application of MTSET

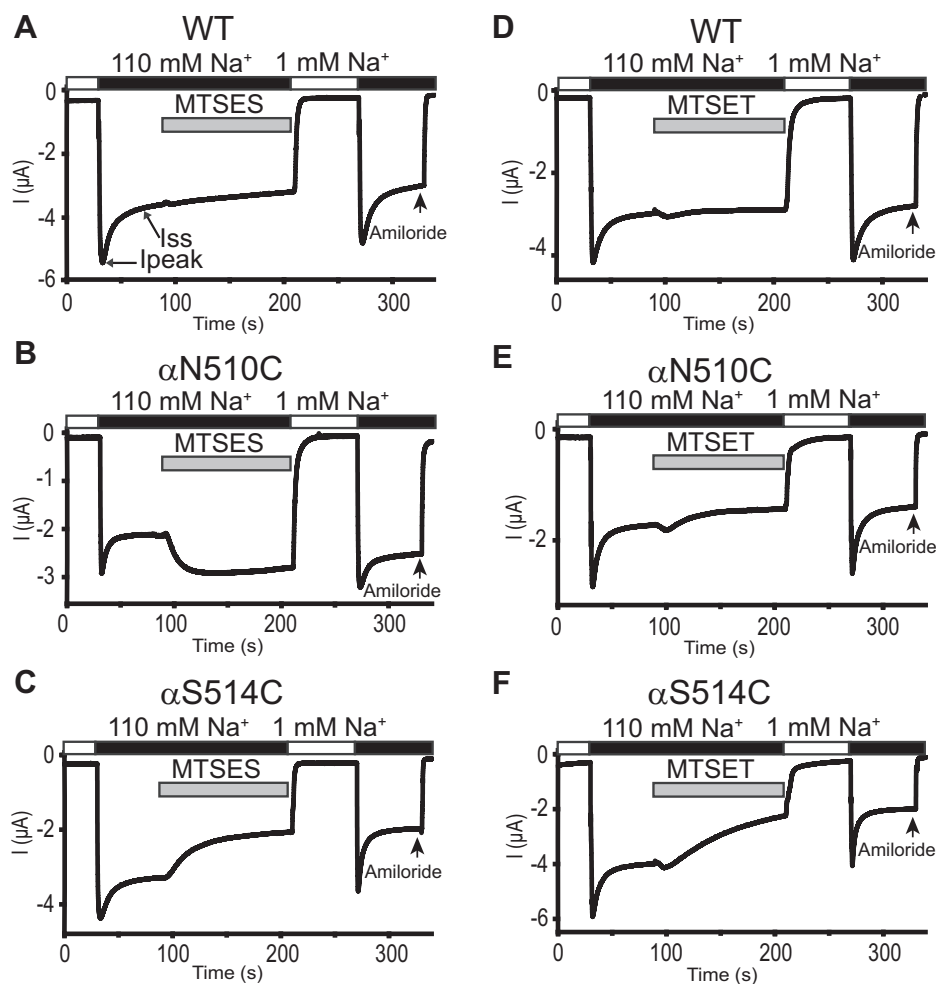


Figure 2. Select α subunit β 10 residues are functionally accessible to MTSES and MTSET. Oocytes expressing wildtype or mutant mouse ENaC channels were clamped at a holding potential of -100 mV. Whole-cell Na^+ currents were measured in oocytes perfused with solutions containing either a 1 mM (white bar) or a 110 mM Na^+ (black bar), as noted. *A–C*, representative recordings of wildtype (WT), αN510C , and αS514C channels, respectively, showing the effects of 2 mM MTSES, added to the bath as indicated by the gray bar. Ipeak, peak current after switching from a 1 mM to a 110 mM Na^+ bath solution. I_{ss}, steady state current at 40 s after Ipeak. *D–F*, representative recordings of wildtype, αN510C , and αS514C channels, respectively, showing the effects of 1 mM MTSET, added to the bath as indicated by the gray bar. Arrow indicates addition of amiloride (10 μM) to the bath. MTSES, sodium (2-sulfonatoethyl) methanethiosulfonate; MTSET, [2-(trimethylammonium) ethyl] methanethiosulfonate bromide.

(Figs. 2 and 3B). For other mutants, responses to MTSET were similar to wildtype ENaC (Fig. 3B). The effects on currents in oocytes expressing ENaC mutants were sustained after the reagent was washed out, consistent with irreversible channel modification.

Modification of specific β 10 Cys-substituted residues with MTS reagents alters the Na^+ self-inhibition response

We examined the Na^+ self-inhibition response of wildtype and mutant channels that showed significant changes in current in response to MTS reagents, by measuring the I_{ss} to Ipeak ratio following the switch from a 1 mM to 110 mM Na^+ bath (see Fig. 2A). The Na^+ self-inhibition response was determined prior to and following MTSES or MTSET application. The percent change in the Na^+ self-inhibition response (ΔSI) following MTS treatment, relative to the Na^+ self-inhibition response prior to MTS, was determined using the formula described in the Figure 4 legend. A positive ΔSI reflects an enhanced Na^+ self-inhibition response after MTSES or MTSET treatment, while negative ΔSI reflects a reduced Na^+ self-inhibition response after

MTSES or MTSET treatment. Wildtype ENaCs showed a similar and modest increase in Na^+ self-inhibition after MTSES and MTSET treatment (Fig. 4, A–D). This increase is likely not due to the MTS reagent, as we have observed that repetitive tests of Na^+ self-inhibition in the same oocyte often led to a modest increase in the Na^+ self-inhibition response. To ascertain this was the case, we examined Na^+ self-inhibition responses in oocytes expressing wildtype ENaCs twice with the same time interval as the MTS application shown in Figure 2, A and D (*i.e.*, 2 min). The representative recording and summary data are shown in Figure 4, E and F, demonstrating a similar level of increase in the Na^+ self-inhibition response of wildtype channels as observed after MTS application (Fig. 4, A–D). This increase in Na^+ self-inhibition may be related to a time-dependent decrease in ENaC activity that has been observed when oocytes are bathed with a high concentration of extracellular Na^+ and clamped at hyperpolarization potential (27, 28). Compared to wildtype, MTSES significantly reduced the Na^+ self-inhibition response of αN510C but increased that of αS514C . MTSET, on the

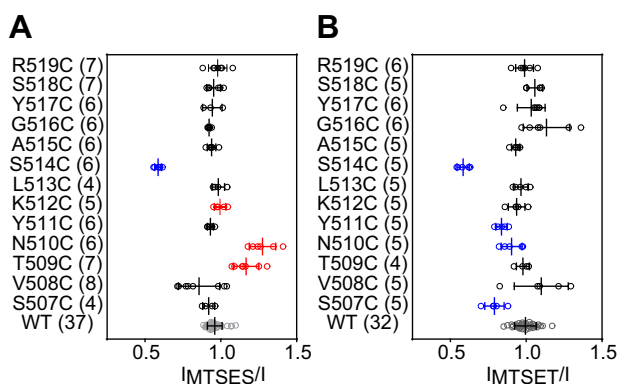


Figure 3. External MTSES and MTSET alter the activity of multiple α subunit $\beta 10$ Cys mutants. *A and B*, scatterplots of I_{MTSES}/I and I_{MTSET}/I , measured in channels with α subunit $\beta 10$ Cys mutants. I_{MTSES}/I and I_{MTSET}/I are ratios of amiloride-sensitive currents after (I_{MTSES} or I_{MTSET}) and prior to (I) application of the reagents. Bars are mean \pm S.D. Numbers of oocytes in each experiment are listed in parentheses. Wildtype mouse $\alpha\beta\gamma$ ENaCs were always examined and compared with the mutant channels in the same batch of oocytes. Statistically significant differences in the MTS response of wildtype and mutant channels were determined in the same batches of oocytes by one-way ANOVA followed by Dunnett's tests. The values for wildtype channels (WT, shown in gray) in the charts were from all batches of oocytes used in these experiments and are shown for display purpose only. Values that are not significantly different from that measured with wildtype ENaC are shown in black. Values that are significantly reduced or increased when compared with wildtype ($p < 0.05$) are shown in blue or red, respectively. ENaC, epithelial Na^+ channel; MTS, methanethiosulfonate; MTSES, sodium (2-sulfonatoethyl) methanethiosulfonate; MTSET, [2-(trimethylammonium) ethyl] methanethiosulfonate bromide.

other hand, did not significantly alter the Na^+ self-inhibition response of $\alpha\text{N510C}\beta\gamma$ but increased the Na^+ self-inhibition response of $\alpha\text{S514C}\beta\gamma$. These results suggest that MTSES and MTSET modify the Na^+ self-inhibition response of specific mutant channels.

MTSES does not activate αN510C channels containing a βS518K mutation

The strong activation of $\alpha\text{N510C}\beta\gamma$ by MTSES was associated with a significant reduction in the Na^+ self-inhibition response (Figs. 2B and 3A), consistent with an MTSES-dependent increase in channel open probability in the presence of a high extracellular $[\text{Na}^+]$. An increase in current could also reflect an increase in unitary channel conductance. To rule out this possibility, we examined the effect of MTSES on αN510C channels that also had a βS518K mutation. Previous studies have shown that βS518K channels have an intrinsic high open probability (29–31). If MTSES activation involves an increase in unitary conductance, it should activate $\alpha\text{N510C}\beta\text{S518K}\gamma$ channels. We observed that MTSES did not activate $\alpha\text{N510C}\beta\text{S518K}\gamma$ ($p = 0.77$, before versus after MTSES treatment, $n = 11$, paired Student's t test, Fig. 5). Consistent with a high open probability state, the Na^+ self-inhibition response of $\alpha\text{N510C}\beta\text{S518K}\gamma$ was absent prior to and after MTSES application (Fig. 5A).

Four α subunit $\beta 10$ mutations alter Na^+ self-inhibition response

We examined the Na^+ self-inhibition response of each α subunit $\beta 10$ Cys mutant and compared it to the wildtype Na^+ self-inhibition response. As shown in Figure 6, two mutations

(αV508C and αY517C) reduced and two mutations (αT509C and αN510C) enhanced the Na^+ self-inhibition response. The data suggest that these residues have a role in Na^+ self-inhibition. As the magnitude of Na^+ self-inhibition is correlated with open probability (23), mutant channels with a reduced Na^+ self-inhibition response should display an elevated whole-cell ENaC current, reflecting an increase in channel open probability. Indeed, amiloride-sensitive currents in oocytes expressing $\alpha\text{V508C}\beta\gamma$ and $\alpha\text{Y517C}\beta\gamma$ were significantly greater than that in oocytes expressing wildtype $\alpha\beta\gamma$ mouse ENaC (Fig. 6C). Interestingly, currents in oocytes expressing either of these mutant channels were not significantly altered by either MTSES or MTSET (Fig. 3).

Cys residues introduced at the proximal part of the $\beta 10$ strand of the β subunit are functionally accessible to MTS reagents

To determine whether $\beta 10$ strand residues in β and γ subunits exhibit a similar accessibility to MTS reagents, we introduced Cys mutations at four β and γ subunit $\beta 10$ residues, homologous to the α subunit $\beta 10$ residues where Cys substitutions either significantly reduced Na^+ self-inhibition or rendered mutant channels MTS-sensitive.

As shown in Figure 7, MTSES significantly reduced currents in oocytes expressing $\alpha\beta\text{D448C}\gamma$ (homologous to $\alpha\text{V508C}\beta\gamma$) and $\alpha\beta\text{Q450C}\gamma$ (homologous to $\alpha\text{N510C}\beta\gamma$), while MTSES increased $\alpha\beta\text{T454C}\gamma$ (homologous to $\alpha\text{S514C}\beta\gamma$) currents. It did not significantly change $\alpha\beta\text{M457C}\gamma$ (homologous to $\alpha\text{Y517C}\beta\gamma$) currents. MTSET inhibited $\alpha\beta\text{T454C}\gamma$ currents but increased $\alpha\beta\text{D448C}\gamma$ currents (Fig. 8). These results suggest that βD448C , βQ450C , and βT454C are functionally accessible to MTS reagents. Therefore, MTS accessibility is conserved between βQ450C and βT454C and their homologous sites in the α subunit (αN510C and αT514C). In contrast, while βD448C channels were responsive to MTS reagents, the homologous α subunit mutation (αV508C) is functionally inaccessible to MTS reagents (Figs. 3, 7 and 8).

Compared to wildtype, $\alpha\beta\text{Q450C}\gamma$ and $\alpha\beta\text{M457C}\gamma$ showed a significantly reduced Na^+ self-inhibition response (Figs. 7, 8 and 9A). The MTSES-induced current decrease in $\alpha\beta\text{D448C}\gamma$ and $\alpha\beta\text{Q450C}\gamma$ was associated with an enhanced Na^+ self-inhibition response (Fig. 9B). Furthermore, the MTSES-induced increase in $\alpha\beta\text{T454C}\gamma$ current was accompanied with a decreased Na^+ self-inhibition response (Fig. 9B). Finally, the MTSET-induced current decrease in $\alpha\beta\text{T454C}\gamma$ was followed by a significantly increased Na^+ self-inhibition response (Fig. 9C). These results suggest that several $\beta 10$ residues of β subunit have a role in Na^+ self-inhibition response.

Cys residues introduced at proximal part of the $\beta 10$ strand of the γ subunit are functionally accessible to MTS reagents

Among the four γ subunit mutants studied, $\alpha\beta\gamma\text{F465C}$ (homologous to $\alpha\text{V508C}\beta\gamma$), $\alpha\beta\gamma\text{E467C}$ (homologous to $\alpha\text{N510C}\beta\gamma$), and $\alpha\beta\gamma\text{T471C}$ (homologous to $\alpha\text{S514C}\beta\gamma$) were inhibited by MTSES, whereas $\alpha\beta\gamma\text{L474C}$ (homologous to $\alpha\text{Y517C}\beta\gamma$) was not affected (Fig. 10). MTSET reduced $\alpha\beta\gamma\text{F465C}$ and $\alpha\beta\gamma\text{E467C}$ currents, while increasing

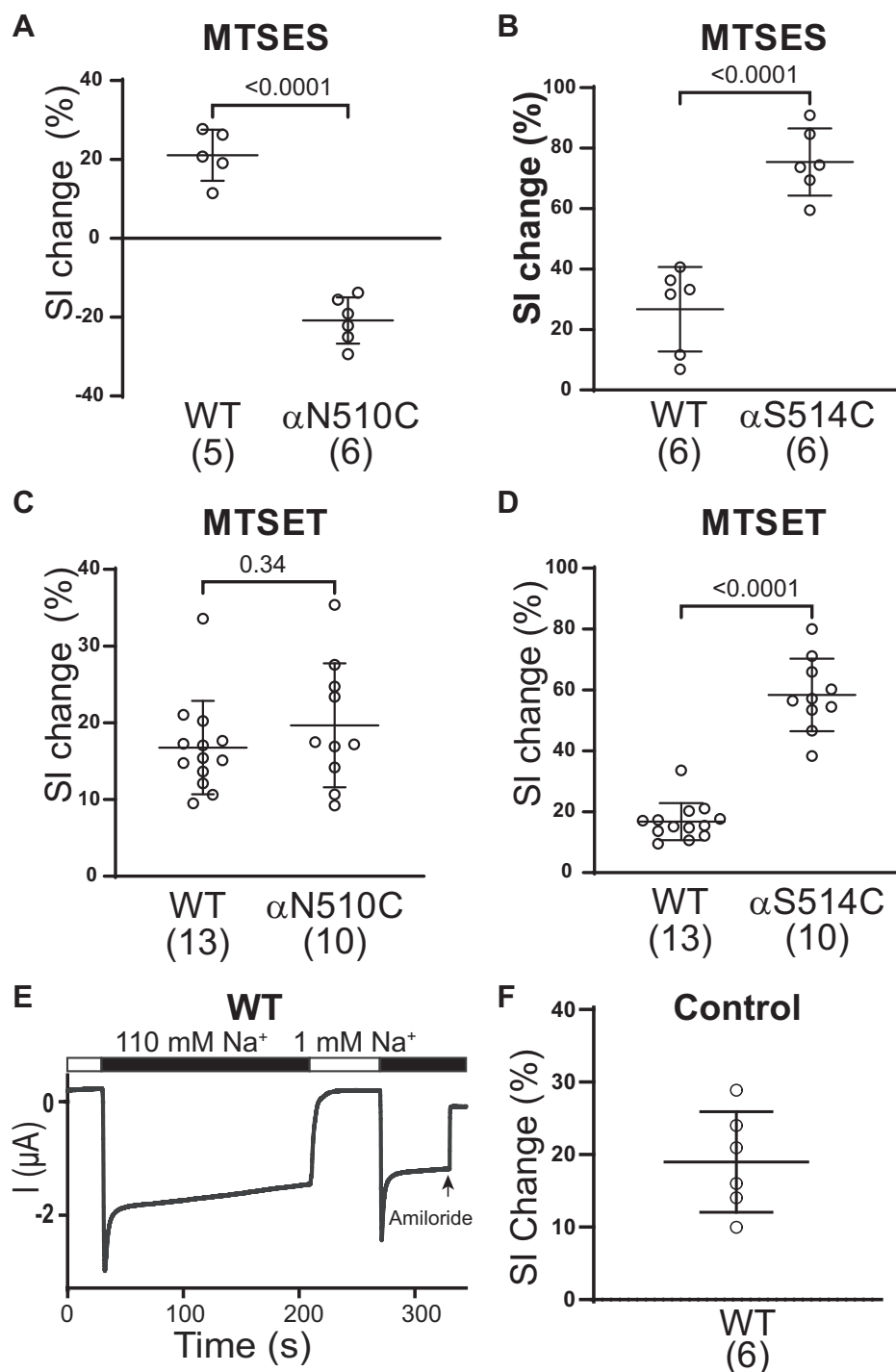


Figure 4. Effects of MTSES and MTSET on Na⁺ self-inhibition. Percentage change of the Na⁺ self-inhibition response following MTSES (A and B) or MTSET (C and D) treatment were calculated from the following formula: $(SI_2 - SI_1)/SI_1$, where SI_2 reflects the percentage of the Na⁺ self-inhibition response after MTSES or MTSET [$100 \times (I_{ss} - I_{peak})/I_{peak}$] and SI_1 reflects the percentage of the Na⁺ self-inhibition response prior to MTSES or MTSET treatment [$100 \times (I_{ss} - I_{peak})/I_{peak}$]. Data were from experiments shown in Figure 2. Bars are mean \pm S.D., and p values were from unpaired *Student's t* test with Welch's correction. E, representative recording of an oocyte expressing wildtype ENaC showing repetitive Na⁺ self-inhibition responses ($n = 6$). The experiment had the same time course as in Figure 2, A and D, except that no MTSES or MTSET was applied. F, Na⁺ self-inhibition change (%) from experiments illustrated in (E). Note the similar values to that in (A-D) for wildtype. MTSES, sodium (2-sulfonatoethyl) methanethiosulfonate; MTSET, [2-(trimethylammonium) ethyl] methanethiosulfonate bromide.

$\alpha\beta\gamma$ T471C currents. It did not affect $\alpha\beta\gamma$ L474C currents (Fig. 11). These results suggest that γ F465C, γ E467C, and γ T471C are functionally accessible to MTS reagents. Interestingly, MTS reactivity is conserved between three γ subunit

residues ($\alpha\beta\gamma$ F465C, $\alpha\beta\gamma$ E467C, and $\alpha\beta\gamma$ T471C) and their homologous β subunit residues (β D448C, β Q450C, and β T454C). While γ E467C, γ T471C, and homologous α subunit residues (α N510C and α T454C, respectively) are accessible to

ENaC palm domain

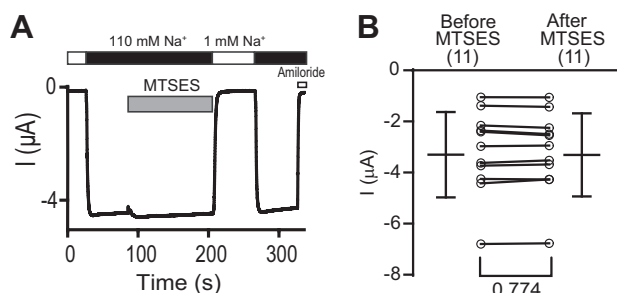


Figure 5. MTSES activation of α N510C mutant is absent in channels containing the β S518K mutant. *A*, representative recording showing the effect of MTSES on α N510C β S518K γ . Oocytes were clamped at -100 mV and perfused with either a 1 mM or a 110 mM Na^+ bath solution, as indicated by white and black bars, respectively. MTSES (2 mM) was applied for 2 min as indicated by the gray bar. Amiloride (10 μM , open bar) was applied at the end of the experiment. Representative of 11 experiments. *B*, amiloride-sensitive currents before and after MTSES treatment are shown as circles connected by lines. Similar currents were observed prior to MTSES (-3.2 ± 1.6 μA) and after MTSES (-3.2 ± 1.6 μA , $n = 11$, $p = 0.774$ from paired Student *t* test) treatment. Bars on the left and right are mean \pm S.D. before and after MTSES treatment, respectively. MTSES, sodium (2-sulfonatoethyl) methanethiosulfonate.

MTS reagents, we did not observe a consistent MTS response with γ F465C (functionally responsive) and the homologous α V508C (functionally nonresponsive, Fig. 3).

The Na^+ self-inhibition response of $\alpha\beta\gamma$ F465C (enhanced) and $\alpha\beta\gamma$ E467C (reduced) differed from wildtype (Fig. 12A), while the Na^+ self-inhibition response of the other γ subunit mutants was similar to wildtype. Following the inhibitory effect of MTSES, the Na^+ self-inhibition response of $\alpha\beta\gamma$ F465C and $\alpha\beta\gamma$ T471C was enhanced compared to the response prior to MTSES. In contrast, the Na^+ self-inhibition response of $\alpha\beta\gamma$ E467C was not altered by MTSES (Fig. 12B). MTSET inhibited $\alpha\beta\gamma$ E467C and enhanced the mutant's Na^+ self-inhibition response, whereas MTSET activated $\alpha\beta\gamma$ T471C and reduced the mutant's Na^+ self-inhibition response (Fig. 12C). These data suggest that several γ subunit β 10 residues have a role in Na^+ self-inhibition.

Cys residues introduced at select β 10 sites are functionally accessible to Cd^{2+}

We found that Cys residues introduced at multiple sites in the proximal parts of the β 10 strands in all three subunits were accessible to MTS reagents. These MTS reagents are considered bulky, with estimated dimensions of 5 (short axis) by 10 (long axis) \AA (32). We also examined accessibility and functional effects of a smaller, thiophilic cation, Cd^{2+} (10^{-7} M to 3×10^{-3} M) on currents in oocytes expressing wildtype channels or channels with a mutant γ subunit (Fig. 13A). The mutants $\alpha\beta\gamma$ F465C and $\alpha\beta\gamma$ E467C responded to both low and high concentrations of Cd^{2+} with significant and large increases in currents in a reversible manner, compared to wildtype. $\alpha\beta\gamma$ T471C responded to high concentrations of Cd^{2+} with significant and moderate increases in currents. In contrast, wildtype and $\alpha\beta\gamma$ L474C channels showed modest increases in current at high [Cd^{2+}], which then fell at a [Cd^{2+}] of 3×10^{-3} M. This modest activation was similar to what we previously observed with wildtype (33). The effects of Cd^{2+}

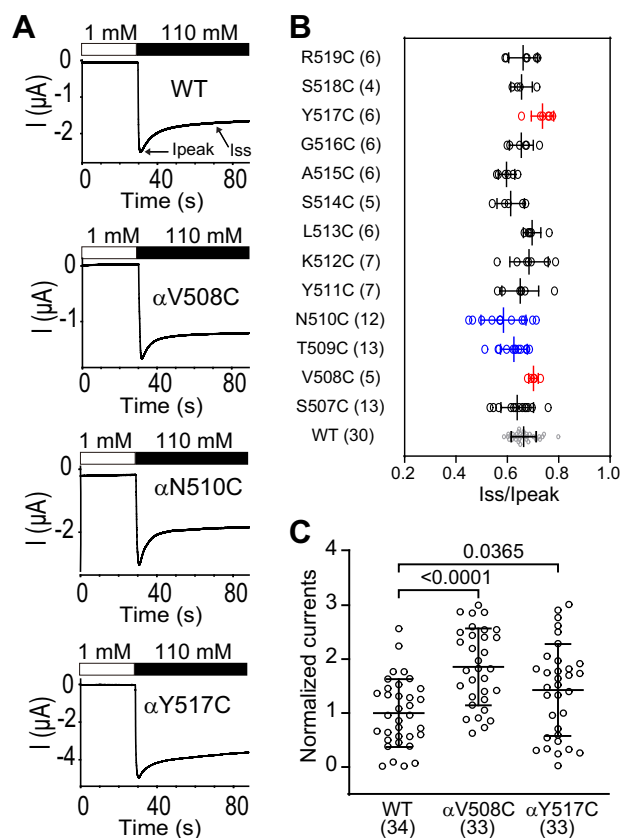


Figure 6. Selected α subunit β 10 Cys substitutions alter the Na^+ self-inhibition response. Na^+ self-inhibition responses were examined as described in the Experimental procedures. Oocytes expressing wildtype and mutant α subunit and wildtype β and γ subunits were perfused with bath solutions containing a 1 mM or a 110 mM Na^+ , as indicated by the open and filled bars in (A), while clamped at -100 mV. *A*, representative recordings showing the Na^+ self-inhibition responses in wildtype and selected mutants. *B*, dot plots of I_{ss}/I_{peak} representing the magnitude of Na^+ self-inhibition. *peak* and I_{ss} are peak and steady state currents, respectively, as depicted in top panel in (A). Bars are mean \pm S.D. Numbers of oocytes in each experiment are listed in parentheses. Wildtype mouse $\alpha\beta\gamma$ ENaCs were always examined and compared with mutant channels in the same batch of oocytes. Statistical significances between wildtype and mutant channels were determined in the same batch of oocytes by one-way ANOVA followed by Dunnett's tests. The values for wildtype channels (WT, shown in gray) in (B) were from all batches of oocytes used in these experiments and are shown for display purpose only. Values that are not significantly different from that measured with wildtype ENaC are shown in black. Values that are significantly reduced or increased when compared with wildtype ($p < 0.05$) are shown in blue or red, respectively. *C*, dot plot of the normalized currents (individual amiloride-sensitive currents divided by the mean wildtype current). Bars are mean \pm S.D. Numbers of oocytes in each experiment are listed in parentheses. The *p* values were from one-way ANOVA followed by Dunnett's tests. ENaC, epithelial Na^+ channel.

were analyzed after normalizing amiloride-sensitive currents in the presence of Cd^{2+} to currents measured prior to Cd^{2+} . Dose-response curves are shown in Figure 13B, and fitting parameters are summarized in Table 1. For $\alpha\beta\gamma$ F465C, $\alpha\beta\gamma$ E467C, and $\alpha\beta\gamma$ T471C, data fit well with a two-site model, previously used to fit the response of ENaC to Zn^{2+} (34). The EC_{50} s (\pm SD) for ENaC activation by Cd^{2+} (μM , $n = 4-5$) were 11 ± 2 , 3 ± 1 , and 124 ± 21 for $\alpha\beta\gamma$ F465C, $\alpha\beta\gamma$ E467C, and $\alpha\beta\gamma$ T471C, respectively. We next examined the effects of Cd^{2+} on α V508C $\beta\gamma$ and $\alpha\beta$ D448C γ channels (homologous to γ F465C). Both mutants responded to Cd^{2+} with significant

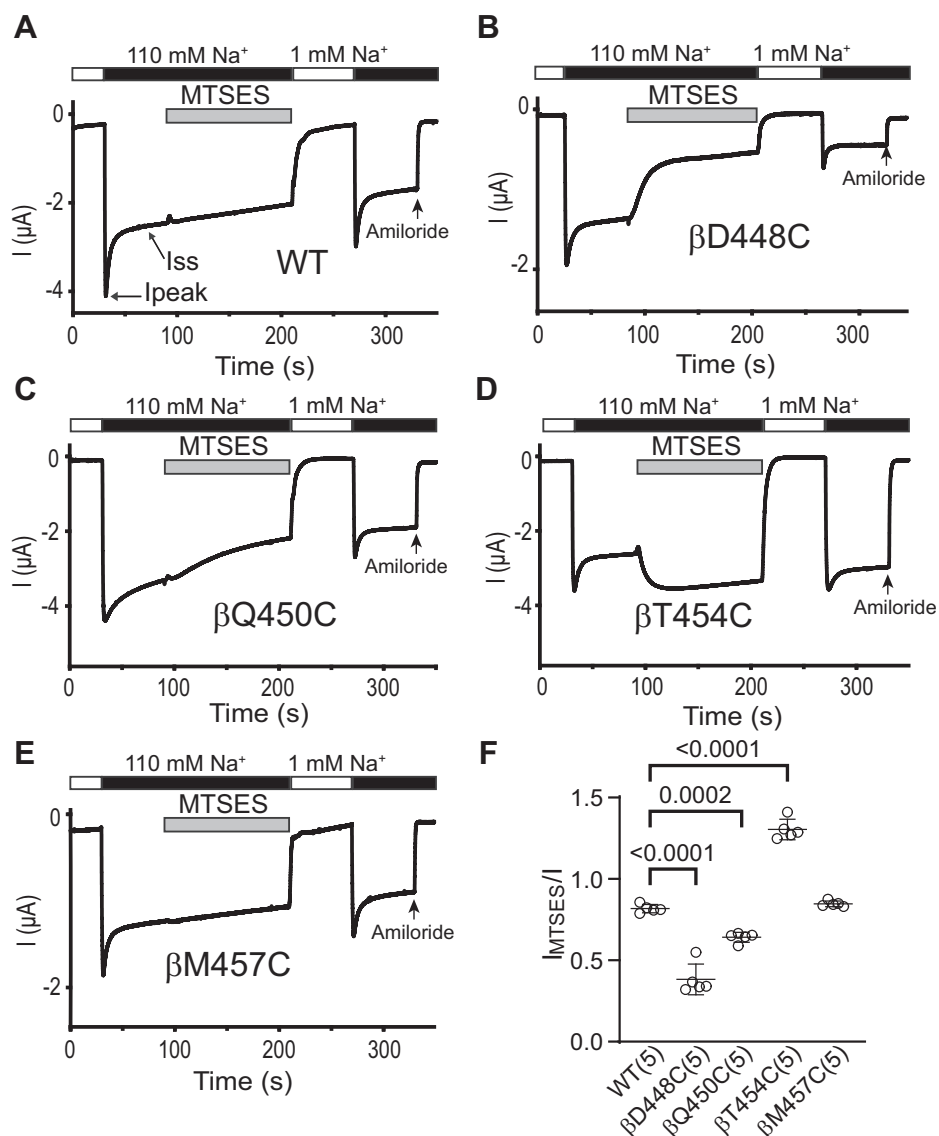


Figure 7. Three proximal β subunit $\beta 10$ residues are functionally accessible to MTSES. Oocytes expressing wildtype or mutant β ENaC subunits together with wildtype α and γ subunits were clamped at a holding potential of -100 mV. Whole-cell Na^+ currents were measured in oocytes perfused with solutions containing either a 1 mM (white bar) or a 110 mM Na^+ (black bar), as noted. A–E, MTSES (2 mM) was added to the bath, as indicated by the gray bar. Traces are representative of five experiments. I_{peak} , peak current after switching from a 1 mM to a 110 mM Na^+ bath solution. I_{ss} , steady-state current at 40 s after I_{peak} . The arrow indicates the addition of amiloride (10 μM) to the bath. F, I_{MTSES}/I , determined as described in the Figure 3 legend. Mean \pm S.D. ($n = 5$). The p values (above brackets) were from one-way ANOVA followed by Dunnett's tests. ENaC, epithelial Na^+ channel; MTSES, sodium (2-sulfonatoethyl) methanethiosulfonate.

increases in currents (Fig. 13C), with estimated $\text{EC}_{50\text{s}}$ (μM , $n = 4$ –5) of 253 ± 28 ($\alpha\text{V508C}\beta\gamma$) and 8 ± 1 ($\alpha\beta\text{D448C}\gamma$) (Fig. 13D). These results suggest that the binding of Cd^{2+} to substituted Cys residues at specific sites in the $\beta 10$ strand of each subunit activates the channel.

Potential pathways for MTS reagents to reach introduced Cys residues

As the $\beta 10$ strand is located within a three-fold axis of symmetry (Fig. 14, A and B) and most of its residues are not exposed to the surface, charged MTS molecules must travel to the introduced sulfhydryl groups through an aqueous tunnel. Inspection of a surface-rendered model of mouse ENaC did not reveal apparent openings to solvents. We used CAVER

Analyst 2.0 (35) and CAVER Web 1.1 (36) to probe potential pathways for MTS reagents to access $\beta 10$ residues. A search with a starting point at αN510 yielded three independent tunnels opening to the surface at various locations (Fig. 14D). The most promising aqueous tunnel (blue) with the largest bottleneck radius (1.4 \AA) and shortest length (8 \AA) opens to the surface at the junction of the α subunit palm, thumb, and β -ball domains (blue tunnel). A similar search starting at αS514 also revealed three tunnels (Fig. 14E). The most prominent tunnel leads from αS514 to the surface at the α (palm domain) and γ (thumb domain) interface (blue tunnel). Aqueous tunnels were also found to provide access to residues homologous to αN510 in the β (βQ450 , Fig. 14G) and γ subunits (γE467 , Fig. 14J), as well as access to residues

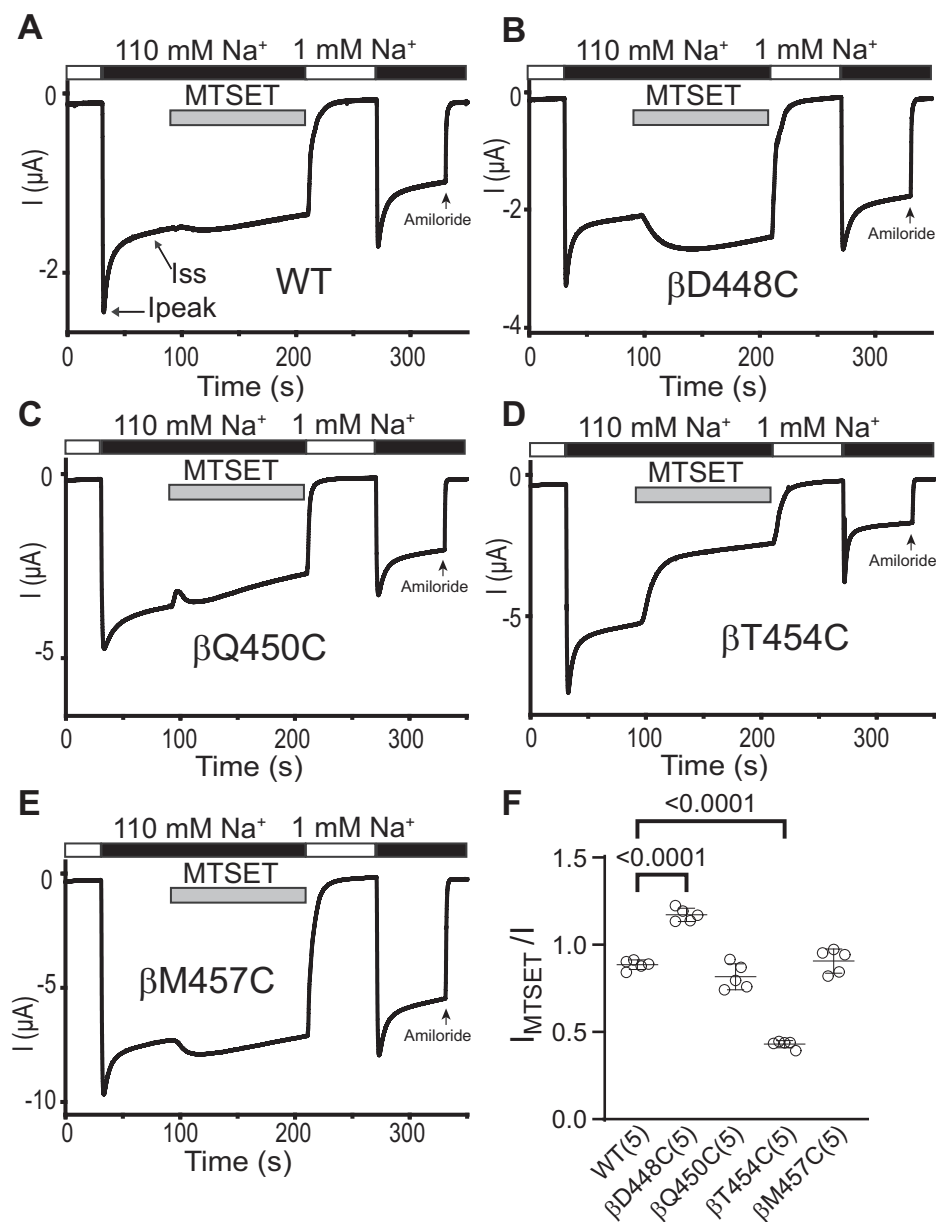


Figure 8. Two proximal β subunit β 10 residues are functionally accessible to MTSET. Oocytes expressing wildtype or mutant β ENaC subunits together with wildtype α and γ subunits were clamped at a holding potential of -100 mV. Whole-cell Na^+ currents were measured in oocytes perfused with solutions containing either a 1 mM (white bar) or a 110 mM Na^+ (black bar), as noted. A–E, 1 mM MTSET was added to the bath, as indicated by the gray bar. Traces are representative of five identical experiments. I_{peak} , peak current after switching from a 1 mM to a 110 mM Na^+ bath solution. I_{ss} , steady-state current at 40 s after I_{peak} . The arrow indicates the addition of amiloride (10 μM) to the bath. F, I_{MTSET}/I , determined as described in the Figure 3 legend. Mean \pm S.D. (n = 5). The p values (above brackets) were from one-way ANOVA followed by Dunnett's tests. ENaC, epithelial Na^+ channel; MTSET, [2-(trimethylammonium) ethyl] methanethiosulfonate bromide.

homologous to αS514 in the β (βT454 , Fig. 14H) and γ subunits (γT471 , Fig. 14K). For αV508 and its homologous residues in the β and γ subunits (βD448 and γF465), their locations were too close to the surface to allow for reliable detection of tunnels. Using the same search parameters, no promising tunnel was identified for αY517 and its homologous residues in the β and γ subunits (βM457 and γL474), consistent with the functional insensitivity of their corresponding Cys mutants to MTS reagents. To determine whether substituted Cys affected the predicted tunnels, we repeated tunnel analyses on mutant ENaC models (generated by PyMol)

containing the substituted Cys at sites selected as the starting point. These tunnels appear to be somewhat similar to tunnels based on the wildtype ENaC model. Representative tunnel models based on channels with specific Cys substitutions at three sites are shown in Figure 14F: (αC514), 14I (βC454), and 14L (γC471).

Discussion

We used scanning Cys mutagenesis to explore the functional accessibility of β 10 residues in the α subunit and whether MTS modifications affected channel gating as

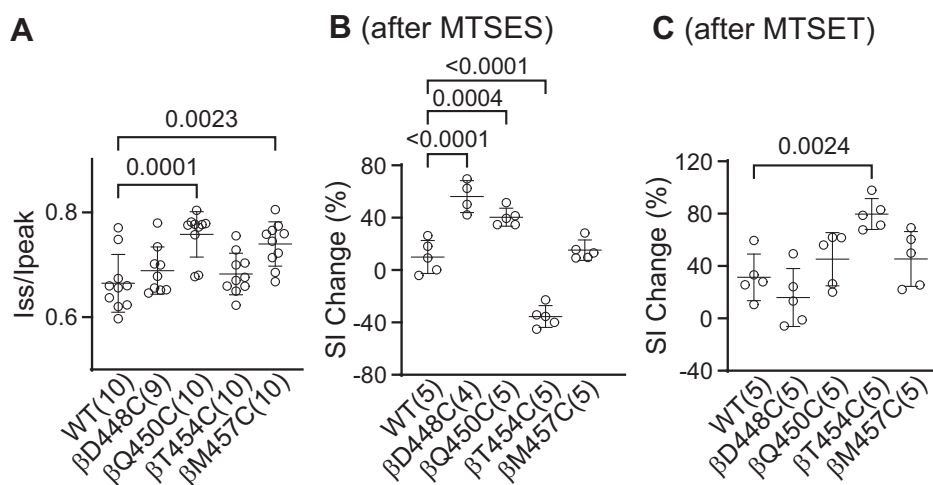


Figure 9. Select β Cys substitutions alter the Na^+ self-inhibition response before and/or after MTS reagent treatment. Na^+ self-inhibition responses in oocytes expressing wildtype $\alpha\beta\gamma$ (WT) and mutant β plus wildtype α and γ ENaC subunits were examined prior to and after MTSES or MTSET treatment, as shown in Figures 7 and 8. **A**, dot plot of I_{ss}/I_{peak} . The I_{ss}/I_{peak} values were obtained from the experiments shown in Figure 7 (prior to MTSES) and 8 (prior to MTSET). Bars are mean \pm S.D. ($n=9-10$). I_{ss} and I_{peak} are defined in Figures 7A and 8A. **B and C**, Na^+ self-inhibition (SI) change (%) after MTSES (from experiments shown in Fig. 7) and MTSET (from experiments shown in Fig. 8). The values were calculated as described in the Figure 4 legend. Bars are mean \pm S.D. ($n=4-5$). All p values (above brackets) were from one-way ANOVA followed by Dunnett's tests. ENaC, epithelial Na^+ channel; MTSES, sodium (2-sulfonatoethyl) methanethiosulfonate; MTSET, [2-(trimethylammonium) ethyl] methanethiosulfonate bromide.

reflected in changes in the Na^+ self-inhibition response. At least four of the first eight Cys substituted residues in the proximal aspect of α subunit $\beta 10$ ($\alpha S507C$, $\alpha T509C$, $\alpha N510C$, $\alpha S514C$) were found to be functionally accessible to an MTS reagent, based on a large and significant change in current (Figs. 2 and 3). In contrast, none of the five Cys substituted residues in the distal aspect of $\beta 10$ ($\alpha A515C$ - $\alpha R519C$) responded to an MTS reagent with a significant change in current (Fig. 3). These observations are consistent with the concept that the proximal aspect of $\beta 10$ within the palm domain contributes to the solvent accessible central vestibule, analogous to ASIC1 (6, 20). In addition, MTS reagents significantly altered the Na^+ self-inhibition response in mutants that showed a strong response to these reagents, suggesting that MTS modifications of these introduced Cys residues within the α subunit $\beta 10$ strand affected ENaC gating. Our study also showed that Cys mutations at multiple sites within $\beta 10$ significantly altered the Na^+ self-inhibition response.

In contrast to the proximal part of the $\beta 10$ strand, all five sites with Cys introduced distal to $\alpha S514$ were not functionally modified by either MTSES or MTSET. Our results clearly show differences in the functional accessibility of MTS reagents between the proximal and distal parts of $\beta 10$ (Fig. 14A). However, we cannot rule out the possibility that sites in the distal aspect of $\beta 10$ were chemically modified by MTS reagents. Our observations are consistent with the notion that distal palm domain provides a structural scaffold, while the proximal palm enables dynamic changes in conformations associated with channel gating (7, 20). The resolved structure of ASIC1 predicts a central aqueous pore/tunnel within the extracellular and transmembrane domains (37, 38). Our accessibility data and the tunnel computations do not support the notion of permeant ions entering the ENaC pore through an opening at the most distal aspects of the palm domain,

unlike the long pore architecture found in pentameric acetylcholine receptors (39). Recent studies suggest that such a central pathway is unlikely to be an ion permeation pathway in P2X receptor channels (40, 41), which share a similar architecture with ASIC1 (42). Permeant cations and small pore blockers (*i.e.*, amiloride) likely gain access to the pore through the fenestrations formed at subunit interfaces near the transmembrane domain (6, 7). MTS reagents probably do not gain access to the introduced Cys residues in $\beta 10$ strand through the same fenestrations, as these are only open to the vestibule within the pore, which is separated from the central vestibule by a net of lower palm domain $\beta 11$ and $\beta 12$ strands in resolved structures of ASIC1 and ENaC (7, 9, 10).

We also examined selected $\beta 10$ residues in the β and γ subunits, focusing on sites homologous to α subunit $\beta 10$ residues where channels with Cys substitutions were responsive to MTS reagents or where the Na^+ self-inhibition response was altered. As expected, channels with Cys substitutions at sites homologous to $\alpha N510C$ ($\beta Q450C$ and $\gamma E467C$) and homologous to $\alpha S514C$ ($\beta T454C$ and $\gamma T471$) were functionally accessible to MTS reagents, whereas channels with distal $\beta 10$ Cys substitutions homologous to $\alpha Y517C$ ($\beta M457C$ and $\gamma L474C$) were unresponsive to these reagents (Figs. 7, 8, 10 and 11). While channels with an $\alpha V508C$ mutation did not respond to MTS reagents (Fig. 3), channels with Cys substitutions at homologous sites in the β and γ subunits ($\beta D448C$ and $\gamma F465C$) were functionally accessible to both MTS reagents (Figs. 7, 8, 10 and 11). Our observations regarding functional MTS accessible α , β , and γ subunit $\beta 10$ residues are illustrated in Figure 14A and Table 2. It is interesting to note that not all accessible residues point their side chains to the central vestibule in the resolved ENaC structure (9, 10). Structural studies of ASIC1 (7, 20, 43) suggest that the proximal part of the $\beta 10$ strand has a dynamic conformation and that side chain orientations are not static. The functional

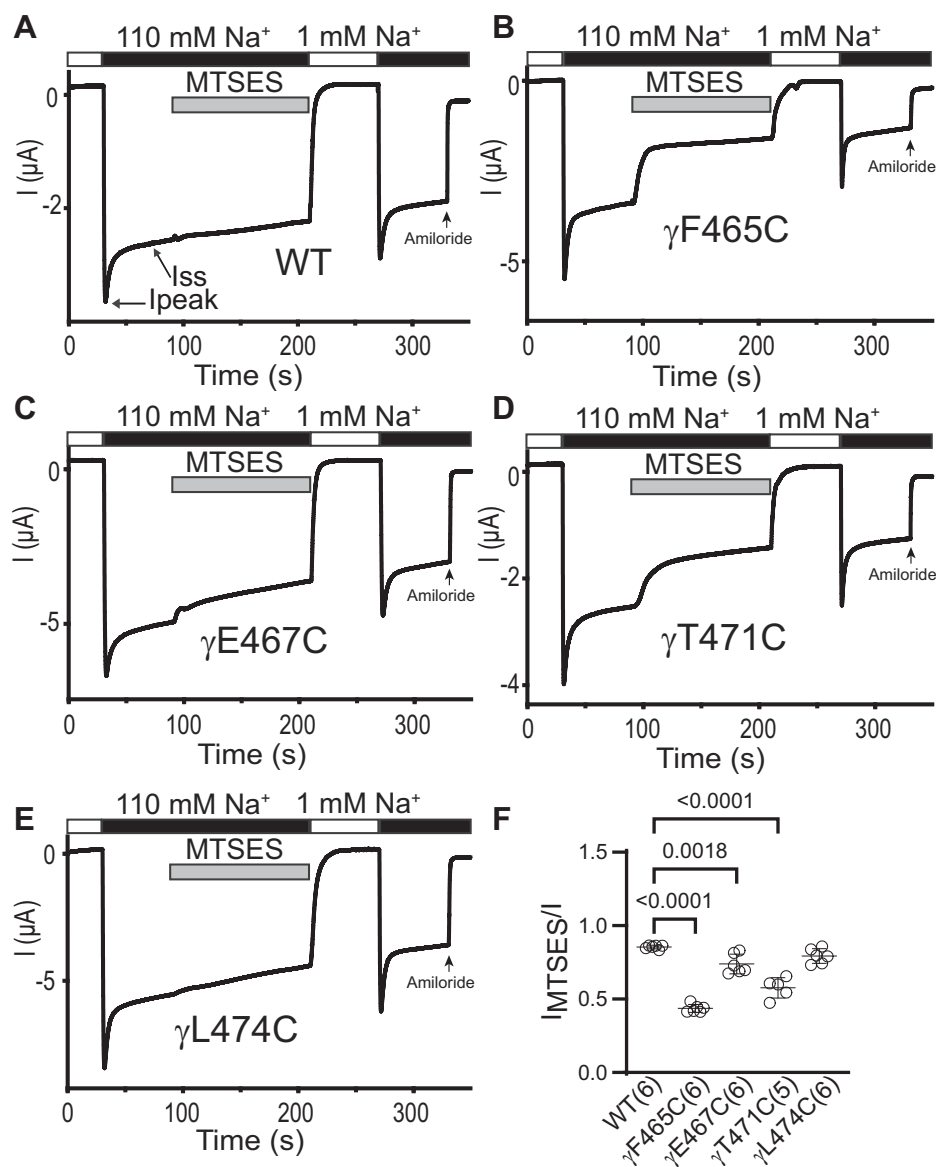


Figure 10. Three proximal γ subunit β 10 residues are functionally accessible to MTSES. Oocytes expressing wildtype or mutant γ ENaC subunits together with wildtype α and β subunits were clamped at a holding potential of -100 mV. Whole-cell Na^+ currents were measured in oocytes perfused with solutions containing either a 1 mM (white bar) or a 110 mM Na^+ (black bar), as noted. A–E, 2 mM MTSES was added to the bath, as indicated by the gray bar. Traces are representative of five or six identical experiments. I_{peak}, peak current after switching from a 1 mM to a 110 mM Na^+ bath solution. I_{ss}, steady-state current at 40 s after I_{peak}. The arrow indicates the addition of amiloride (10 μM) to the bath. F, I_{MTSES}/I , determined as described in the Figure 3 legend. Mean \pm S.D. (n = 5–6). The p values (above brackets) were from one-way ANOVA followed by Dunnett’s tests. ENaC, epithelial Na^+ channel; MTSES, sodium (2-sulfonatoethyl) methanethiosulfonate.

effects of MTS reagents do not follow a pattern where Cys substitutions at every other residue in the β 10 strand are functionally modified by an MTS reagent, suggesting the aqueous accessibility is not limited to the central vestibule. The effects of MTS reagents on several mutants (αY511C and αK512C) were quite modest (Fig. 3) and were not included among the accessible residues in Figure 14A.

The results from experiments on the homologous β 10 residues in the three ENaC subunits are summarized in Table 2 and revealed several patterns regarding MTS-induced effects on mutant channels. First, channels with Cys substitutions that were responsive to MTSES were also responsive to MTSET, with the exception of βQ450C . Second, the effects of MTS

reagents on channel activity (*i.e.*, increase or decrease) were dependent on the charge of the reagent for some mutants (αN510C , βD448C , βT454C , and γT471C). The effects of MTS reagents on other mutants (αS514C , γE467C , and γF465C) were not charge dependent. While both reagents inhibited both γF465C and γE467C mutants, the effect of MTSES was much greater than that of MTSET on the γF465C mutant and effect of MTSET was much larger than that of MTSES on the γE467C mutant (Figs. 10 and 11, Table 2). There are several charged residues in the β 10 strands and nearby strands which may have a role on how mutant channels respond to charged MTS reagents. For example, γE467 in β 10 is close to αR407 (β 9 strand, 2.5 Å), well within the distance for salt bridge (44).

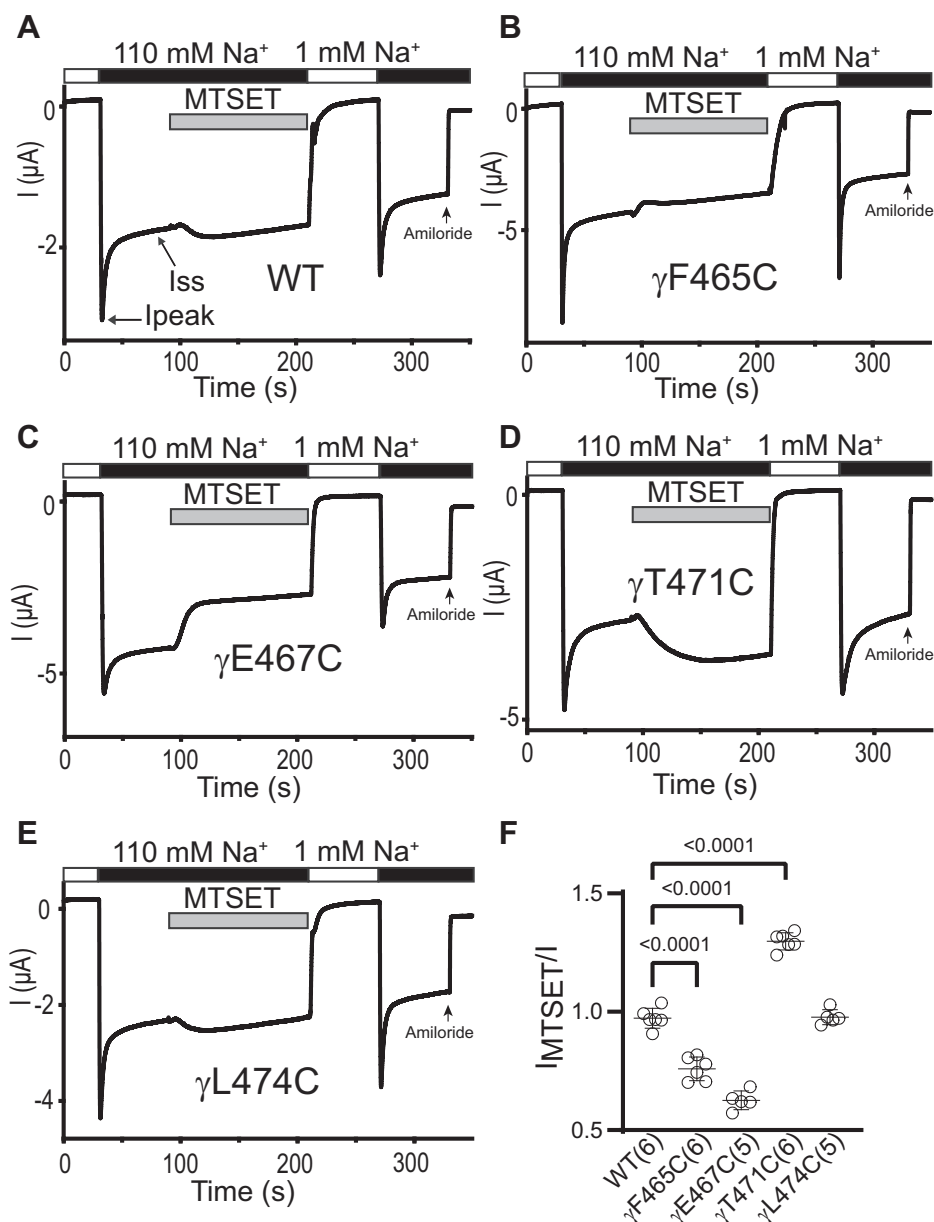


Figure 11. Three proximal γ subunit β 10 residues are functionally accessible to MTSET. Oocytes expressing wildtype or mutant γ ENaC subunits together with wildtype α and β subunits were clamped at a holding potential of -100 mV. Whole-cell Na^+ currents were measured in oocytes perfused with solutions containing either a 1 mM (white bar) or a 110 mM Na^+ (black bar), as noted. A–E, 1 mM MTSET was added to the bath, as indicated by the gray bar. Traces are representative of five or six identical experiments. I_{peak} , peak current after switching from a 1 mM to a 110 mM Na^+ bath solution. I_{ss} , steady-state current at 40 s after I_{peak} . The arrow indicates the addition of amiloride (10 μM) to the bath. F, I_{MTSET}/I , determined as described in the Figure 3 legend. Mean \pm S.D. ($n = 5$ –6). The p values (above brackets) were from one-way ANOVA followed by Dunnett's tests. ENaC, epithelial Na^+ channel; MTSET, [2-(trimethylammonium) ethyl] methanethiosulfonate bromide.

MTSET modification of γE467C would not allow a salt bridge with αR407 , consistent with the strong inhibition of $\alpha\beta\gamma\text{E467C}$ activity in response to MTSET (Fig. 11C). In contrast, MTSET had a small effect on $\alpha\beta\gamma\text{E467C}$ channel activity (Fig. 10C). Third, at homologous sites within the three ENaC subunits, the effects of both MTSES and MTSET were often subunit dependent. Functional ENaC subunit dependence has been well documented in many studies (12, 33, 45–53) and are consistent with the notion that homologous sites in ENaC subunits often have asymmetric functions (46–48). MTS reagents likely changed channel activity by altering ENaC gating,

as suggested by their relatively rapid effect and significant change in the Na^+ self-inhibition response induced by MTS modification. A lack of activation of $\alpha\text{N510C}\beta\text{S518K}\gamma$ by MTSES (Fig. 5) also supports this notion.

The transition metal Cd^{2+} has been used to identify functional sites in ion channels (54). We examined whether ENaCs with Cys substitutions at specific sites in β 10 responded to Cd^{2+} with a change in activity. Channels with Cys mutants at the three sites in the γ subunit that were MTS accessible (γF465C , γE467C , and γT471C) were also activated by external Cd^{2+} (Fig. 13, A and B). The most robust activation by Cd^{2+}

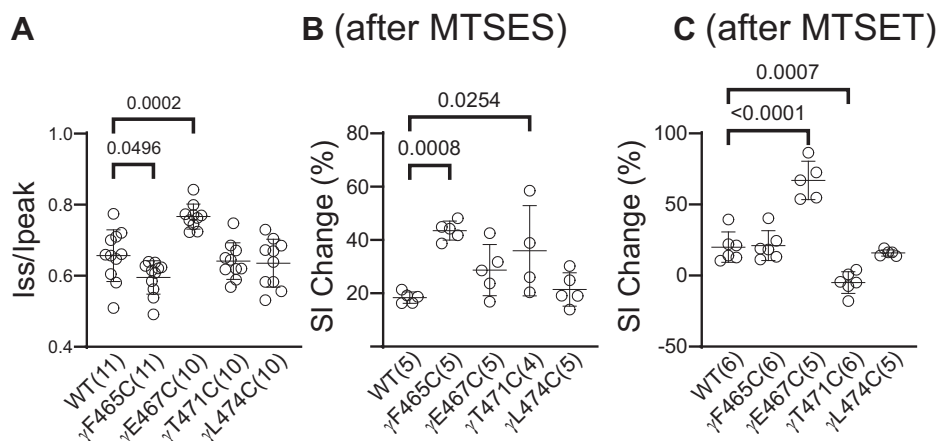


Figure 12. Select γ Cys substitutions alter the Na^+ self-inhibition response before and/or after MTS reagents. Na^+ self-inhibition responses in oocytes expressing wildtype $\alpha\beta\gamma$ (WT) and mutant γ plus wildtype α and β ENaC subunits were examined prior to and after MTSES or MTSET treatment, as shown in Figures 10 and 11. A, dot plot of I_{ss}/I_{peak} . The I_{ss}/I_{peak} values were obtained from experiments shown in Figure 10 (prior to MTSES) and Figure 11 (prior to MTSET). Bars are mean \pm S.D. ($n = 10$ – 11). I_{ss} and I_{peak} are depicted in Figures 10A and 11A. B and C, Na^+ self-inhibition (SI) change (%) after MTSES (from experiments shown in Fig. 10) and MTSET (from experiments shown in Fig. 11), respectively. The values were calculated as described in the Figure 4 legend. Bars are mean \pm S.D. ($n = 4$ – 6). All p values (above brackets) were from one-way ANOVA followed by Dunnett's tests. ENaC, epithelial Na^+ channel; MTSES, sodium (2-sulfonatoethyl) methanethiosulfonate; MTSET, [2-(trimethylammonium) ethyl] methanethiosulfonate bromide.

was seen with the $\alpha\beta\gamma$ F465C mutant. Channels with Cys substitutions at homologous sites in the α and β subunits (α V508C and β D448C) were also activated by Cd^{2+} (Fig. 13, C and D). The EC_{50} of Cd^{2+} activation varied among the mutants that were studied (Fig. 13). The Cd^{2+} EC_{50} is dependent on the numbers and types of side chains that form a Cd^{2+} -binding site (54). ENaC mutants with EC_{50} s of less than $12 \mu\text{M}$ (γ F465C, γ E467C, and β D448C) likely have a Cd^{2+} -binding site that includes the introduced sulfhydryl group as well as nearby residues that coordinate Cd^{2+} binding (*i.e.*, Asp, Glu, and His). Coordinated Cd^{2+} binding is likely not present in ENaC mutants with higher EC_{50} s (γ T471C [$124 \mu\text{M}$] and α V508C [$253 \mu\text{M}$]) (54). These observations support the notion that these modified β 10 residues have functionally important roles in ENaC gating. While most Cys mutants examined resulted in Cd^{2+} -dependent activation, we saw either no effect or variable effects on channel activity in response to MTSES or MTSET (see Table 2). While the reason for these distinct effects Cd^{2+} and MTS reagents on ENaC activity is not clear, we speculate that the addition of different charged moieties with different sizes (Cd^{2+} versus MTSES and MTSET) likely perturbs local structures in distinct ways to alter channel activity. For example, the resolved ENaC structure shows a ring of polar residues, including α N510, β Q450, and γ E467, which project their side chains to the central vestibule and contact multiple polar side chains from palm domains of the same or neighboring subunit (*i.e.*, γ E467 may form a salt bridge with R407 within β 9 strand of the α subunit). It is not surprising that modifying an introducing Cys residue with a bulky side chain at one of these sites will either enhance or disrupt interactions that affect channel structure and activity. In addition, Cd^{2+} coordination by an introduced sulfhydryl group and other native groups may strengthen polar interactions favoring an open state. Cd^{2+} binding might induce a collapsed central vestibule, favoring an open channel state (described in the later part of the article).

To further explore the aqueous accessibility of the proximal aspect of the β 10 strands in the three ENaC subunits, we used CAVER Analyst 2.0 ((35)) and CAVER Web v1.1 (36) to identify extracellular aqueous tunnels in our mouse ENaC model. Potential tunnels were detected using empiric search parameters when α N510, α S514, or their homologous sites in the β or γ subunits were chosen as starting points (Fig. 14). The narrowest (bottleneck) radii of these tunnels were 1.4 to 1.9 \AA , smaller than the 2.5 \AA radius of MTSES or MTSET (32). Given the dynamic nature of protein structures, we predict that these tunnels allow the MTS reagents and Cd^{2+} to reach their targets. Only one tunnel was detected using β Q450 as starting point. The tunnel was similar to the most promising tunnel for α N510. Interestingly, the most promising tunnels (in blue) for α S514, β T454, and γ T471 were also similar. No tunnels were detected for α Y517, β M457, and γ L474 using the same search parameters, consistent with the observations that their corresponding Cys mutants did not respond to MTS reagents. For all sites studied, no tunnels transiting along the three-fold symmetry axis from the top of the extracellular domain were identified.

Several β 10 mutations significantly altered the channel's Na^+ self-inhibition response. Among the 13 α mutants studied, α Y517C and α V508C exhibited reduced Na^+ self-inhibition and greater amiloride-sensitive currents, compared to wild-type (Fig. 6). These observations are consistent with an increased channel open probability, as predicted from the close correlation between the magnitude of Na^+ self-inhibition and channel open probability (23). Interestingly, the gain-of-function human ENaC variant α V481M, homologous to mouse α V508, had a reduced Na^+ self-inhibition response (55). Two β ENaC mutations (β Q450C and β M457C) and one γ ENaC mutation (γ E467C) exhibited a significantly reduced Na^+ self-inhibition response (Figs. 9A and 12A), while three mutants (α T509C, α N510C, and γ F465C) had an enhanced Na^+ self-inhibition response (Figs. 6 and 12A). Our results

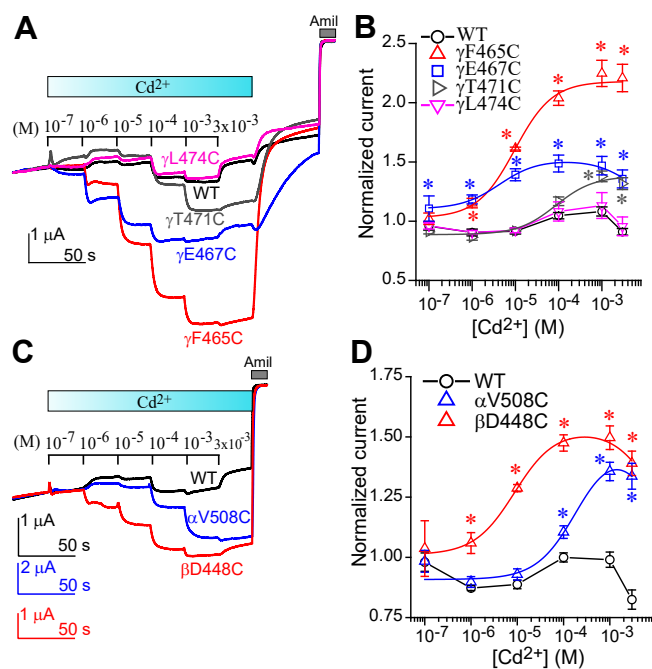


Figure 13. Cd²⁺ activates ENaCs with Cys substitutions in proximal β 10 residues. Effects of Cd²⁺ on whole-cell amiloride-sensitive currents in oocytes expressing wildtype and mutant ENaCs. Oocytes were perfused with a bath solution (NaCl-110) containing increasing concentrations of CdCl₂, at a holding potential of -100 mV. *A*, representative recordings showing the effects of Cd²⁺ on wildtype $\alpha\beta\gamma$, $\alpha\beta\gamma$ F465C, $\alpha\beta\gamma$ E467C, $\alpha\beta\gamma$ T471C, and $\alpha\beta\gamma$ L474C. Traces were superimposed to align the basal currents prior to Cd²⁺ treatment and the currents in the presence of 10 μ M amiloride with approximately the same current and time scales. Cd²⁺ application is indicated by gradient cyan bars, and Cd²⁺ concentrations are shown above traces. *B*, dose responses of Cd²⁺ on amiloride-sensitive currents in oocytes expressing wildtype and the γ mutants. Normalized currents were the ratios of currents measured at the end of 30-s applications of Cd²⁺ and the basal currents measured immediately prior to 10⁻⁷ M Cd²⁺ application. Data are shown as mean \pm S.D. (n = 5). Asterisks indicate that the values of mutant channels were significantly greater than that of wildtype channels ($p < 0.01$, one-way ANOVA followed by Dunnett's tests). Values for $\alpha\beta\gamma$ L474C did not differ from wildtype at all Cd²⁺ concentrations ($p > 0.05$). Smooth lines were from the best fit with the equation described in the [Experimental procedures](#). The dose responses of Cd²⁺ on wildtype and $\alpha\beta\gamma$ L474C channels were not fit successfully, and the data points are simply connected with straight lines. *C*, representative recordings showing the effects of Cd²⁺ on wildtype $\alpha\beta\gamma$, α V508C $\beta\gamma$, and β D448C γ . Traces were superimposed in a similar way to (*A*), but with distinct scales. *D*, dose responses of Cd²⁺ on amiloride-sensitive currents in oocytes expressing wildtype and the mutant channels. Asterisks indicate that the values of mutant channels were significantly greater than that of wildtype channels ($p < 0.0001$, one-way ANOVA followed by Dunnett's tests). Smooth lines were from the best fit with the aforementioned equation. The dose responses of Cd²⁺ on wildtype channels were not fit successfully, and the data points are connected with black straight lines. EC₅₀s and IC₅₀s (\pm S.D.) are listed in [Table 1](#). ENaC, epithelial Na⁺ channel.

suggest that these eight sites with β 10 residues have a role in the mechanism of Na⁺ self-inhibition, likely influencing allosteric transitions that occur following Na⁺ binding. These β 10

Table 1
Fitting parameters for the dose responses of Cd²⁺ on mutant ENaCs

Channel	Imax	Imin	EC ₅₀ (μ M)	EC ₅₀ (95% CI)	IC ₅₀ (mM)	R ²	n
α V508C	1.5 \pm 0.02	0.9 \pm 0.03	253 \pm 28	219–287	8.7 \pm 2.7	0.93 \pm 0.07	5
β D448C	1.5 \pm 0.04	1.0 \pm 0.02	8 \pm 1	7–9	9.4 \pm 3.0	0.98 \pm 0.03	4
γ F465C	2.2 \pm 0.11	1.0 \pm 0.04	11 \pm 2	8–13	N.D.	0.99 \pm 0.01	5
γ E467C	1.5 \pm 0.06	1.0 \pm 0.03	3 \pm 1	1–5	7.4 \pm 3.1	0.98 \pm 0.01	4
γ T471C	1.5 \pm 0.04	0.9 \pm 0.02	124 \pm 21	98–151	7.6 \pm 2.1	0.98 \pm 0.01	5

Note: Values are mean \pm S.D.

95% CI, confidence interval at 95% for EC₅₀ (μ M); R², square of correlation coefficient; N.D., not determined.

residues are not in the vicinity of the previously defined α subunit Na⁺-binding site (10, 17).

ENaC structures (9, 10) and our structural model suggest that hydrophobic contacts from α Y517, β M457, and γ L474 within the distal part of β 10 strands seal the central axis at a site distal to the solvent-accessible central vestibule ([Fig. 14B](#)). This hydrophobic seal likely supports the scaffold formed by the distal parts of β 10 strands. Our models predict that the α Y517C mutation creates a separation between the α Y517C, β M457, and γ L474 ([Fig. 14C](#)). The β M457C mutation also creates a separation between β M457C and γ L474, though it retains close contact with α Y517. In contrast, γ L474C appears to be less disruptive. The observations are consistent with the suppressed Na⁺ self-inhibition response observed with α Y517C and β M457C, while γ L474C did not affect Na⁺ self-inhibition ([Figs. 6, 9A and 12A](#)). Given the proximity of this hydrophobic seal to a hydrophobic patch in the knuckle domain implicated in Na⁺ self-inhibition response (47), we speculate that the hydrophobic seal and the knuckle domain hydrophobic patch function as an integral nonpolar anchor within the extracellular domain. Stability of this anchor may facilitate conformational changes of other flexible parts in response to extracellular Na⁺ or other channel modulators. Consistent with this notion, mutations within the β 10 hydrophobic seal, the hydrophobic knuckle patch, or deletion of the knuckle domain in the α subunit reduce or eliminate Na⁺ self-inhibition ([Figs. 6 and 9A and \(47\)](#)).

Our results regarding the effects of β 10 Cys substitutions on Na⁺ self-inhibition and the response to MTS reagents and Cd²⁺ suggest that the β 10 strands in ENaC subunits, which reside at the three-fold symmetry axis, have functional roles in ENaC gating. The β 10 strands interface with thumb and knuckle domains, which also have roles in modulating ENaC gating (47, 48). Moreover, β 10 within the α subunit is flanked by residues (α C506 and α W520, [Fig. 1C](#)) where introduced mutations alter ENaC gating. Mouse α C506 is homologous to human α C479, where a Cys-to-Arg mutation was found in a pair of siblings with a Liddle syndrome phenotype (56). We previously showed that α C506 and α C421 form a disulfide bond, and disruption of this bond affects Na⁺ self-inhibition (49). α W520 is homologous to human α W493, a site where a gain-of-function variant (α W493R) was identified (57, 58). Our results suggest that nonsynonymous variants of human ENaC at specific β 10 sites are likely to alter ENaC activity. In addition, the β 10 strand may convey conformational changes from peripheral ENaC helical domains to structures that directly control ENaC gating. The central locations of the β 10 strands allow for extensive intrasubunit and intersubunit

ENaC palm domain

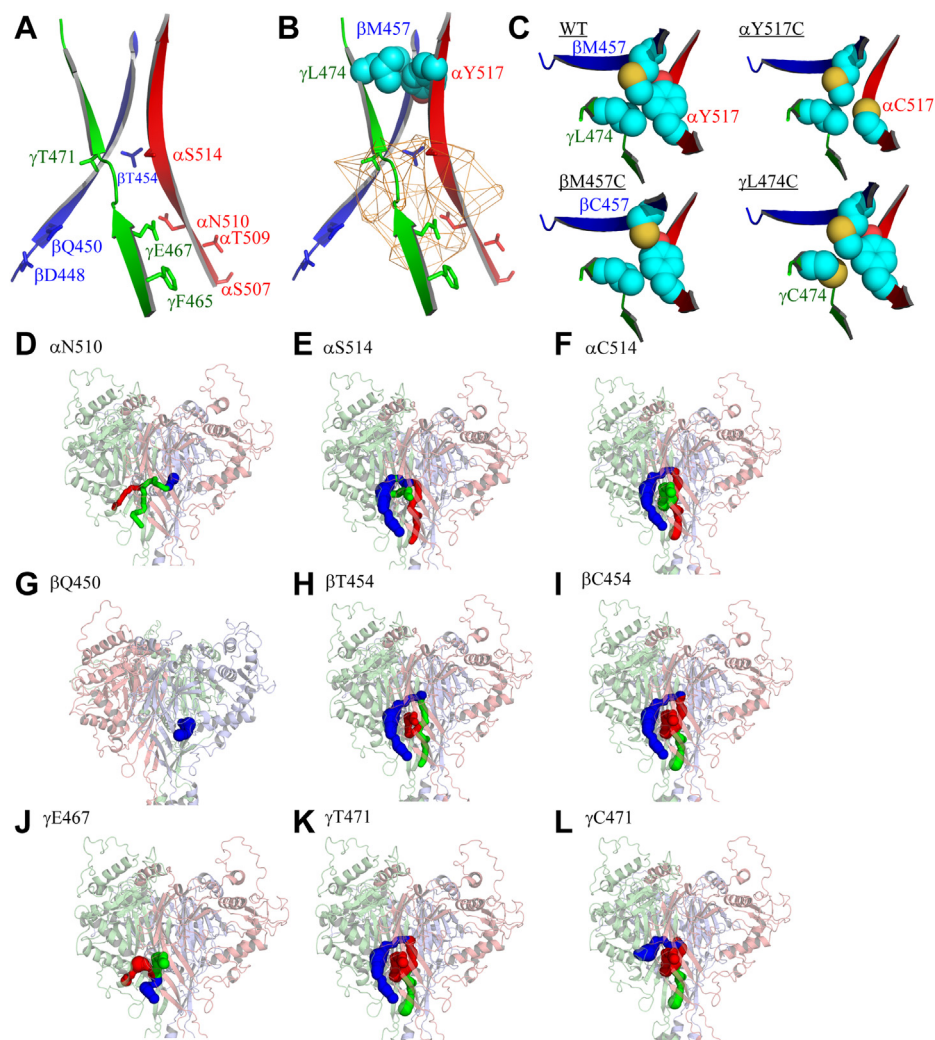


Figure 14. Access tunnels in mouse ENaC. *A*, a model of three mouse ENaC β 10 strands (α subunit [red], β subunit [blue], and γ subunit [green]). Side chains of β 10 residues that were accessible to MTSES or MTSET are shown as sticks. All 13 Cys mutants were examined for MTS accessibility, whereas only four β Cys mutants (β D448C, β Q450C, β T454C, and β M457C) and γ Cys mutants (γ F465C, γ E467C, γ T471C, and γ L474C) were examined. *B*, a similar model to (*A*), with illustrated central vestibule and top seal. The central vestibule, shown as orange mesh, was calculated by CAVER Analyst 2.0 (35). Accessible residues are not labeled for clarity. Side chains of the three inaccessible residues (α Y517, β M457, and γ L474) that form a hydrophobic seal are shown as spheres with carbon in cyan, oxygen in red, and sulfur in yellow. *C*, top views of three β 10 strands showing residues forming a hydrophobic seal at the central axis. Wildtype and mutant channels are labeled as WT, α Y517C, β M457C, β C457C, and γ L474C. For mutants, only the mutated residue is labeled for clarity. Four panels were drawn with same rotation and scale to highlight the contact differences. The Cys substitutions were made in PyMol 2.4 using default rotamer. *D-L*, mouse ENaC models showing the top score tunnels identified by CAVER Web 1.1, with α N510 (*D*), α S514 (*E*), α C514 (*F*), β Q450 (*G*), β T454 (*H*), β C454 (*I*), γ E467 (*J*), γ T471 (*K*), or γ C471 (*L*) as starting points. Mouse α , β , and γ subunits are shown in light red, light blue, and light green, respectively. The most prominent tunnel is shown in blue, while the second and third optimal tunnels are shown in green and red, respectively. The three tunnels for α N510 are overlapping. To optimally reveal the most promising blue tunnel in (*D*), the green and red tunnels are shown as thinner tunnels. There was only one tunnel identified with β Q450 as a starting point (*G*). For *F*, *I*, and *L*, a model with a single Cys substitution was used as the structural input. For others, a wildtype ENaC model was used. Tunnel search parameters are described in [Experimental procedures](#). All models were visualized using PyMol 2.4 (75). ENaC, epithelial Na^+ channel; MTSES, sodium (2-sulfonatoethyl) methanethiosulfonate; MTSET, [2-(trimethylammonium) ethyl] methanethiosulfonate bromide.

contacts that likely have roles in modulating ENaC gating. Intersubunit interactions between palm and thumb domains have been demonstrated to contribute to ENaC gating and regulation by extracellular Cl^- and Cu^{2+} (52, 53, 59). Previous work examining the functional effects of varying length bifunctional cross-linkers also highlights the importance of intersubunit interactions (53).

The proximal aspect of the ASIC palm domains has been implicated in channel activation and desensitization (7, 19, 20, 43, 60–63). ENaCs do not undergo desensitization, and it is unclear whether ENaCs Na^+ self-inhibition response resembles ASIC desensitization. Functionally

relevant acidic residues in the proximal palm domains of ASICs are not present in ENaC subunits, consistent with distinct mechanisms regulating channel gating. Within ASIC1a, unique acidic residues E80 (β 1), E417 (β 12), E412 (β 11- β 12 linker), and E374 (β 10) contribute to protonation and Ba^{2+} -binding sites (6, 64). The proposed Ba^{2+} -binding sites in the central vestibule of ASIC1a, involving Q277, E374, E412, and E417 (64), are not present in ENaC.

Various roles of the central vestibule in ASIC1 have been proposed, including serving as a cation reservoir, as well as roles in channel desensitization and modulator binding (7, 20, 43, 64, 65). We speculate that the major function of the

Table 2Summary of changes in the Na⁺ self-inhibition response and response to MTS reagent treatment of ENaCs with Cys substitutions

Channel	S-I	MTSES	MTSET	MTSES versus MTSET	Accessible
αY517C	↓	-	-	-	No
βM457C	↓	-	-	-	No
γL474C	-	-	-	-	No
αS514C	-	↓↓	↓↓	Similar	Yes
βT454C	-	↑↑	↓↓	Opposite	Yes
γT471C	-	↓↓	↑	Opposite	Yes
αN510C	↑	↑↑	↓	Opposite	Yes
βQ450C	↓	↓	-	-	Yes
γE467C	↓	↓	↓↓	Similar	Yes
αV508C	↓	-	-	-	No
βD448C	-	↓↓	↑	Opposite	Yes
γF465C	↑	↓↓	↓	Similar	Yes

Channels with substitutions at homologous sites within ENaC subunits are clustered.

Note: S-I, Na⁺ self-inhibition: upward arrow, increased (or enhanced) Na⁺ self-inhibition; downward arrow, decreased (or blunted) Na⁺ self-inhibition; -, no significant change. MTSES and MTSET: upward arrow, increased current in response to the MTS reagent; downward arrow, decreased current in response to the MTS reagent; -, no significant change. Double arrows indicate greater changes than single arrows. MTSES versus MTSET: Similar, similar effect; Opposite, opposite effect; -, no comparison. Accessibility: No, no effect from both MTSES and MTSET; Yes, increase and/or decrease current in response to either MTSES or MTSET.

ENaC, epithelial Na⁺ channel; MTSES, sodium (2-sulfonatoethyl) methanethiosulfonate; MTSET, [2-(trimethylammonium) ethyl] methanethiosulfonate bromide.

central vestibule of ENaC is to facilitate conformational changes associated with channel opening and closing. Consistent with this notion, certain ions or small molecules may modulate ENaC gating by binding to residues within the central vestibule and altering channel gating. Extracellular ions such as Na⁺, H⁺, Cl⁻, and certain divalent cations and small molecules are important ENaC-gating modulators (1, 2, 11–14, 34, 50, 52, 53, 59, 66–71). The mechanisms by which these ions or small molecules alter channel gating are not fully understood. Binding within the central vestibule provides a plausible pathway for certain modulators to influence ENaC gating, similar to what has been suggested for ASICs (64). Small molecules may gain access to the central vestibule through the routes identified in our study. Although binding sites for Na⁺, H⁺, and Cl⁻ have been reported outside of the central vestibule (10, 17, 52, 72), a βENaC Val (V348) was identified as a central vestibule residue that facilitates ENaC activation by small molecules (S3969 and 8-(4-chlorophenylthio)adenosine 3',5'-cyclic monophosphate) (69, 73). In addition, mouse αN510 is homologous to guinea pig αI481, a site implicated in ENaC activation by 8-(4-chlorophenylthio)adenosine 3',5'-cyclic monophosphate (68).

Previous studies suggest that ASIC1 palm domain β sheets lining the central vestibule undergo conformational changes in association with channel gating (7, 20). During proton activation, ASIC1 undergoes a slight contraction of the central vestibule (7, 64). We speculate that the ENaC central vestibule exhibits similar conformational changes in association with gating. A potential coordination of Cd²⁺ by multiple ligands from introduced sulfhydryl groups (*i.e.*, γE467C, γF465C, or βD448C) and native groups is consistent with a reduction of the central vestibule space in association with channel activation. Clearly additional studies are needed to ascertain changes in the structure of ENaC's central vestibule during gating transitions.

In summary, our study identified solvent-accessible residues within the proximal parts of the palm domain β10 strands of the three ENaC subunits. Furthermore, several β10 residues were found to have roles in modulating ENaC gating.

Experimental procedures

Site-directed mutagenesis

Point mutations in mouse ENaC α, β, and γ subunits were introduced using QuickChange II XL site-directed mutagenesis kit (Agilent). Mutations were confirmed by DNA sequencing conducted in the Genomics Research Core of University of Pittsburgh. Linearized DNAs following restriction enzyme digestion were purified by GeneJET PCR Purification Kit (Thermo Fisher Scientific). Wildtype and mutant mouse ENaC cRNAs were generated *via* T3 RNA polymerase (mMESSAGE mMACHINE T3 Kit, Invitrogen) and purified by RNeasy MinElute Cleanup Kit (QIAGEN). Concentrations of plasmid DNAs and cRNAs were quantified by spectrophotometry.

ENaC expression

Oocytes from female *Xenopus laevis* were harvested according to a protocol approved by the University of Pittsburgh's Institutional Animal Care and Use Committee and treated with type II collagenase (Sigma-Aldrich). cRNA (0.5 or 1 ng) of each mouse ENaC subunit (wildtype or mutant α, wildtype or mutant β, and wildtype or mutant γ) was injected into stage V or stage VI oocytes, and oocytes were incubated at 18 °C in a modified Barth's solution: 88 mM NaCl, 1 mM KCl, 2.4 mM NaHCO₃, 15 mM Hepes, 0.3 mM Ca (NO₃)₂, 0.41 mM CaCl₂, 0.82 mM MgSO₄, 10 μg/ml streptomycin sulfate, 100 μg/ml gentamycin sulfate, and 10 μg/ml sodium penicillin, pH 7.4.

Two-electrode voltage clamp

Two-electrode voltage clamp studies were performed at room temperature (20–24 °C) 1 to 2 days after injection using Axoclamp 900A Computer-Controlled Microelectrode Amplifier and DigiData 1440A controlled by pClamp 10.4 (Molecular Devices). Oocytes were placed in a chamber with constant flow (~5 ml/min). Glass pipettes filled with 3 M KCl were inserted into oocytes, and the intracellular potential was clamped at -100 mV.

ENaC palm domain

Na⁺ self-inhibition

The Na⁺ self-inhibition response was assessed as previously reported (12). Oocytes expressing wildtype or mutant channels were perfused with a 1 mM Na⁺ bath solution (NaCl-1: 1 mM NaCl, 109 mM N-methyl-D-glucamine, 2 mM KCl, 2 mM CaCl₂, and 10 mM Hepes, pH 7.4) for 60 s and switched abruptly to a 110 mM Na⁺ bath solution (NaCl-110: 110 mM NaCl, 2 mM KCl, 2 mM CaCl₂, and 10 mM Hepes, pH 7.4). Currents were recorded by a two-electrode voltage clamp. After 60 s of NaCl-110 perfusion, 10 μM amiloride was applied to determine the amiloride-sensitive current. Upon the change from NaCl-1 to NaCl-110, currents rapidly increased to a peak (I_{peak}) and slowly declined to a steady-state level (I_{ss}, measured 40 s after I_{peak}).

Effects of MTSET and MTSES

MTSES (Toronto Research Chemicals) powder was freshly dissolved in NaCl-110 at a concentration of 2 mM and used for experiments within 2 h. MTSET (Toronto Research Chemicals) solution was prepared in NaCl-110 at a concentration of 1 mM and used immediately. MTSES and MTSET solutions were perfused for 2 min, when currents were stable. Amiloride-sensitive Na⁺ currents prior to and after MTSES or MTSET application were measured as I and I_{MTSES} or I_{MTSET}, respectively.

Effects of Cd²⁺

The effects of Cd²⁺ on selected mutant and wildtype channels were examined by monitoring the current changes following 30 s applications of increasing concentrations of CdCl₂, in the range of 10⁻⁷ to 3 × 10⁻³ M. A CdCl₂ stock (1 M) was prepared by dissolving CdCl₂ powder in deionized water and diluted to various concentrations of CdCl₂ in the NaCl-110 bath solution prior to use. Oocytes were perfused with NaCl-110 containing 10 μM amiloride after 3 mM CdCl₂ or after washout with NaCl-110 for 1 min in order to measure the amiloride-insensitive component of the whole-cell current. The Cd²⁺ dose response was analyzed using a two-site equation $I = (I_{max} - I_{min}) \frac{C}{C + EC_{50}} \left(\frac{IC_{50}}{C + IC_{50}} \right) + I_{min}$, as previously described (34). The I, I_{max}, and I_{min} are the observed, maximal, and minimal values of the normalized currents, respectively, while C, EC₅₀, and IC₅₀ are the [Cd²⁺] used in our studies, the [Cd²⁺] that achieved 50% channel activation, and the [Cd²⁺] that achieved 50% channel inhibition, respectively. Chelators were not added to the NaCl-110 solution. Concentrations of CdCl₂ added to the bath solution were used to represent [Cd²⁺], which was not the free Cd²⁺ concentrations that would be calculated using a chelator. Nonlinear regression fitting was performed with Origin Pro 2018 (OriginLab Corporation).

Molecular modeling

A structural model of mouse ENaCs was generated with SWISS-MODEL (22). Templates were automatically searched from input

amino acid sequences Q61180 (SCNNA_MOUSE), Q9WU38 (SCNNB_MOUSE), and Q9WU39 (SCNNG_MOUSE). Eight templates with the highest quality, originated in PDB 6BQN (9) but with varying lengths, were automatically selected for modeling. A template originated in the structure of human ENaC (PDB 6WTH (10)) was deemed less suitable for modelling than the selected eight templates. Models were built based on target-template alignment using ProMod3 (22) and ranked according to sequence identity and other parameters. The final model was chosen based on its highest sequence identity (84.4) and quaternary structure quality estimate (0.85 (74)). Models were illustrated using PyMol 2.4 (75). Solvent access pathways were analyzed by CAVER Analyst 2.0 (35) and CAVER Web 1.1 (36). Search configuration parameters were empirically optimized after a series of trials with varying parameter inputs using CAVER Analyst 2.0. The numbers of tunnels were minimized by using the most stringent search parameters which still allowed identification of at least one tunnel with a meaningful length (>5 Å). Final lists of tunnels for each mutant mouse ENaC were obtained from CAVER Web 1.1 using following search parameters: probe radius, 1.4; shell radius, 5; shell depth, 4; and clustering threshold, 5. Tunnel analyses were performed using wildtype and mutant ENaC models as structural inputs. The mutant models containing single Cys substitution were generated by PyMol 2.4.

Statistical analyses

Data are presented as mean ± S.D. Given the inherent batch-to-batch variation in expression levels in *Xenopus* oocytes, all comparisons between mutant and wildtype channels were done in the same batches of oocytes. Significance between two groups was determined by Student's *t* test with Welch's correction and for multiple groups by one-way ANOVA followed by Dunnett's correction. *p* < 0.05 was considered statistically significant. All significance comparisons and normality tests (Shapiro–Wilk test) were performed using GraphPad Prism 9.

Data availability

All data are contained within the manuscript.

Author contributions—L. Z., X. W., J. C., and S. S. data curation; L. Z. and S. S. formal analysis; L. Z., X. W., J. C., T. K., and S. S. investigation; L. Z. writing-original draft; L. Z., T. K., and S. S. writing-review and editing; T. K. and S. S. conceptualization; T. K. resources; T. K. and S. S. supervision; T. K. funding acquisition; T. K. and S. S. project administration.

Funding and additional information—This work was supported by National Institutes of Health Grants R01 HL147818 and P30 DK079307 and the Xiangya Scholar Fund (to L. Z. and X. W.) from The Third Xiangya Hospital, Central South University, China.

Conflict of interests—The authors declare that they have no conflicts of interest with the contents of this article.

Abbreviations—The abbreviations used are: ACIC, acid-sensing ion channel; ENaC, epithelial Na⁺ channel; MTS, methanethiosulfonate;

MTSES, sodium (2-sulfonatoethyl) methanethiosulfonate; MTSET, [2-(trimethylammonium) ethyl] methanethiosulfonate bromide..

References

- Kleyman, T. R., Kashlan, O. B., and Hughey, R. P. (2018) Epithelial Na⁺ channel regulation by extracellular and intracellular factors. *Annu. Rev. Physiol.* **80**, 263–281
- Kleyman, T. R., and Eaton, D. C. (2020) Regulating ENaC's gate. *Am. J. Physiol. Cell Physiol.* **318**, C150–c162
- Kashlan, O. B., and Kleyman, T. R. (2011) ENaC structure and function in the wake of a resolved structure of a family member. *Am. J. Physiol. Ren. Physiol.* **301**, F684–696
- Pitzer, A. L., Van Beurden, J. P., Kleyman, T. R., and Kirabo, A. (2020) ENaC in salt-sensitive hypertension: Kidney and beyond. *Curr. Hypertens. Rep.* **22**, 69
- Mutchler, S. M., Kirabo, A., and Kleyman, T. R. (2021) Epithelial sodium channel and salt-sensitive hypertension. *Hypertension* **77**, 759–767
- Jasti, J., Furukawa, H., Gonzales, E. B., and Gouaux, E. (2007) Structure of acid-sensing ion channel 1 at 1.9 Å resolution and low pH. *Nature* **449**, 316–323
- Yoder, N., Yoshioka, C., and Gouaux, E. (2018) Gating mechanisms of acid-sensing ion channels. *Nature* **555**, 397–401
- Yoder, N., and Gouaux, E. (2020) The His-Gly motif of acid-sensing ion channels resides in a reentrant 'loop' implicated in gating and ion selectivity. *Elife* **9**, e56527
- Noreng, S., Bharadwaj, A., Posert, R., Yoshioka, C., and Bacongus, I. (2018) Structure of the human epithelial sodium channel by cryo-electron microscopy. *Elife* **7**, e39340
- Noreng, S., Posert, R., Bharadwaj, A., Houser, A., and Bacongus, I. (2020) Molecular principles of assembly, activation, and inhibition in epithelial sodium channel. *Elife* **9**, e59038
- Chraïbi, A., and Horisberger, J. D. (2002) Na self inhibition of human epithelial Na channel: Temperature dependence and effect of extracellular proteases. *J. Gen. Physiol.* **120**, 133–145
- Sheng, S., Bruns, J. B., and Kleyman, T. R. (2004) Extracellular histidine residues crucial for Na⁺ self-inhibition of epithelial Na⁺ channels. *J. Biol. Chem.* **279**, 9743–9749
- Collier, D. M., and Snyder, P. M. (2009) Extracellular protons regulate human ENaC by modulating Na⁺ self-inhibition. *J. Biol. Chem.* **284**, 792–798
- Collier, D. M., and Snyder, P. M. (2009) Extracellular chloride regulates the epithelial sodium channel. *J. Biol. Chem.* **284**, 29320–29325
- Hughey, R. P., Bruns, J. B., Kinlough, C. L., Harkleroad, K. L., Tong, Q., Carattino, M. D., Johnson, J. P., Stockand, J. D., and Kleyman, T. R. (2004) Epithelial sodium channels are activated by furin-dependent proteolysis. *J. Biol. Chem.* **279**, 18111–18114
- Carattino, M. D., Sheng, S., and Kleyman, T. R. (2004) Epithelial Na⁺ channels are activated by laminar shear stress. *J. Biol. Chem.* **279**, 4120–4126
- Kashlan, O. B., Blobner, B. M., Zuzek, Z., Tolino, M., and Kleyman, T. R. (2015) Na⁺ inhibits the epithelial Na⁺ channel by binding to a site in an extracellular acidic cleft. *J. Biol. Chem.* **290**, 568–576
- Wichmann, L., Dulai, J. S., Marles-Wright, J., Maxeiner, S., Szczesniak, P. P., Manzini, L., and Althaus, M. (2019) An extracellular acidic cleft confers profound H⁺-sensitivity to epithelial sodium channels containing the delta-subunit in *Xenopus laevis*. *J. Biol. Chem.* **294**, 12507–12520
- Springauf, A., Bresenitz, P., and Grunder, S. (2011) The interaction between two extracellular linker regions controls sustained opening of acid-sensing ion channel 1. *J. Biol. Chem.* **286**, 24374–24384
- Bacongus, I., and Gouaux, E. (2012) Structural plasticity and dynamic selectivity of acid-sensing ion channel-spider toxin complexes. *Nature* **489**, 400–405
- Chen, J., Kleyman, T. R., and Sheng, S. (2013) Gain-of-function variant of the human epithelial sodium channel. *Am. J. Physiol. Ren. Physiol.* **304**, F207–213
- Waterhouse, A., Bertoni, M., Bienert, S., Studer, G., Tauriello, G., Gumienny, R., Heer, F. T., de Beer, T. A. P., Rempfer, C., Bordoli, L., Lepore, R., and Schwede, T. (2018) SWISS-MODEL: Homology modeling of protein structures and complexes. *Nucleic Acids Res.* **46**, W296–w303
- Maarouf, A. B., Sheng, N., Chen, J., Winarski, K. L., Okumura, S., Carattino, M. D., Boyd, C. R., Kleyman, T. R., and Sheng, S. (2009) Novel determinants of epithelial sodium channel gating within extracellular thumb domains. *J. Biol. Chem.* **284**, 7756–7765
- Sheng, S., Carattino, M. D., Bruns, J. B., Hughey, R. P., and Kleyman, T. R. (2006) Furin cleavage activates the epithelial Na⁺ channel by relieving Na⁺ self-inhibition. *Am. J. Physiol. Ren. Physiol.* **290**, F1488–F1496
- Sheng, S., Li, J., McNulty, K. A., Kieber-Emmons, T., and Kleyman, T. R. (2001) Epithelial sodium channel pore region. structure and role in gating. *J. Biol. Chem.* **276**, 1326–1334
- Snyder, P. M., Olson, D. R., and Bucher, D. B. (1999) A pore segment in DEG/ENaC Na⁺ channels. *J. Biol. Chem.* **274**, 28484–28490
- Kellenberger, S., Gautschi, I., Rossier, B. C., and Schild, L. (1998) Mutations causing Liddle syndrome reduce sodium-dependent downregulation of the epithelial sodium channel in the *Xenopus* oocyte expression system. *J. Clin. Invest.* **101**, 2741–2750
- Volk, T., Konstas, A. A., Bassalay, P., Ehmke, H., and Korbmacher, C. (2004) Extracellular Na⁺ removal attenuates rundown of the epithelial Na⁺-channel (ENaC) by reducing the rate of channel retrieval. *Pflugers Arch.* **447**, 884–894
- Snyder, P. M., Bucher, D. B., and Olson, D. R. (2000) Gating induces a conformational change in the outer vestibule of ENaC. *J. Gen. Physiol.* **116**, 781–790
- Condliffe, S. B., Zhang, H., and Frizzell, R. A. (2004) Syntaxin 1A regulates ENaC channel activity. *J. Biol. Chem.* **279**, 10085–10092
- Carattino, M. D., Sheng, S., Bruns, J. B., Pilewski, J. M., Hughey, R. P., and Kleyman, T. R. (2006) The epithelial Na⁺ channel is inhibited by a peptide derived from proteolytic processing of its alpha subunit. *J. Biol. Chem.* **281**, 18901–18907
- Akabas, M. H. (2015) Cysteine modification: Probing channel structure, function and conformational change. *Adv. Exp. Med. Biol.* **869**, 25–54
- Sheng, S., Perry, C. J., Kashlan, O. B., and Kleyman, T. R. (2005) Side chain orientation of residues lining the selectivity filter of epithelial Na⁺ channels. *J. Biol. Chem.* **280**, 8513–8522
- Chen, J., Winarski, K. L., Myerburg, M. M., Pitt, B. R., and Sheng, S. (2012) Probing the structural basis of Zn²⁺ regulation of the epithelial Na⁺ channel. *J. Biol. Chem.* **287**, 35589–35598
- Jurcik, A., Bednar, D., Byska, J., Marques, S. M., Furmanova, K., Daniel, L., Kokkonen, P., Brezovsky, J., Strnad, O., Stourac, J., Pavelka, A., Manak, M., Damborsky, J., and Kozlikova, B. (2018) CAVER analyst 2.0: Analysis and visualization of channels and tunnels in protein structures and molecular dynamics trajectories. *Bioinformatics* **34**, 3586–3588
- Stourac, J., Vavra, O., Kokkonen, P., Filipovic, J., Pinto, G., Brezovsky, J., Damborsky, J., and Bednar, D. (2019) Caver Web 1.0: Identification of tunnels and channels in proteins and analysis of ligand transport. *Nucleic Acids Res.* **47**, W414–W422
- Edelheit, O., Ben-Shahar, R., Dascal, N., Hanukoglu, A., and Hanukoglu, I. (2014) Conserved charged residues at the surface and interface of epithelial sodium channel subunits—roles in cell surface expression and the sodium self-inhibition response. *FEBS J.* **281**, 2097–2111
- Hanukoglu, I. (2017) ASIC and ENaC type sodium channels: Conformational states and the structures of the ion selectivity filters. *FEBS J.* **284**, 525–545
- Unwin, N. (2013) Nicotinic acetylcholine receptor and the structural basis of neuromuscular transmission: Insights from Torpedo postsynaptic membranes. *Q. Rev. Biophys.* **46**, 283–322
- Samways, D. S., Khakh, B. S., Dutertre, S., and Egan, T. M. (2011) Preferential use of unobstructed lateral portals as the access route to the pore of human ATP-gated ion channels (P2X receptors). *Proc. Natl. Acad. Sci. U. S. A.* **108**, 13800–13805
- Kawate, T., Robertson, J. L., Li, M., Silberberg, S. D., and Swartz, K. J. (2011) Ion access pathway to the transmembrane pore in P2X receptor channels. *J. Gen. Physiol.* **137**, 579–590
- Gonzales, E. B., Kawate, T., and Gouaux, E. (2009) Pore architecture and ion sites in acid-sensing ion channels and P2X receptors. *Nature* **460**, 599–604

43. Bacongus, I., Bohlen, C. J., Goehring, A., Julius, D., and Gouaux, E. (2014) X-ray structure of acid-sensing ion channel 1-snake toxin complex reveals open state of a Na⁺-selective channel. *Cell* **156**, 717–729
44. Donald, J. E., Kulp, D. W., and DeGrado, W. F. (2011) Salt bridges: Geometrically specific, designable interactions. *Proteins* **79**, 898–915
45. Schild, L., Schneeberger, E., Gautschi, I., and Firsov, D. (1997) Identification of amino acid residues in the alpha, beta, and gamma subunits of the epithelial sodium channel (ENaC) involved in amiloride block and ion permeation. *J. Gen. Physiol.* **109**, 15–26
46. Li, J., Sheng, S., Perry, C. J., and Kleyman, T. R. (2003) Asymmetric organization of the pore region of the epithelial sodium channel. *J. Biol. Chem.* **278**, 13867–13874
47. Chen, J., Ray, E. C., Yates, M. E., Buck, T. M., Brodsky, J. L., Kinlough, C. L., Winarski, K. L., Hughey, R. P., Kleyman, T. R., and Sheng, S. (2015) Functional roles of clusters of hydrophobic and polar residues in the epithelial Na⁺ channel knuckle domain. *J. Biol. Chem.* **290**, 25140–25150
48. Sheng, S., Chen, J., Mukherjee, A., Yates, M. E., Buck, T. M., Brodsky, J. L., Tolino, M. A., Hughey, R. P., and Kleyman, T. R. (2018) Thumb domains of the three epithelial Na⁺ channel subunits have distinct functions. *J. Biol. Chem.* **293**, 17582–17592
49. Sheng, S., Maarouf, A. B., Bruns, J. B., Hughey, R. P., and Kleyman, T. R. (2007) Functional role of extracellular loop cysteine residues of the epithelial Na⁺ channel in Na⁺ self-inhibition. *J. Biol. Chem.* **282**, 20180–20190
50. Sheng, S., Perry, C. J., and Kleyman, T. R. (2002) External nickel inhibits epithelial sodium channel by binding to histidine residues within the extracellular domains of alpha and gamma subunits and reducing channel open probability. *J. Biol. Chem.* **277**, 50098–50111
51. Shi, S., Ghosh, D. D., Okumura, S., Carattino, M. D., Kashlan, O. B., Sheng, S., and Kleyman, T. R. (2011) Base of the thumb domain modulates epithelial sodium channel gating. *J. Biol. Chem.* **286**, 14753–14761
52. Collier, D. M., and Snyder, P. M. (2011) Identification of epithelial Na⁺ channel (ENaC) intersubunit Cl⁻ inhibitory residues suggests a trimeric alpha beta gamma beta channel architecture. *J. Biol. Chem.* **286**, 6027–6032
53. Collier, D. M., Tomkovicz, V. R., Peterson, Z. J., Benson, C. J., and Snyder, P. M. (2014) Intersubunit conformational changes mediate epithelial sodium channel gating. *J. Gen. Physiol.* **144**, 337–348
54. Linsdell, P. (2015) Metal bridges to probe membrane ion channel structure and function. *Biomol. Concepts* **6**, 191–203
55. Ray, E. C., Chen, J., Kelly, T. N., He, J., Hamm, L. L., Gu, D., Shimmin, L. C., Hixson, J. E., Rao, D. C., Sheng, S., and Kleyman, T. R. (2016) Human epithelial Na⁺ channel missense variants identified in the GenSalt study alter channel activity. *Am. J. Physiol. Ren. Physiol.* **311**, F908–F914
56. Salih, M., Gautschi, I., van Bemmelen, M. X., Di Benedetto, M., Brooks, A. S., Lugtenberg, D., Schild, L., and Hoorn, E. J. (2017) A missense mutation in the extracellular domain of alphaENaC causes Liddle syndrome. *J. Am. Soc. Nephrol.* **28**, 3291–3299
57. Azad, A. K., Rauh, R., Vermeulen, F., Jaspers, M., Korbmacher, J., Boissier, B., Bassinet, L., Fichou, Y., des Georges, M., Stanke, F., De Boeck, K., Dupont, L., Balascakova, M., Hjelte, L., Lebecque, P., *et al.* (2009) Mutations in the amiloride-sensitive epithelial sodium channel in patients with cystic fibrosis-like disease. *Hum. Mutat.* **30**, 1093–1103
58. Rauh, R., Diakov, A., Tzschoppe, A., Korbmacher, J., Azad, A. K., Cuppens, H., Cassiman, J. J., Dotsch, J., Sticht, H., and Korbmacher, C. (2010) A mutation of the epithelial sodium channel associated with atypical cystic fibrosis increases channel open probability and reduces Na⁺ self inhibition. *J. Physiol.* **588**, 1211–1225
59. Chen, J., Myerburg, M. M., Passero, C. J., Winarski, K. L., and Sheng, S. (2011) External Cu²⁺ inhibits human epithelial Na⁺ channels by binding at a subunit interface of extracellular domains. *J. Biol. Chem.* **286**, 27436–27446
60. Della Vecchia, M. C., Rued, A. C., and Carattino, M. D. (2013) Gating transitions in the palm domain of ASIC1a. *J. Biol. Chem.* **288**, 5487–5495
61. Krauson, A. J., Rued, A. C., and Carattino, M. D. (2013) Independent contribution of extracellular proton binding sites to ASIC1a activation. *J. Biol. Chem.* **288**, 34375–34383
62. Roy, S., Boiteux, C., Alijevic, O., Liang, C., Berneche, S., and Kellenberger, S. (2013) Molecular determinants of desensitization in an ENaC/degenerin channel. *FASEB J.* **27**, 5034–5045
63. Wu, Y., Chen, Z., and Canessa, C. M. (2019) A valve-like mechanism controls desensitization of functional mammalian isoforms of acid-sensing ion channels. *Elife* **8**, e45851
64. Yoder, N., and Gouaux, E. (2018) Divalent cation and chloride ion sites of chicken acid sensing ion channel 1a elucidated by x-ray crystallography. *PLoS One* **13**, e0202134
65. Dawson, R. J., Benz, J., Stohler, P., Tetaz, T., Joseph, C., Huber, S., Schmid, G., Hügin, D., Pflimlin, P., Trube, G., Rudolph, M. G., Hennig, M., and Ruf, A. (2012) Structure of the acid-sensing ion channel 1 in complex with the gating modifier Psalmotoxin 1. *Nat. Commun.* **3**, 936
66. Sheng, S., Perry, C. J., and Kleyman, T. R. (2004) Extracellular Zn²⁺ activates epithelial Na⁺ channels by eliminating Na⁺ self-inhibition. *J. Biol. Chem.* **279**, 31687–31696
67. Yu, L., Eaton, D. C., and Helms, M. N. (2007) Effect of divalent heavy metals on epithelial Na⁺ channels in A6 cells. *Am. J. Physiol. Ren. Physiol.* **293**, F236–F244
68. Renauld, S., Allache, R., and Chraïbi, C. (2008) Ile481 from the Guinea pig alpha-subunit plays a major role in the activation of ENaC by cpt-cAMP. *Cell Physiol. Biochem.* **22**, 101–108
69. Molina, R., Han, D. Y., Su, X. F., Zhao, R. Z., Zhao, M., Sharp, G. M., Chang, Y., and Ji, H. L. (2011) Cpt-cAMP activates human epithelial sodium channels via relieving self-inhibition. *Biochim. Biophys. Acta* **1808**, 1818–1826
70. Nie, H. G., Zhang, W., Han, D. Y., Li, Q. N., Li, J., Zhao, R. Z., Su, X. F., Peng, J. B., and Ji, H. L. (2010) 8-pCPT-cGMP stimulates alphabeta-gamma-ENaC activity in oocytes as an external ligand requiring specific nucleotide moieties. *Am. J. Physiol. Ren. Physiol.* **298**, F323–334
71. Van Driessche, W., and Zeiske, W. (1985) Ionic channels in epithelial cell membranes. *Physiol. Rev.* **65**, 833–903
72. Collier, D. M., Peterson, Z. J., Blokhin, I. O., Benson, C. J., and Snyder, P. M. (2012) Identification of extracellular domain residues required for epithelial Na⁺ channel activation by acidic pH. *J. Biol. Chem.* **287**, 40907–40914
73. Lu, M., Echeverri, F., Kalabat, D., Laita, B., Dahan, D. S., Smith, R. D., Xu, H., Staszewski, L., Yamamoto, J., Ling, J., Hwang, N., Kimmich, R., Li, P., Patron, E., Keung, W., *et al.* (2008) Small molecule activator of the human epithelial sodium channel. *J. Biol. Chem.* **283**, 11981–11994
74. Bertoni, M., Kiefer, F., Biasini, M., Bordoli, L., and Schwede, T. (2017) Modeling protein quaternary structure of homo- and hetero-oligomers beyond binary interactions by homology. *Sci. Rep.* **7**, 10480
75. Schrödinger, LLC (2021) *The PyMOL Molecular Graphics System, Version 2.4*, Schrödinger, LLC, New York, NY
76. Madeira, F., Park, Y. M., Lee, J., Buso, N., Gur, T., Madhusoodanan, N., Basutkar, P., Tivey, A. R. N., Potter, S. C., Finn, R. D., and Lopez, R. (2019) The EMBL-EBI search and sequence analysis tools APIs in 2019. *Nucleic Acids Res.* **47**, W636–W641