Proton Sensing of CLC-0 Mutant E166D

Sonia Traverso, Giovanni Zifarelli, Rita Aiello, and Michael Pusch

Istituto di Biofisica, Consiglio Nazionale delle Ricerche, I-16149 Genova, Italy

INTRODUCTION

CLC Cl⁻ channels are homodimers in which each subunit has a proper pore and a (fast) gate. An additional slow gate acts on both pores. A conserved glutamate (E166 in CLC-0) is a major determinant of gating in CLC-0 and is crucially involved in Cl⁻/H⁺ antiport of CLC-ec1, a CLC of known structure. We constructed tandem dimers with one wild-type (WT) and one mutant subunit (E166A or E166D) to show that these mutations of E166 specifically alter the fast gate of the pore to which they belong without effect on the fast gate of the neighboring pore. In addition, both mutations activate the common slow gate. E166A pores have a large, voltage-independent open probability of the fast gate (p_open), whereas p_open of E166D pores is dramatically reduced. Similar to WT, p_open of E166D was increased by lowering pH_{int}. At negative voltages, E166D presents a persistent inward current that is blocked by p-chlorophenoxy-acetic acid (CPA) and increased at low pH_{ext}. The pH_{ext} dependence of the persistent current is analogous to a similar steady inward current in WT CLC-0. Surprisingly, however, the underlying unitary conductance of the persistent current in E166D is about an order of magnitude smaller than that of the transient deactivating inward Cl⁻ current. Collectively, our data support the possibility that the mutated CLC-0 channel E166D can assume two distinct open states. Voltage-independent protonation of D166 from the outside favors a low conductance state, whereas protonation from the inside favors the high conductance state.

Correspondence to Michael Pusch: pusch@ibf.cnr.it

Abbreviations used in this paper: CPA, p-chlorophenoxy-acetic acid; WT, wild type.
straightforward correlation of the structure of the bacterial CLC-ec1 and the function of the vertebrate CLC-0 is also in agreement with other studies that suggest a structural conservation of CLC proteins (Estévez et al., 2003; Lin and Chen, 2003). However, other studies suggested that the fast gating of CLC-0 involves an additional rearrangement of the intracellular part that is not revealed by the crystal structure of E148A (Accardi and Pusch, 2003; Traverso et al., 2003). In fact, the functional equivalence of CLC-0 and CLC-ec1 was challenged when Accardi and Miller demonstrated that CLC-ec1 is actually not a Cl⁻ ion channel but an electrogenic Cl⁻/H⁺ antiporter with an apparent stoichiometry of 2 Cl⁻:1 H⁺ (Accardi and Miller, 2004). Moreover it has been recently shown that also mammalian proteins of the same family, CLC-3, CLC-4, and CLC-5, exhibit Cl⁻/H⁺ antiporter activity (Picollo and Pusch, 2005; Scheel et al., 2005). In contrast, CLC-0 is clearly an ion channel with well-defined, relatively large single channel events (Hanke and Miller, 1983; Bauer et al., 1991) and Nernstian dependence of the reversal potential on the chloride concentration.

The molecular mechanism of transport of CLC-ec1 and CLC-3–5 is not understood and it is currently unclear how the gating and permeation properties of CLC-0 are correlated to it. It seems, however, likely that the proton dependence of the fast gate of CLC-0 is somehow related to the Cl⁻/H⁺ antiport of CLC-ec1. For example, extracellular acidification opens CLC-0 (Chen and Chen, 2001; Dutzler et al., 2003), probably by protonating E166, mimicking the effect of mutating E166 to a neutral amino acid (Dutzler et al., 2003), probably somehow related to the Cl⁻/H⁺ antiport of CLC-ec1. The analogous mutations of CLC-ec1 (E148A) and CLC-5 (E211A) abolish H⁺ transport (Accardi and Miller, 2004; Picollo and Pusch, 2005; Scheel et al., 2005). Also intracellular acidification strongly activates CLC-0 (Hanke and Miller, 1983) and similarly CLC-1 (Rychkov et al., 1996) by apparently shifting the activation curve to negative voltages.

To better understand the role of protons in the mechanism of protopore gating of CLC-0 we mutated the critical glutamate 166 to the similar amino acid aspartate. Despite the small difference between these two amino acids (one extra CH₂ group in the side chain of glutamate) the kinetics of the WT and of the mutant are very different (Traverso et al., 2003). In the present work, we show that indeed both mutants, E166A and E166D, have a drastically altered protopore gate. However, both mutations, despite their disparate effect on the fast gate, appear to eliminate slow gating processes, locking the slow gate open. We then varied pH_int and pH_ext and compared the effects on E166D with those described for WT CLC-0. In contrast with what would be expected from the behavior of WT CLC-0, extracellular pH had no effect on E166D outward currents but affected only a persistent inward current present at negative voltages, a current that appears to represent a different conductance state of the channel. Decreasing intracellular pH drastically increased the p_open of the channel in a manner that suggests that the protonation from the inside represents one of the major voltage-dependent steps in the opening of the fast gate.

**MATERIALS AND METHODS**

**Molecular Biology and Heterologous Expression**

Mutations were introduced by recombinant PCR as previously described (Accardi et al., 2001). Tandem dimers (WT-ED, ED-WT, WT-EE, and EAE-WT) were generated as previously described (Ludewig et al., 1996). In brief, the stop codon of the NH₂-terminal subunit was replaced with an Spel and a Kpnl restriction site. The same sites were introduced before the start codon of the COOH-terminal subunit. The Spe I site was used to link both subunits. The linker sequence consisted of four amino acids (G-T-F-S). All constructs were in the PTLN vector (Lorenz et al., 1996). cRNA was transcribed and injected in *Xenopus* oocytes as previously described (Accardi and Pusch, 2000).

**Electrophysiology**

Currents were recorded using the two-electrode voltage-clamp method and excised patch-clamp recording as previously described (Pusch et al., 2000). For whole oocyte voltage clamp measurements, the bath solution contained (in mM) 100 NaCl (or 100 Nal), 4 MgSO₄, 5 HEPES, pH 7.3, and the holding potential was chosen close to the resting membrane potential (−30 to −50 mV). For patch clamping, the intracellular solution contained (in mM): 100 NMDG-Cl, 2 MgCl₂, 10 HEPES, 2 EGTA, pH 7.2, whereas the standard extracellular solution contained 100 NMDG-Cl, 5 MgCl₂, 10 HEPES, pH 7.2. In both solutions HEPES was substituted by MES for solutions with 5 < pH < 6.5, bis-Tris-propane for solutions with pH > 7.8, and glutamate for solutions with pH < 5. Experiments shown in the figures were performed using regular pH of 7.2 for the extracellular solution (for patch-clamp and voltage-clamp recordings) and the intracellular solution (for patch-clamp recordings) unless otherwise noted.

All substances were purchased from Sigma-Aldrich. Solutions in patch-clamp experiments were changed by inserting the patch pipette into perfusion tubes of ~0.5 mm diameter. Patch-clamp data were recorded using an EPC-7 amplifier (HEKA) and the Pulse acquisition program (HEKA) or a custom acquisition program (GePulse) (the acquisition program is available at http://www.ge.cnrs-france.fr/ICB/conti_moran_pusch/programs-pusch/software-mik.htm).

The holding potential in patch clamp measurements was 0 mV. Voltage clamp measurements employed an NPI-TEC 05 amplifier (NPI Electronics), and were performed as described previously (Traverso et al., 2003).

**Capacity Subtraction**

For all (macroscopic) patch-clamp experiments, the capacitive transients were subtracted offline in the following manner. All pulse protocols contained a final pulse to 0 mV with a duration equal or superior to the longest segment of the voltage-clamp pulse protocol. Since at 0 mV (very close to the reversal potential) no ionic current is expected to flow, the current response reflects only the capacitive transient. This response, after appropriate scaling, was used for the subtraction of the capacitive transients at the other test potentials.
Single Channel Analysis
Single channel recordings were generally filtered at 1 kHz or 500 Hz. For the construction of amplitude histograms a bin width of 5 fA was used. Amplitude histograms were fitted with the sum of Gaussian functions, $G_i$, one for each peak, $i$,

$$H(I) = \sum_i G_i(I) = \sum_i a_i \exp\left(\frac{-(I - \mu_i)^2}{2\sigma_i^2}\right),$$

where each Gaussian function is characterized by a mean $\mu_i$, a width $\sigma_i$, and amplitude $a_i$. The relative area, $A_i$, that is occupied by each Gaussian component was calculated by

$$A_i = \frac{a_i}{\sum_j a_j}$$

and was taken as a measure of the probability to dwell in the conductance state associated with mean $\mu_i$.

Nonstationary Noise Analysis
Nonstationary noise analysis was performed essentially as described earlier (Pusch et al., 1994). In brief, a test pulse was repeatedly applied, and the variance was calculated from the squared difference of consecutive current responses. For the variance-mean analysis, the current range was subdivided into a certain number of bins for a clearer graphical representation. Background variance was measured at the baseline (at 0 mV) and subtracted. The variance-mean plots were fitted with Eq. 1 (see below) with two free parameters, the single channel current $i$, and the number of channels, $N$. All primary data analysis was performed with the custom analysis program downloadable at http://www.ge.cnr.it/ICB/conti_moran_pusch/programs-pusch/software-mik.htm. Figures were prepared with SigmaPlot (SPSS Inc.).

pH Measurements
We measured the extracellular pH close to the oocyte surface with a pH-sensitive microelectrode as described by Picollo and Pusch (2005). In brief, silanized (with dichlorodimethylsilane; Sigma-Aldrich) microelectrodes were filled with proton ionophore B (Fluka) and then with a solution containing (in mM) 150 NaCl, 23 NaOH, 40 KH$_2$PO$_4$, pH 6.8. Pipettes were connected to a custom built high impedance ($>10^{12}$ Ohm) amplifier and responded with a slope of 57–63 mV per pH unit. The pH-sensitive microelectrodes were gently pushed against the vitelline membrane without penetrating the oocyte. The pH-related signal was recorded as a second input channel in parallel to the membrane current. The extracellular solution for pH measurements contained 100 mM NaCl, 4 mM MgCl$_2$, 0.1 mM HEPES, pH 6.4.

RESULTS
Noise Analysis of Mutant E166D Reveals a Slightly Reduced Conductance
We analyzed mutations of the glutamate E166 of CLC-0 to aspartate (ED) and alanine (EA). Mutating E166 in CLC-0 to alanine leads to an almost constitutively open channel (Dutzler et al., 2003; Traverso et al., 2003), whereas E166D slows down opening at positive potentials and increases the rate of closure at negative potentials (Traverso et al., 2003). In addition, mutant E166D consistently expressed much less current than WT CLC-0 or mutant E166A. In fact, in order to keep currents at a manageable magnitude that could be measured with the two electrode voltage clamp, <1 ng of cRNA was injected for CLC-0, and currents were measured after 1–2 d. In contrast, ~20 ng had to be injected for mutant E166D, and oocytes had to be incubated for at least 3 d to achieve a sizable current (unpublished data). To find out whether a reduced single channel conductance of E166D was responsible for the smaller currents we performed nonstationary noise analysis (Fig. 1). This method provides a good order-of-magnitude estimate of the single channel current and may allow the determination of the absolute open probability (Heinemann and Conti, 1992). Fig. 1 A shows the mean of 80 traces obtained each by stepping the voltage from 0 to 120 mV in an inside-out patch. Fig. 1 B shows the corresponding variance trace, whereas in Fig. 1 C the variance is plotted versus the mean current (symbols) together with a fit of Eq. 1 (line) with the particular parameters $i = 0.70$ pA, $N = 10^3$.

$$\sigma^2 = i^2 - I^2/N, \quad (1)$$

where $\sigma^2$ is the variance, $I$ the macroscopic current, $i$ the single channel current, and $N$ the number of channels. The average single-channel current obtained from noise analysis at 120 mV was $0.55 \pm 0.14$ pA (mean $\pm$ SD, $n = 6$). Assuming a linear single-channel i-V, this corresponds to a conductance of 4.6 pS. This value is only ~35% smaller than the conductance of WT CLC-0 (~7 pS) (Accardi and Pusch, 2003) and this reduction can thus not explain the small macroscopic currents of mutant E166D. From the nonstationary noise analysis it was not possible to obtain a reliable es-
estimate for the number of channels, and consequently of the absolute open probability, because the variance-mean plots showed little curvature. This indicates that the maximal open probability is significantly smaller than 0.5, as is indeed the case (see below).

**Tandem Mutant-WT and WT Mutant Dimers Differentiate Effects on Fast and Slow Gate**

The next question we asked was: In what specific manner do mutations E166A and E166D affect the fast (protopore) gate and the slow (common) gate? The slow gate of CLC-0 is voltage dependent with activation favored at negative voltages (Miller and Richard, 1990; Pusch et al., 1997) (Fig. 2 A). No hyperpolarization activation could be detected for either E166A (Fig. 2 B) or E166D (Fig. 2 C). A further hint that the slow gate is locked open in mutant E166D was obtained from the study of the double mutant E166D/C212S that includes the mutation C212S, that locks open the slow gate of CLC-0 (Lin et al., 1999). The double mutant E166D/C212S had properties indistinguishable from the single mutant E166D (unpublished data). These results indicate that the slow gate is either locked open or rendered voltage independent by both mutations E166A and E166D.

We next made four tandem dimeric constructs consisting of one WT and one mutant subunit: WT-ED, WT-EA, ED-WT, and EA-WT. For example, the notation WT-
ED indicates that the first subunit is WT and the second bears the E166D mutation. No difference could be observed between heterodimers with opposite order (i.e., ED-WT versus WT-ED and EA-WT versus WT-EA) (unpublished data). All dimeric constructs, including a control WT-WT dimer, expressed similar levels of current (conductance ranged between 50 and 200 pA after 1 d of incubation), suggesting that the E166D mutation has no (dominant) effect on protein processing or stability. However, we cannot completely rule out that mutation E166D alters protein trafficking.

Interestingly, all dimeric constructs partially recovered a voltage dependence of the slow gate (Fig. 2, D and E). The fact that the slow gate was only partially recovered demonstrates that for all dimeric constructs, both subunits contribute to channel gating. Macroscopic currents of EA-WT dimers on a faster time scale from inside-out patches are shown in Fig. 3 A. The voltage dependence of the fast gate, plotted in Fig. 3 B, differs from that of WT CLC-0 mainly by an increased offset at negative voltages, reflecting probably the voltage-independent contribution of the E166A pores. This interpretation was further confirmed by single channel analysis.

Fig. 4 A shows a single channel trace of the dimer EA-WT at −100 mV. For most of the time the channel behaves as the superposition of a WT pore and a pore, of similar conductance, that is almost always open. Occasionally, currents reach the baseline (indicated by arrows in Fig. 4 A). These events probably represent longer closures of the “EA pore.” A similar behavior has been also previously observed in homomeric E166A channels (Traverso et al., 2003). These closures are not closures of the slow gate because the neighboring “WT pore” continues to open and close. Whether these slow transitions of the EA pore reflect “residual” fast gate transitions remains to be studied. An amplitude histogram over a stretch without such long closures (see bracket with * in Fig. 4 A) yielded a \( p_{\text{open}} \) of 0.64 of the fluctuating pore (Fig. 4 C), relatively close to the WT \( p_{\text{open}} \) at −100 mV (\( p_{\text{open}} \)[WT] \( \sim 0.75; \) Accardi and Pusch, 2003). This strongly suggests that indeed the fast fluctuating conductance level represents the WT pore whereas the long open times correspond to the EA pore, demonstrating that the mutation strongly affects the fast protopore gate, without affecting the fast gate of the neighboring WT pore.

The fast gate properties of the ED-WT resemble those of homodimeric WT CLC-0 as illustrated in Fig. 3 (C and D). The same holds true for WT-ED dimers (unpublished data). In particular, at positive voltage, no slowly activating component similar to that seen in Fig. 1 is visible in patch or voltage-clamp recordings from dimers containing E166D. Thus, there seems to be no contribution of the ED subunit to the “heterodimeric” ED/WT currents, even though we know from the slow-gate recovery, that the ED subunit is present in the dimer. This might be caused by a very small open probability of the fast gate of mutant E166D as suggested by the noise analysis described above. To directly test this hypothesis we measured single ED-WT channels. The advantage of using the dimer instead of measuring directly single E166D channels is that the presence of
only one channel in the patch can be assured by the presence of a single WT-like pore. Indeed, single channel events of WT-ED dimers almost behaved as if they consisted of an isolated single WT pore. This is illustrated in Fig. 5 A, which shows a recording of a patch subjected to voltage pulses to first −100 mV and then +80 mV. At −100 mV, a single pore switches between open and closed states, with an apparent open probability (p ≈ 0.77) close to that of the fast gate of CLC-0 at this voltage (p_{open}[WT] ≈ 0.75; Accardi and Pusch, 2003). At +80 mV, the pore is almost permanently open, which is consistent with the high open probability of the fast gate of CLC-0 at this voltage. However, closer inspection of several traces recorded at 80 mV (Fig. 5 B) reveals rare short openings to a higher conductance level (see arrow in Fig. 5 B). Also many brief interruptions to the baseline can be seen, representing probably brief closures of the WT fast gate. In fact, the expected mean closed time of the WT fast gate is given by 1/α (where α is the opening rate) being <1%. Similar results were seen in a total of four single-channel patches (one patch WT-EA, three patches EA-WT).

Figure 5. Phenotype of dimer WT-ED. In A, a current trace recorded from a patch with a single WT-ED dimer is shown. The voltage was stepped from 0 to −100 mV, back to 0 mV for a brief time and then to 80 mV. Currents appear almost like a single WT pore at −100 mV (with a p_{open} ≈ 0.7) and at 80 mV with a p_{open} of almost 1. However, brief openings to a second open level are visible at 80 mV. To visualize the “spikes” at 80 mV, B shows the superposition of 10 consecutive records at an expanded time scale showing only the pulse to 80 mV. To quantify the p_{open} of the ED pore on top of the WT pore at 80 mV, the amplitude histogram of all records at 80 mV was constructed and limited to the part I > 0.7 pA (C, solid line). In this way, interferences from short closures were eliminated. The amplitude histogram was fitted by the sum of two Gaussian functions (dashed line in C). Since the p_{open} of the WT pore is close to one, the relative area of the higher peak directly reflects the p_{open} of the ED pore. In this case it amounts to 0.51%. Similar results were seen in a total of six single-channel patches (two patches WT-ED, four patches ED-WT).
rent. Given that the open probability of the fast gate of WT is practically one at 80 mV, this contribution directly reflects the open probability of the fast gate of E166D if the openings are interpreted as arising from an E166D pore. The conductance of the putative ED pore estimated from the histogram analysis at 80 mV (~4.7 pS) is very similar to that obtained from the non-stationary noise analysis at 120 mV (~4.6 pS), consistent with this interpretation of the single-channel results. Thus, the almost complete lack of an obvious contribution of E166D pores to macroscopic and single channel currents in WT/ED heteromers probably arises from the very small open probability of E166D pores even at 80 mV.

Collectively, results from macroscopic and single channel current measurements show that both E166 mutations (E166A and E166D) strongly affect the fast gate, without influence on the fast gate of the neighbor subunit, and that the conservative mutation E166D leads to a drastic reduction of the open probability of the fast gate.

**Dependence of E166D on Extracellular pH**

Having established that E166D strongly alters the fast gate, our next purpose was to analyze the effects of different extracellular and intracellular pH on this mutant and compare it to the published effects on WT CLC-0. In two-electrode voltage clamp measurements we varied pHext from 5.8 to 8.3. WT CLC-0 is strongly activated by a reduction of pHext (Chen and Chen, 2001; Dutzler et al., 2003). Given that the open probability of E166D is very small (see above and below), we expected that its $p_{\text{open}}$ would be strongly augmented at low extracellular pH. Surprisingly, almost no change of E166D currents were observed at positive voltages, and only the inward currents at negative voltages were significantly enhanced (Fig. 6, A and B). The latter phenomenon was studied in further detail using outside-out patches. Changing pHext from 7.2 to 5.8 in outside-out patches outward currents were almost unchanged, whereas we observed a significant increase of the steady-state inward current present at $-140 \text{ mV}$ (Fig. 6, C and D). This current is not a leak current as it is blocked by $\beta$-chlorophenoxy-acetic acid (CPA) (see below, Fig. 9 A). A more detailed investigation of its properties is presented below.

**Dependence of E166D on Intracellular pH**

In contrast to pHext, pHint had a drastic effect on the currents carried by mutant E166D. In Fig. 7 A, currents measured from the same inside-out patch are shown at different pHint (pH 7.2, pH 6.8, pH 6.3, and pH 5.8). These currents were elicited by pulses up to 220 mV and channel activation was monitored by a tail pulse to $-140 \text{ mV}$. Currents are clearly activated by low pHint. This can be seen directly from the current measured at the variable test voltages. But also the initial current at the constant tail pulse to $-140 \text{ mV}$ is clearly increased at low pH up to 5.3 (Fig. 7 A, insets). A qualitatively different behavior was seen when the pH was further lowered down to 4.3. Fig. 7 B shows current traces from a different inside-out patch at pHint 7.2, 5.8, 4.8, and 4.3.
Surprisingly, currents at pH_int 4.8 were smaller than currents at pH_int 5.8 but increased again at pH_int 4.3. Most importantly, the tail currents at the fixed tail voltage of −140 mV were significantly smaller at pH_int 4.8 and even smaller at pH_int 4.3 compared with pH_int 5.8 (Fig. 7 B, insets). Thus, reducing pH_int has a biphasic effect on tail current amplitude of mutant E166D: tail currents increase up to pH ~5.3 and then decrease again. In fact, the tail currents at pH_int < 5.3 were too small to allow a quantitative analysis. We noted also that it took several minutes to reach a steady-state current level after perfusing patches with pH_int < 5.3, and also recovery after washing with the control solution was much slower than the speed of the solution exchange. Because of these complications we restricted the quantitative analysis of the effect of pH_int on the open probability to values pH_int > 5. For the quantitative analysis we assumed that the initial current at the constant final “tail” pulse is proportional to the p_open at the end of the prepulse to V_p. In Fig. 8 A the normalized initial tail currents are plotted versus V_p. Currents were normalized to the maximum response seen in the same patch for voltages ≥200 mV and pH ≤5.8. This normalization is justified because curves saturated at high voltages at low pH_int. The normalization implicitly assumes that the single-channel current at −140 mV is not influenced by pH_int. In principle, this is a reasonable assumption because intracellular H⁺ are expected to be pushed away from the pore at these negative voltages. For pH_int > 5, the assumption seems to be justified also by the data, whereas for more acidic pH, tail currents decrease in an apparently paradoxical manner (Fig. 7 B). For pH_int > 5 the I-V curves were fitted by

\[ p(V) = p_{\text{min}} + \frac{(1 - p_{\text{min}})}{1 + \exp((V - V_{1/2})/k)} \]

where the parameter p_{min} accounts for possible leak current and the persistent inward current carried by E166D. The fits resulted in estimates of the voltage of half-maximal activation, V_{1/2}, as a function of pH_int.
Overall it can be concluded that E166D is dramatically activated by intracellular protons. The $p_{\text{open}}(V)$ curve is shifted by $\approx 81$ mV per pH unit (see solid line in Fig. 8 B). Assuming that the maximal $p_{\text{open}}$ achieved at high voltages and low $p_{\text{Hint}}$ is close to unity, allows to estimate the absolute $p_{\text{open}}$ at all other voltages and pH values. For example at $p_{\text{Hint}}$ 7.2 and $V = 80$ mV a $p_{\text{open}}$ of 0.95% is estimated (neglecting $p_{\text{min}}$ that accounts for possible leak current and the persistent inward current). This is relatively close to the value estimated from the single channel analysis of ED-WT heterodimers (0.5%, see above). However, it has to be kept in mind that the assumption that the open probability approaches one at saturating voltages is probably not fully justified (see Discussion). The low $p_{\text{open}}$ at physiological pH values inferred from these measurements and from the single channel analysis most likely explains the small macroscopic current amplitude in voltage clamp experiments. As can be seen in the insets in Fig. 7 A, $p_{\text{Hint}}$ affects also the kinetics of deactivation: deactivation is slightly faster at high $p_{\text{Hint}}$.

The Persistent Inward Current Is Possibly Mediated by a Different Open State

We characterized the properties of the persistent inward currents at $-140$ mV in more detail. First, to assure that it is not an unspecific leak current, we applied 5 and 20 mM CPA in the intracellular solution (Accardi and Pusch, 2003; Estévez et al., 2003). Most of the persistent inward current is indeed blocked by 5 mM CPA and practically all inward current is blocked by 20 mM CPA, in a reversible manner (Fig. 9 A). Since the size of the inward current strictly correlated with the size of the outward current (unpublished data), this result shows that the current is carried by E166D proteins and is not an artifact. A further proof of the specificity of the persistent inward current was obtained by reducing intracellular chloride: reducing $[\text{Cl}^-]_{\text{int}}$ to 14 mM abolished the persistent inward current almost completely (Fig. 9 B).
In noise analysis experiments such as that shown in Fig. 1, we noted that the persistent inward current was associated with a surprisingly small variance. To study this in detail we applied high-resolution nonstationary noise analysis to the deactivating and steady-state part of the current at −140 mV under various conditions. Fig. 10 shows examples performed at various values of pH_{ext}. Data are from different inside-out patches at the indicated pH values. In each case at least 50% of the persistent current at −140 mV was blocked by the application of 5 mM CPA to the intracellular side of the patch showing that the current is not caused by leak (unpublished data). Clearly, at pH_{ext} 6.4, and even more so at pH_{ext} 5.4, the persistent current is much larger relative to the transient inward current (Fig. 10, A–C, a). Actually, at pH_{ext} 5.4, the inward current at −140 mV is practically exclusively composed of an activating component without a transient deactivating component. In each case, the variance associated with the persistent current was very small (Fig. 10, A–C, b).

In the subpanels c (Fig. 10, A–C) the variance of the current during the pulse to −140 mV is plotted versus the absolute value of the corresponding mean current, after appropriate binning (circles). For pH_{ext} 7.2, the data are reasonably fitted by Eq. 1 (Fig. 10 A, c, solid line). However, the data are better fitted by a straight line with slope 0.8 pA, that does not cross the origin (Fig. 10 A, c, dashed line; overlaps with data points). At pH_{ext} 6.4 (Fig. 10 B) it is obvious that the data cannot be well fitted by Eq. 1 because the variance is close to zero at steady state even though the current is substantial (Fig. 10 B, c, solid line). The dashed line in Fig. 10 B, c, that fits the data well, has a slope of ~1 pA. This shows that the transient, deactivating response of E166D at −140 mV is associated with an elementary current of ~1 pA, corresponding to a single-channel conductance of ~7 pS. Assuming that the persistent current is carried by ion channel activity, the small variance of the steady-state current could be due to a small unitary conductance or a larger unitary conductance associated with a close-to unity open probability. However, since the persistent current is mediated by E166D proteins, very many of which must be present in the patch illustrated in Fig. 10 to generate the sizeable outward current at 120 mV, the latter possibility can be excluded: a close-to unity open probability together with a conductance similar to that estimated for the transient inward current would generate a much larger inward current than observed. We can therefore conclude that the elementary conductance of the persistent inward current is small. To estimate the elementary current of the steady-state component we use the equation

$$\sigma^2 = i^* I^* (1 - p),$$

and assuming for simplicity a small open probability $i = \sigma^2 / I$. From the measured values of the persistent current, $I$, and the associated variance, $\sigma^2$, an elementary current of ~0.11 pA at pH_{ext} 6.4 can be calculated, about 10-fold smaller than the elementary current asso-

![Figure 10](image-url)

Figure 10. Small unitary conductance underlying the persistent current. In each box (A–C) are shown the results of a nonstationary noise analysis conducted with an inside-out patch with the indicated pH_{ext} values. In each case, subpanel a shows the mean current response from >60 stimulations evoked by a step from 0 to 160 mV and then to −140 mV. Subpanel b shows the corresponding baseline-subtracted variance. Subpanel c shows the plot of the binned variance versus the absolute value of the mean for the segment of the records at −140 mV. Solid lines are best fits of Eq. 1 with $i = 0.68$ pA (A), $i = 0.7$ pA (B), $i = 0.13$ pA (C). The number of channels was very large in A and B, and $N = 583$ in C. The dashed lines in A and B are linear fits with slopes of 0.79 pA (A) and 1 pA (B) and a current offset of 1.1 pA (A) and 4.2 pA (B). The residual variance at the end of the −140 mV pulse was 0.46 pA² in B.
The Persistent Inward Current Is Not Associated with H⁺ Transport

It might be hypothesized that the persistent inward current reflects Cl⁻/H⁺ antiport. This would explain the marked dependence on pHext and the small variance. To test for this we measured the extracellular pH close to the oocyte surface using a pH-sensitive microelectrode in a solution of low buffer capacity (0.1 mM HEPES) and a slightly acidic pH of 6.4 to increase the magnitude of the inward current. To assay for H⁺ transport we applied a train of pulses to negative voltages (between −100 and −140 mV). In CLC-5–expressing oocytes, tested at positive voltages in the same solution and at similar current levels (Fig. 11 A), a robust change of the extracellular pH could be recorded (Fig. 11 B; Picollo and Pusch, 2005). Since inward currents generated by mutant E166D are relatively small (e.g., Fig. 6), we used only oocytes that expressed currents >12 μA at 80 mV for this analysis (Fig. 11 C). However, even in such highly expressing oocytes, no significant increase of the extracellular pH close to the oocyte surface could be detected (Fig. 11 D). This result suggests that the persistent inward current is not mediated to a large extent by protons.

DISCUSSION

The recent discovery that CLC-ec1 is not a Cl⁻ channel but a Cl⁻/H⁺ antiporter induced us to investigate better the role of protons in gating of CLC-0. Dutzler et al. (2003) have shown that a major element that is responsible for CLC gating is the glutamate residue E166. Mutating it to alanine, glutamine, or serine leads to a complete loss of voltage and chloride dependence of gating of CLC-0 (Dutzler et al., 2003; Traverso et al., 2003) with channels appearing almost permanently open. X-ray crystallographical analysis of the equivalent mutations of the bacterial CLC-ec1 (E148A, E148Q) beautifully revealed that the location of the presumably negatively charged side chain of E148 in the WT structure was occupied by a Cl⁻ ion in the mutant structures (Dutzler et al., 2003). Accardi and Miller found that the Cl⁻/H⁺ antiport activity of CLC-ec1 was abolished by the mutation E148A and that it behaves like a passive Cl⁻-selective channel or uniporter (Accardi and Miller, 2004). These results indicate that there is an intimate relationship between gating of CLC-0 and Cl⁻/H⁺ antiport of CLC-ec1. A Cl⁻/H⁺ antiport function was recently described also for the mammalian proteins CLC-4 and CLC-5 (Scheel et al., 2005; Picollo and Pusch, 2005), demonstrating that the function of the bacterial proteins is of far greater relevance to human physiology than previously thought.

In the present work we sought to obtain more insight into the relationship between gating and H⁺ transport by analyzing in detail the properties of an interesting mutation of the glutamate E166 in CLC-0; a mutation that behaves like a passive Cl⁻-selective antiport induced us to investigate further the role of protons in gating of CLC-0. Dutzler et al. (2003) have shown that a major element that is responsible for CLC gating is the glutamate residue E166. Mutating it to alanine, glutamine, or serine leads to a complete loss of voltage and chloride dependence of gating of CLC-0 (Dutzler et al., 2003; Traverso et al., 2003) with channels appearing almost permanently open. X-ray crystallographical analysis of the equivalent mutations of the bacterial CLC-ec1 (E148A, E148Q) beautifully revealed that the location of the presumably negatively charged side chain of E148 in the WT structure was occupied by a Cl⁻ ion in the mutant structures (Dutzler et al., 2003). Accardi and Miller found that the Cl⁻/H⁺ antiport activity of CLC-ec1 was abolished by the mutation E148A and that it behaves like a passive Cl⁻-selective channel or uniporter (Accardi and Miller, 2004). These results indicate that there is an intimate relationship between gating of CLC-0 and Cl⁻/H⁺ antiport of CLC-ec1. A Cl⁻/H⁺ antiport function was recently described also for the mammalian proteins CLC-4 and CLC-5 (Scheel et al., 2005; Picollo and Pusch, 2005), demonstrating that the function of the bacterial proteins is of far greater relevance to human physiology than previously thought.

In the present work we sought to obtain more insight into the relationship between gating and H⁺ transport by analyzing in detail the properties of an interesting mutation of the glutamate E166 in CLC-0; a mutation that behaves like a passive Cl⁻-selective antiport induced us to investigate further the role of protons in gating of CLC-0. Dutzler et al. (2003) have shown that a major element that is responsible for CLC gating is the glutamate residue E166. Mutating it to alanine, glutamine, or serine leads to a complete loss of voltage and chloride dependence of gating of CLC-0 (Dutzler et al., 2003; Traverso et al., 2003) with channels appearing almost permanently open. X-ray crystallographical analysis of the equivalent mutations of the bacterial CLC-ec1 (E148A, E148Q) beautifully revealed that the location of the presumably negatively charged side chain of E148 in the WT structure was occupied by a Cl⁻ ion in the mutant structures (Dutzler et al., 2003). Accardi and Miller found that the Cl⁻/H⁺ antiport activity of CLC-ec1 was abolished by the mutation E148A and that it behaves like a passive Cl⁻-selective channel or uniporter (Accardi and Miller, 2004). These results indicate that there is an intimate relationship between gating of CLC-0 and Cl⁻/H⁺ antiport of CLC-ec1. A Cl⁻/H⁺ antiport function was recently described also for the mammalian proteins CLC-4 and CLC-5 (Scheel et al., 2005; Picollo and Pusch, 2005), demonstrating that the function of the bacterial proteins is of far greater relevance to human physiology than previously thought.

In the present work we sought to obtain more insight into the relationship between gating and H⁺ transport by analyzing in detail the properties of an interesting mutation of the glutamate E166 in CLC-0; a mutation that behaves like a passive Cl⁻-selective antiport induced us to investigate further the role of protons in gating of CLC-0. Dutzler et al. (2003) have shown that a major element that is responsible for CLC gating is the glutamate residue E166. Mutating it to alanine, glutamine, or serine leads to a complete loss of voltage and chloride dependence of gating of CLC-0 (Dutzler et al., 2003; Traverso et al., 2003) with channels appearing almost permanently open. X-ray crystallographical analysis of the equivalent mutations of the bacterial CLC-ec1 (E148A, E148Q) beautifully revealed that the location of the presumably negatively charged side chain of E148 in the WT structure was occupied by a Cl⁻ ion in the mutant structures (Dutzler et al., 2003). Accardi and Miller found that the Cl⁻/H⁺ antiport activity of CLC-ec1 was abolished by the mutation E148A and that it behaves like a passive Cl⁻-selective channel or uniporter (Accardi and Miller, 2004). These results indicate that there is an intimate relationship between gating of CLC-0 and Cl⁻/H⁺ antiport of CLC-ec1. A Cl⁻/H⁺ antiport function was recently described also for the mammalian proteins CLC-4 and CLC-5 (Scheel et al., 2005; Picollo and Pusch, 2005), demonstrating that the function of the bacterial proteins is of far greater relevance to human physiology than previously thought.

Figure 11. Persistent inward current is not associated with H⁺ inward movement. The extracellular pH was measured with a pH-sensitive microelectrode close to the oocyte surface as described in MATERIALS AND METHODS. Currents recorded from a CLC-5–expressing oocyte are shown in A (pulses are from −120 to 80 mV with a constant “tail” pulse to 60 mV). In B, the pH response, shown as a function of time, was evoked by a train of 300-ms pulses to 60 mV (current at 60 mV is ~1.8 μA) with a 300-ms holding period between the pulses at −20 mV. The arrow indicates the switch off of the voltage clamp, nulling the current and leading to a recovery of pHext. Results from a similar experiment from an oocyte from the same batch expressing mutant E166D. The train of 300-ms pulses was delivered to −100 mV (Vhold = −30 mV), where a current of ~2 μA was measured. No significant pH change could be detected in >10 oocytes with large expression of E166D, whereas a pH change was robustly detected in all CLC-5–expressing oocytes.
E166D has drastic effects on gating. E166D slows down opening at positive potentials (Traverso et al., 2003), increases the rate of closure to negative potentials, and has a very low open probability at physiological pH and voltages <100 mV. Our first aim was to understand whether this drastically different gating of E166D (and E166A) was due to a specific alteration of the fast gate or of the slow gate. From the published single channel data of the mutant E166A (Dutzler et al., 2003; Traverso et al., 2003) it was clear that the fast gating transitions were abolished in the mutant E166A. However, no single channel data were available for E166D. Interestingly, we found here that both mutations (E166A and E166D) appear to lock the slow gate in an open state, similar to the C212S mutation (Lin et al., 1999). Slow-gate closing was partially recovered in tandem heterodimers containing one mutant and one WT subunit. The mechanism of the slow gate and its relationship with the fast gate, however, remain an enigma.

Based on single-channel analysis of dimeric constructs containing one WT and one mutant subunit, we could definitely conclude that in addition to their effect on the slow gate, both mutants strongly alter the fast gate. E166A strongly increases the open probability and renders it insensitive to voltage and chloride concentration, whereas E166D strongly reduces $p_{open}$. An effect of these mutations on the fast gate might seem almost trivial since the glutamate side chain is directly “occluding” the individual “protopores” in the WT CLC-ec1 structure (Dutzler et al., 2002). However, mutating only one amino acid upstream of E166 in CLC-0, namely K165 into arginine, a mutation that leads to a strong inwardly rectifying phenotype (Ludewig et al., 1997), drastically affects mainly the slow gate, rendering it much faster in a manner that the overall macroscopic gating relaxations are reflecting mostly slow gate transitions (unpublished data), with little direct effect on the fast gate.

In addition, the dimeric ED-WT (and WT-ED) constructs allowed us to determine the absolute open probability of the fast gate of the ED pore. This was not possible using nonstationary noise analysis, because this method fails if the $p_{open}$ is significantly smaller than 0.5. It turned out that at 80 mV the fast gate of E166D pores has a $p_{open}$ of <0.01, whereas WT CLC-0 has a maximal $p_{open}$ of 1 at this voltage. It would have been practically almost impossible to determine such a low $p_{open}$ using direct single channel recording of ED homomers because of the difficulty in determining the number of channels if each has a low $p_{open}$ (Colquhoun and Hawkes, 1990).

Having established that the E166A and E166D mutations affect the fast gate, we next investigated the fast gate modification of E166D by pH$_{int}$ and pH$_{ext}$. The fast gate of WT CLC-0 is known to be affected by pH but in a qualitatively different manner by pH$_{int}$ and pH$_{ext}$. Changing pH$_{int}$ mainly “shifts” the activation curve (Hanke and Miller, 1983), whereas lowering pH$_{ext}$ mainly increases the “residual” $p_{open}$ at negative voltages (Chen and Chen, 2001). The differential effect of internal and external pH on the open probability is related to the two possible routes by which the fast gate of CLC-0 can open (Chen and Miller, 1996). The opening rate constant shows a biphasic voltage dependence, rising both at negative as well as at positive voltages (Chen and Miller, 1996; Chen and Chen, 2001), however with different voltage dependencies. Extracellular protons increase the rate of opening favored at negative voltages and have no effect on the closing rate, whereas intracellular protons mostly seem to affect the closing rate (Hanke and Miller, 1983; Chen and Chen, 2001).

The molecular acceptor for intracellular protons is unknown. In contrast, it is believed that the increase of $p_{open}$ of WT CLC-0 at low pH$_{ext}$ is caused by a protonation of E166 and a consequent “unblocking” of the external Cl$^-$ site, $S_{ext}$ (Dutzler et al., 2003). Therefore, since $p_{open}$ of the mutant E166D is so low we expected that decreasing pH$_{ext}$ would dramatically increase currents over the whole voltage range by protonation of Asp166. Surprisingly, practically the only effect of lowering pH$_{ext}$ was to increase the persistent current at negative voltages. Qualitatively, the effect of reducing pH$_{ext}$ in WT CLC-0 and mutant E166D seems to be nevertheless very similar: steady inward currents are increased, whereas the “voltage-dependent part” of the $p_{open}$–voltage relationship is only slightly affected. There is, however, a significant difference. In WT CLC-0, single channel events that reflect the “persistent” conductance at negative voltages have the same conductance as the single channel events seen at more positive voltages. In contrast, in mutant E166D the persistent current is carried by a different, lower-conductance, open state. Several possibilities exist to explain this behavior. First, the persistent current of E166D could be mechanistically different from that in WT CLC-0. Even though we are not able to exclude this possibility, the similar pH$_{ext}$ dependence and the relative voltage insensitivity suggest that these phenomena reflect the same molecular mechanism, i.e., opening of the channel by protonation of E166/D166 from the extracellular side. The major difficulty with this interpretation is that the conductance of this state in mutant E166D is ~10-fold smaller than the depolarization-induced open state.

Lowering pH$_{int}$ dramatically increased currents carried by E166D. For pH$_{int}$ values >5 we could describe the activation by a shift of the $p_{open}$–V curve along the voltage axis. At more acidic pH$_{int}$ (pH < 5), a qualitatively new behavior appeared that was not followed further in detail. In particular, at very acidic pH$_{int}$ inward
“tail” currents became very small, despite the large outward currents. Future studies are needed to characterize this interesting phenotype in more detail.

For pH$_{int}$ > 5, the mechanism of action of intracellular protons seems to be similar to that of WT CLC-0, i.e., lowering pH$_{int}$ “shifts” the p$_{open}$ (V) curve to more negative voltages. In contrast to WT CLC-0 the voltage of half-maximal activation was very positive (+74 mV) even at the lowest pH for which we were able to perform a Boltzmann analysis (5.3). Activation saturated at voltages ≥200 mV and pH$_{int}$ = 5.8, even if it is not entirely clear if the open probability approaches unity under these conditions. Assuming a saturating p$_{open}$ of 1 it is clear that the open probability was actually below unity, meaning that the value of 0.95% is an overestimation of the true open probability.

Hanke and Miller (1983) described the effect of pH$_{int}$ on CLC-0 with a four-state model

\[
\begin{align*}
\text{C} & \xrightarrow{\alpha} \text{O} \\
K_C & \quad \text{O} \\
\text{C}_H & \xrightarrow{\beta} \text{O}_H
\end{align*}
\]

(Model 1)

in which unprotonated channels open and close with rate constants $\alpha$ and $\beta$, respectively, whereas protonated channels open and close with rate constants $\alpha_H$ and $\beta_H$, respectively. In the model, protonation of closed and open states occurs with binding constants $K_C$ and $K_O$, respectively. Protonation favors opening if $\alpha_H/\beta_H > \alpha/\beta$. Assuming microscopic reversibility, Model 1 predicts the following dependence of the open probability on [H] = [H]$_{int}$:

\[
p_{open} = p_O + p_{OH} = \frac{[H]/K_O}{1 + \beta/\alpha + [H]/K_O + [H]/K_O \cdot \beta_H/\alpha_H}.
\]

Hanke and Miller (1983) concluded that most of the voltage dependence of opening should be attributed to the rate constants $\alpha$ and $\beta$ (and $\alpha_H$ and $\beta_H$), whereas protonation and deprotonation, characterized by the constants $K_O$ and $K_C$, was deduced to be almost voltage independent. The dependence of the voltage of half-maximal activation, $V_{1/2}$, on pH$_{int}$ was thus described by the equation

\[
V_{1/2} = \frac{RT}{zF} \ln \left( \frac{K_1(0)(1 + [H]/K_O)}{1 + [H]/K_C} \right).
\]

where $z$ is the apparent gating valence that describes the steepness of the voltage dependence of the open probability (Eq. 18 in Hanke and Miller, 1983). For the Torpedo channel, Hanke and Miller obtained a value for $z \sim 1$ (Hanke and Miller, 1983), whereas for E166D we found a slightly smaller value of $z \sim 0.74$ (Fig. 8, legend). $K_1(0)$ is the value of $\alpha/\beta$ at 0 mV. Eq. 5 predicts that $V_{1/2}$ levels off at low [H] and high [H] at values $-RT/zF \ln(K_1(0))$ and $-RT/zF \ln(K_1[0]*K_C/K_O)$, respectively. In contrast to this prediction of the model of Hanke and Miller (1983), no clear saturation of the $V_{1/2}$ values is seen for E166D at either low or high pH values (Fig. 8 B). Indeed, the data shown in Fig. 8 B can only be well fitted by Eq. 5 if the parameter $z$ is adjusted to a value of 0.59, significantly smaller than the steepness of the $p_{open}(V)$ curve at pH 5.3 and pH 5.8 (dashed line in Fig. 8 B). Furthermore, the fit predicts that the pK of the hypothetical proton-accepting group must change from 12.2 in the closed state to 5.3 in the open state, a change by 7 log units. Such a huge change of pK is rather unlikely. A more consistent description of our data can be obtained if, in disagreement with the conclusion of Hanke and Miller (1983) it is assumed that the protonation/deprotonation reaction carries most of the voltage dependence, whereas the “conformational” rates $\alpha$ and $\beta$ are less voltage dependent. Our data are not detailed enough to allow a precise determination of an exact model. We will thus consider only a simplified model in which opening occurs only for protonated channels. This simplification appears to be justified by the finding that the open probability of E166D in the absence of protons is extremely small.

\[
\begin{align*}
\text{C} & \xrightarrow{\alpha} \text{O} \\
K_C & \quad \text{O} \\
\text{C}_H & \xrightarrow{\beta} \text{O}_H
\end{align*}
\]

(Model 2)

Assuming that $\alpha_H$ and $\beta_H$ are voltage independent, and that instead the protonation constant $K_C$ depends exponentially on voltage

\[
K_C = K_C(0) \exp(-zVF/RT),
\]

Model 2 predicts

\[
\begin{align*}
p_{open} &= \frac{1}{1 + \beta_H/\alpha_H + \beta_H/\alpha_H \cdot K_C/[H]} = \\
&= \frac{\alpha_H}{\alpha_H + \beta_H \cdot \exp \left( \frac{z(V_{1/2} - V)F}{RT} \right)}
\]

Traverso et al. 63
with

\[ V_{1/2} = \frac{RT}{zF} \ln \left( \frac{\beta_H}{\alpha_H + \beta_H [H]} \right) \]

(8)

and if \( \beta_H/\alpha_H << 1 \), the open probability follows practically a Boltzmann distribution. Most importantly, Eq. 8 predicts that the voltage of half maximal activation depends linearly on pH. This is indeed found for the mutant E166D (Fig. 8 B), and seems also to be an appropriate description of the data reported for CLC-0 (see Fig. 5 in Hanke and Miller, 1983). The argument Hanke and Miller used to conclude that protonation/deprotonation is voltage independent was that the apparent gating valence of the Boltzmann distribution describing the voltage dependence of \( p_{\text{open}} \) was independent of pH. However, also Eq. 7 predicts a constant gating valence even though the voltage dependence arises exclusively from protonation/deprotonation. Thus, also the data of Hanke and Miller (1983) may allow the alternative interpretation proposed here that at least part of the voltage dependence lies in the protonation step.

We found a change of \( V_{1/2} \) of \( \sim 81 \) mV per pH unit (see solid line in Fig. 8 B) corresponding to a voltage dependence of \( \sim 0.71 \) elementary charges in Eq. 6, in good agreement with the observed steepness of the voltage dependence of the \( p_{\text{open}}(V) \) curves (\( z \sim 0.74; \) Fig. 8, legend). In this simple model the steepness of the voltage dependence of the activation curve reflects mainly the voltage dependence of the protonation from the intracellular side.

The quantitative conclusions from the above considerations are limited by (at least two) factors. First, the data obtained for E166D are not ideal because the \( p_{\text{open}}(V) \) curve does not saturate for the two more alkaline pH values shown in Fig. 8 B. Thus, the \( V_{1/2} \) values for pH 7.2 and pH 6.8 shown in Fig. 8 B are relatively rough estimates. Unfortunately at more acidic pH values, for which better defined \( V_{1/2} \) values might be expected to be definable, a qualitative new behavior of the mutant emerged, rendering impossible an analysis in terms of the usual open probability. Second, the Model 2 is certainly an oversimplification because the contribution of chloride ions to the voltage dependence of gating is completely neglected. Furthermore, the model does not consider the effect of extracellular protons on the open probability. Despite all these uncertainties, we believe that the idea that one of the major sources of voltage dependence of the gating of CLC-0 arises from a protonation step from the intracellular side is a viable hypothesis. The simple Model 2 assumes protonation directly from the intracellular solution. This seems to be unrealistic, however, if the target of protonation is the residue at position 166. In fact, it is more likely that protonation involves several interme-

Collectively, from our detailed analysis of the conservative mutant E166D, two principal speculations are suggested. First, a major voltage-dependent step of the activation of the fast gate results from a voltage-dependent protonation from the intracellular side. Second, and even more speculatively, protonation of the acidic residue at position 166 (E or D) from the outside and protonation from the inside leads to different open states that have a different single-channel conductance in mutant E166D. In WT CLC-0 these two open states have either a similar conductance or they immediately collapse into a common open state. In contrast, in the mutant E166D the two open states are clearly distinct and not simply interconvertible. In this respect it is noteworthy that a recent theoretical study proposed that the side chain of E166 can adopt an inwardly directed conformation, one that may be susceptible for accepting intracellular protons (Bisset et al., 2005). It will also be highly interesting to study the functional and structural effect of mutating the corresponding glutamate residue to aspartate in the bacterial CLC-ec1. The continuous feedback between functional and structural data will undoubtedly provide an ever better understanding of this unique class of ion channels and transporters.

We thank Laura Elia for expert technical assistance, Alessandra Picollo, and Elena Babini for suggestions on the manuscript, Giacomo Gaggero for help in constructing the perfusion system, and Enrico and Giacomo Gaggero for constructing the high impedance amplifier.

The financial support by Telethon Italy (grant GGP04018) and the Italian Research Ministry (FIRB RBAU01P1MS) is gratefully acknowledged. S. Traverso received a Consiglio Nazionale delle Ricerche doctoral fellowship.

David C. Gadsby served as editor.

Submitted: 31 May 2005
Accepted: 9 December 2005

REFERENCES


Bisset, D., B. Corry, and S.H. Chung. 2005. The fast gating mecha-


