Chloride channelopathy in myotonic dystrophy resulting from loss of posttranscriptional regulation for CLCN1

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Transmembrane chloride ion conductance in skeletal muscle increases during early postnatal development. A transgenic mouse model of myotonic dystrophy type 1 (DM1) displays decreased sarcosomal chloride conductance. Both effects result from modulation of chloride channel 1 (CLCN1) expression, but the respective contributions of transcriptional vs. posttranscriptional regulation are unknown. Here we show that alternative splicing of CLCN1 undergoes a physiological splicing transition during the first 3 wk of postnatal life in mice. During this interval, there is a switch to production of CLCN1 splice products having an intact reading frame, an upregulation of CLCN1 mRNA encoding full-length channel protein, and an increase of CLCN1 function, as determined by patch-clamp analysis of single muscle fibers. In a transgenic mouse model of DM1, however, the splicing transition does not occur. CLCN1 channel function remains low throughout the postnatal interval, and muscle fibers display myotonic discharges. Thus alternative splicing is a posttranscriptional mechanism regulating chloride conductance during muscle development, and the chloride channelopathy in a transgenic mouse model of DM1 results from a failure to execute a splicing transition for CLCN1.

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**CHLORIDE CHANNELOPATHY IN MYOTONIC DYSTROPHY**

**MATERIALS AND METHODS**

*Mouse strains and muscle samples.* HSA	extsuperscript{LR} transgenic mice express human skeletal actin mRNA with ~250 CUG repeats inserted in the 3'-untranslated region (27). HSA	extsuperscript{SR} transgenic mice express skeletal actin with insertion of 5 CUG repeats at the same position. These mice were maintained on an inbred FVB strain background. The HSA	extsuperscript{LR} mice in these experiments were homozygotes from line HSA1KR20b. adr-mto2J mice (CLCN1 null mutant strain) were obtained from Jackson Laboratories (Bar Harbor, MA). Gastrocnemius muscle from mdx mice and wild-type (WT) controls was obtained from Dr. Paula Clemens (University of Pittsburgh, PA). Gastrocnemius muscle from mice with sodium channel myotonia due to a targeted mutation in SCN4a (SCN4a	extsuperscript{M1952V}) (19) and WT littersmates was obtained from Dr. Stephen Cannon (University of Texas, Southwestern, Dallas, TX). Total cellular RNA was isolated from hindlimb muscle using TRI Reagent (Molecular Research, Cincinnati, OH). Surgical denervation of hindlimb muscle was performed under general anesthesia by removing a 4-mm section of the sciatic nerve exposed in the sciatic notch. General anesthesia was induced by intraperitoneal injection of ketamine (100 mg/kg), xylazine (10 mg/kg), and acepromazine (3 mg/kg). Mice were euthanized 4 and 8 days after the procedure. RNA was isolated from gastrocnemius muscle of the denervated and non-denervated hindlimb from each animal. All procedures were approved by the University of Rochester Committee on Animal Research.

**CLCN1 splicing and expression analysis.** To test for alternative splicing, mouse CLCN1 cDNAs extending from the first to the final exon (exons 1–23, nt 1–2671, accession no. AY046403) were amplified by RT-PCR, cloned in pBSK, and sequenced as described (28). Assays for alternative splicing of CLCN1 exon 7a were performed by RT-PCR as described (28). In brief, CLCN1 cDNA was amplified using primers in exons 5 and 8. PCR was performed within the exponential range of amplification. RT-PCR products were resolved on agarose gels, stained with SybrGreen I, scanned on a fluorimager, and quantified using ImageQuant software. RT-PCR products were resolved on agarose gels, stained with SybrGreen I, and scanned on a laser fluorimeter. Loading of PCR products was normalized for equal intensity of the lowest (nominally spliced) band. The relative abundance of exon 7a inclusion and exclusion products was quantified using ImageQuant software. Results were normalized for increased binding of fluorochrome to larger PCR products. Levels of CLCN1 mRNA were determined by competitive RT-PCR assay using an internal standard that extended from exon 21 to 23 (nt 2323–2595 with an internal deletion) and a protocol that has been described in detail elsewhere (39). The assayed portion of CLCN1 was not involved in alternative splicing. In these assays, all RNA samples were reverse transcribed on the same day with the same RT reaction mixture. Under these conditions, expression levels of specific mRNAs were less variable when normalized by the amount of total RNA in the RT reaction than when normalized by a particular “housekeeping” gene. RT-PCR products were resolved on agarose gels, stained with SybrGreen I, scanned on a fluorimeter, and quantified using ImageQuant software. Levels of CLCN1 pre-mRNA were also determined by competitive RT-PCR assay using an internal standard that extended from the exon 1/intron 1 boundary to exon 2 (accession no. AC153915, nt 98333–98079). The RNA was treated with RNase H before the cDNA synthesis, and control reactions without RT were negative.

**Acute dissociation of skeletal muscle fibers.** Individual skeletal muscle fibers used in whole cell patch clamp studies were isolated from fast-twitch flexor digitorum brevis (FDB) muscles of 9- to 20-day-old FVB and HSA	extsuperscript{LR} mice as described previously (3). Briefly, FDB muscles were excised from the foot in a Ringer solution containing (in mM): 146 NaCl, 5 KCl, 2 CaCl	extsubscript{2}, 1 MgCl	extsubscript{2}, and 10 HEPES, pH 7.4 with NaOH, and then gently shaken for 45 min at 37°C in the presence of 1 mg/ml collagenase (Type 1; Roche Diagnostic, Indianapolis, IN). Individual FDB muscle fibers were subsequently dissociated by triturating, using Pasteur pipettes whose tips had been fire polished to produce openings of successively smaller size. Individual FDB fibers were stored at room temperature in Ringer solution and remained experimentally viable for several hours.

**Macroscopic chloride current recordings.** The whole cell variant of the patch clamp technique (18) was used to monitor the magnitude and voltage dependence of macroscopic chloride currents in individual 9- to 20-day-old FDB fibers. Only healthy FDB fibers exhibiting clear striations and clean surfaces were chosen for electrophysiological recordings. The external recording solution contained (in mM): 145 tetraethylammonium (TEA)-Cl, 10 CaCl	extsubscript{2}, 10 HEPES, and 0.003 nifedipine (pH 7.4). The internal solution contained (in mM): 30 CsCl, 110 CsAsp, 5 MgCl	extsubscript{2}, 10 CsEDTA, and 10 HEPES (pH 7.4). The Nernst potential for chloride (ECl) for these solutions was ~35.8 mV. Recording conditions provided adequate blockade of sodium (0 Na	extsuperscript{+}/depolarized holding potential of ~40 mV), calcium (nifedipine), and potassium (TEA/Cs) channel currents. Muscles were whole cell patch clamped using an Axopatch 200A amplifier (Axon Instruments, Foster City, CA). Patch pipettes were pulled using a Flaming Brown micropipette puller (P97; Sutter Instrument, Novato, CA) and fire polished to obtain electrode resistances of 0.4–1 MΩ. In cell-attached configuration, seal resistances were ≥1 GΩ. After achieving whole cell configuration, the internal solution was dialyzed for 5–10 min before all electrophysiological recordings.

Whole cell currents were measured at room temperature (sampled at 10 kHz and filtered at 2 kHz) in response to 250-ms voltage steps from +60 to ~40 mV (in 10-mV increments) immediately following a 200-ms prepulse to +60 mV (to fully activate CLCN1 channels). Individual test pulses were separated by a 10-s interpulse period at a holding potential of ~40 mV. For all experiments, this protocol was delivered first in the absence and then in the presence of 1 mM 9-anthracene carboxylic acid (9-AC), a blocker of CLCN1 channels (7). Offline subtraction of currents recorded in the presence of 9-AC from those recorded in its absence eliminated residual leak and capacitative currents and resulted in 9-AC-sensitive currents that reflect CLCN1 channel activity. Following block of CLCN1 currents, total cell capacitance (Cm), membrane time constant (τm), and uncompensated access resistance (Ra) were determined by integration of the capacity transient resulting from a 10-mV depolarizing pulse applied from the holding potential. The estimated maximal voltage error (peak Cl current at ~140 mV × Ra) for all experiments averaged ~4 mV and was <10 mV even for the largest currents (Table 1). Current density (pA/pF) was then calculated for each record to enable comparison of data obtained from cells of different sizes. Total cell capacitance increased from postnatal day 9 to day 20 to a similar degree in both WT and HSA	extsuperscript{LR} mice (see Table 1). Only experiments in which seal resistance following addition of 9-AC was ≥100 MΩ were analyzed. Instantaneous current vs. voltage relationship (I–V) plots were fitted according to the following modified Boltzmann function

\[
I(V) = I_{\text{max}} - I_0/[1 + \exp((V_{1/2} - V_n)/K_v)] \times I_0
\]

where \(I_{\text{max}}\) is the maximum current at the test potential \((V_n)\), \(I_0\) is a constant offset, \(V_{1/2}\) is the half-maximal activation voltage, and \(K_v\) is a slope factor.

**RESULTS**

As a first step to examine the role of posttranscriptional controls in regulating CLCN1 during development, we cloned and sequenced CLCN1 cDNAs from hindlimb muscle of WT mice. Results from neonatal mice were compared with those obtained from mature WT mice by the same method (28). Among 23 cDNA clones obtained at postnatal day 2 (P2), 10 (43%) showed alternative splicing. Retention of intron 2 (6 instances, leading to a PTC in the retained intron) and inclusion of exon 7a (5 instances, leading to a PTC in exon 7) were the most frequent events. By comparison, these splicing events
were not observed in 25 clones from 6-mo-old WT mice of the same (FVB) inbred strain. Thus CLCN1 undergoes a transition of alternative splicing during postnatal development.

We used RT-PCR splicing assays to assess the frequency of exon 7a inclusion and determine the time course of the postnatal splicing transition. Similar to previous observations in adult HSA\textsuperscript{LR} transgenic mice (28), in the region from CLCN1 exons 5–8, we found three different alternative splice products in neonatal WT mice, of which the exon 7a inclusion isoform was most abundant (Supplemental Fig. 1; supplemental data are available at the online version of this article). Other variant splice products also included an additional exon cassette, exon 8a, or retention of a portion of intron 6. Because all variant splice products included exon 7a, and they all contained a PTC, they were quantified together as “ex7a\textsuperscript{+} isoforms.” The fraction of CLCN1 mRNA that included exon 7a was 45 ± 0.7% at embryonic day 18 (E18) and subsequently declined, reaching levels at P20 (4 ± 1%) similar to adult muscle (5 ± 2%) (Fig. 1). Levels of intron 2 retention could not be quantified by RT-PCR because of the length of this intron, but qualitative analysis showed a similar decline in the interval between P2 and P20 (data not shown).

To determine whether the CUG\textsuperscript{exp} RNA interfered with developmental regulation of CLCN1 splicing, we assessed inclusion of exon 7a in the postnatal interval in HSA\textsuperscript{LR} transgenic mice. Skeletal actin is expressed by E13.5 in mice (5), and nuclear foci of CUG\textsuperscript{exp} RNA are already prominent in HSA\textsuperscript{LR} mice by P2 (25). The results showed a higher fraction of ex7a\textsuperscript{+} isoforms in HSA\textsuperscript{LR} than WT mice at all postnatal time points, ranging from 45–59% (Fig. 1). By comparison, levels of exon 7a inclusion were not increased in disease controls having dystrophin deficiency (10 ± 5% in adult mdx mice vs. 7 ± 2% in WT controls) or sodium channel myotonia (5 ± 2% in SCN4\textsubscript{a}M1592V knockin mice vs. 7 ± 1% in WT littermates) or in mice that overexpress skeletal actin transcripts with a nonexpanded (CUG\textsubscript{3}) repeat (5 ± 1% in HSA\textsuperscript{SR} transgenic mice). Also, section of the sciatic nerve produced only a slight increase in the frequency of exon 7a inclusion in denervated muscle (10 ± 1% in gastrocnemius on day 4 following section and 10 ± 0.5% on day 8 following section vs. 7 ± 3% in the contralateral nondenervated muscle). These results indicate that HSA\textsuperscript{LR} mice fail to execute the postnatal splicing transition for CLCN1. The effect is a specific response to CUG\textsuperscript{exp} RNA rather than a nonspecific consequence of muscular dystrophy, muscle hyperexcitability, loss of nerve-muscle trophic support, or overexpression of actin.

A previous study suggested that transcription of CLCN1 is reduced in DM1 cells (13). However, these studies were performed in cultured myotubes, in which expression of CLCN1 is 100-fold lower than in mature muscle fibers (2). To address this question in mature muscle fibers, we used quantitative RT-PCR to examine levels of mRNA and pre-mRNA for CLCN1 in HSA\textsuperscript{LR} transgenic mice. Barring an effect on kinetics of RNA processing, the steady-state levels of CLCN1 pre-mRNA should reflect relative rates of CLCN1 transcription. The level of CLCN1 mRNA in HSA\textsuperscript{LR} mice was 44 ± 8% of WT controls (Fig. 2A), similar to the value of 43 ± 15% of WT controls that we previously observed in the same transgenic line by quantitative real-time RT-PCR (28). By contrast, quantitative RT-PCR analysis of the pre-mRNA showed no difference in HSA\textsuperscript{LR} transgenic mice compared with WT controls (Fig. 2A). These results argue that the effects of CUG\textsuperscript{exp} RNA on CLCN1 expression are predominantly posttranscriptional.

Relative to their fractional synthetic rate, ex7a\textsuperscript{+} isoforms would be underrepresented at steady state if they undergo accelerated degradation through the nonsense-mediated decay (NMD) pathway. However, the efficiency of NMD varies among genes (reviewed by Maquat, Ref. 29), and some transcripts containing PTCs may escape this mechanism of surveillance. To examine the effects of PTCs on metabolism of CLCN1 mRNA, we identified mice having a PTC in the CLCN1 gene. ad\textsubscript{mdx} 25 mice display severe recessive myotonia resulting from a spontaneous mutation in the BALB inbred strain. Previously, we found a complete absence of immunoreactive CLCN1 protein in these mice using antibodies directed

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Table 1. Linear properties and estimated maximal voltage error

<table>
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<tr>
<th></th>
<th>n</th>
<th>C\textsubscript{m} (\text{pF})</th>
<th>(\tau\text{m} (\text{s})</th>
<th>R\text{m} (\text{M}\Omega)</th>
<th>Peak (I\text{cl} (\text{pA})</th>
<th>Estimated Maximal Voltage Error (\text{mV})</th>
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<tr>
<td>WT day 9</td>
<td>9</td>
<td>320 ± 33</td>
<td>77 ± 13</td>
<td>0.27 ± 0.07</td>
<td>−8.459 ± 1.142</td>
<td>2.0 ± 0.3</td>
</tr>
<tr>
<td>HSA\textsuperscript{LR} day 9</td>
<td>6</td>
<td>267 ± 20</td>
<td>48 ± 5</td>
<td>0.18 ± 0.02</td>
<td>−9.15 ± 0.262</td>
<td>0.2 ± 0.0</td>
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<tr>
<td>WT day 13</td>
<td>4</td>
<td>368 ± 15</td>
<td>255 ± 53</td>
<td>0.68 ± 0.12</td>
<td>−9.355 ± 1.064</td>
<td>6.3 ± 1.3</td>
</tr>
<tr>
<td>HSA\textsuperscript{LR} day 13</td>
<td>11</td>
<td>332 ± 23</td>
<td>117 ± 18</td>
<td>0.37 ± 0.06</td>
<td>−2.099 ± 0.556</td>
<td>0.8 ± 0.2</td>
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<td>WT days 18 and 19</td>
<td>9</td>
<td>660 ± 77</td>
<td>199 ± 41</td>
<td>0.34 ± 0.08</td>
<td>−30.951 ± 3.956</td>
<td>9.3 ± 1.8</td>
</tr>
<tr>
<td>HSA\textsuperscript{LR} days 18 and 19</td>
<td>29</td>
<td>665 ± 19</td>
<td>302 ± 19</td>
<td>0.46 ± 0.03</td>
<td>−11.975 ± 5.129</td>
<td>4.1 ± 0.7</td>
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Values are means ± SE. Average total cell capacitance (C\text{m}), membrane time constant (\(\tau\text{m}\)), uncompensated access resistance (R\text{m}), peak chloride current magnitude (peak \(I\text{cl}\)), and estimated maximum voltage error (peak current \(\times\) R\text{m}) for the no. (n) of experiments shown.
against the carboxyl terminus (28). To identify the mutation, we derived CLCN1 cDNA clones from homozygous adr<sup>pto2J</sup> mice. Sequence analysis showed a single nucleotide deletion in exon 18 at position 2269 (accession no. NM_013491), the only mutation in the coding region. The C2269del→ufs 782X mutation, which caused a frame shift and premature termination codon in exon 19 (of 23 total exons), was confirmed by sequencing genomic DNA. Because this mutation had no effect on splicing of exon 18 or 19 (data not shown), it was unlikely to directly affect splicing at exon 7a.

Several effects on CLCN1 mRNA accumulation would be expected if CLCN1 transcripts containing a PTC are subject to NMD. First, the level of CLCN1 mRNA should be reduced in homozygous adr<sup>pto2J</sup> mice. Second, the fraction of ex7a<sup>+</sup> transcripts should be increased in homozygous adr<sup>pto2J</sup> mice, because all CLCN1 transcripts in these mice contain a frame shift mutation and would be similarly subject to NMD. Third, the level of CLCN1 mRNA in WT mice should increase during postnatal development, as a result of the transition to splice products that encode full-length CLCN1 protein.

To test these predictions, we used quantitative RT-PCR to compare CLCN1 RNA in homozygous adr<sup>pto2J</sup> mice and WT littermates. In accordance with the first prediction, the level of CLCN1 mRNA in adr<sup>pto2J</sup> mice was reduced to 30 ± 3% of WT littermates, indicating that a PTC in exon 19 elicits an ~70% reduction in the half-life of CLCN1 mRNA. This effect was comparable to that observed for other PTC-containing transcripts (29, 33). By comparison, the level of CLCN1 pre-mRNA in adr<sup>pto2J</sup> mice was unchanged (Fig. 2B), which indicates that reduction of the mRNA results from accelerated decay, and that loss of channel function did not induce compensatory upregulation of CLCN1 transcription.

Next, we examined the fraction of ex7a<sup>+</sup> mRNA in homozygous adr<sup>pto2J</sup> mice. In accordance with the second prediction, the fraction of ex7a<sup>+</sup> CLCN1 was increased throughout postnatal development in adr<sup>pto2J</sup> mice relative to WT littermates (Fig. 3; representative gel is shown in online Supplemental Fig. 2). This finding argues that ex7a<sup>+</sup> isoforms are normally subject to NMD, so that placement of a second PTC in a downstream exon caused no additional shortening of their half-life. Because the PTC in ex7a<sup>+</sup> mRNA is at codon 290, it is noteworthy that a point mutation in human CLCN1 causing premature termination at codon 289 also led to marked reduction of CLCN1 mRNA (31).

In accordance with the third prediction, the transition to ex7a-skipped CLCN1 during postnatal development was associated with a threefold rise of CLCN1 mRNA in WT mice (Fig. 4).

The data presented in Figs. 1–4 indicate that levels and splicing of CLCN1 mRNA are regulated during postnatal development and misregulated in response to CUG<sup>esp</sup> RNA. However, alterations in relative mRNA levels may not accurately reflect channel function. In addition, although truncated CLCN1 proteins resulting from aberrantly spliced transcripts do not function alone as chloride channels, they could potentially interfere with residual WT proteins to form dimers having altered function (4). To test these possibilities, we characterized CLCN1 function during postnatal maturation in WT and <i>HSA</i><sup>LR</sup> mice (Fig. 5). For these experiments, whole cell patch clamp recordings were made from individual FDB skeletal muscle fibers dissociated from 9- to 20-day-old FVB and <i>HSA</i><sup>LR</sup> mice. Figure 5, A–C, shows representative macroscopic recordings of raw (Fig. 5A), 9-AC-insensitive (Fig. 5B), and 9-AC-sensitive (Fig. 5C) currents in a FDB fiber of a 19-day-old <i>HSA</i><sup>LR</sup> mouse are shown for comparison in Fig. 5D. For these experiments, identical voltage protocols were used for recording raw and 9-AC-blocked currents. Test potentials were applied to voltages between 60

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**Fig. 2.** Levels of CLCN1 mRNA and pre-mRNA determined by quantitative RT-PCR. In <i>HSA</i><sup>LR</sup> transgenic mice (A) and CLCN1 null mutant mice (B), levels of CLCN1 pre-mRNA are similar to WT controls of the same age and background strain (FVB or BALB) (means ± SD, 4–6 replicates). By comparison, total levels of CLCN1 mRNA are reduced in both <i>HSA</i><sup>LR</sup> (A) and CLCN1 null mice (B) relative to WT control mice (<i>P</i> < 0.01).

**Fig. 3.** ex7a<sup>+</sup> splice products accumulate to higher levels in homozygous adr<sup>pto2J</sup> mice (CLCN1<sup>−/−</sup>) compared with WT littermates (CLCN1<sup>+/+</sup>). Because of a frame shift mutation in <i>CLCN1</i>, all CLCN1 transcripts in adr<sup>pto2J</sup> homozygotes, irrespective of exon 7a skipping or inclusion, contain a premature termination codon and are potentially subject to nonsense-mediated decay. Values for %ex7a<sup>+</sup> splice products in homozygous adr<sup>+</sup> mice were as follows: P2, 53 ± 4%; P10, 39 ± 0.1%; and P20, 22 ± 0.7%. Values in WT littermates were as follows: P2, 29 ± 0.7%; P10, 11 ± 0.2%; and P20, 5.5 ± 1% (means ± SD of triplicate assays) (see Supplemental Fig. 2 for gel showing one set of replicates).

**Fig. 4.** Total levels of CLCN1 mRNA in hindlimb muscle increase during postnatal development in WT mice. CLCN1 mRNA levels were determined by quantitative RT-PCR and expressed as a percentage of the normal level at age 6 mo (means ± SD of triplicate assays).
and −140 mV following a 60-mV prepulse used to fully activate CLCN1 channels. Similar to that observed for heterologously expressed CLCN1 channels (35), macroscopic 9-AC-sensitive currents recorded from individual WT FDB fibers exhibit several hallmarks of CLCN1 currents. First, these currents were completely blocked by 0.1–1 mM 9-AC, a potent CLCN1 antagonist. Second, deactivation kinetics of 9-AC-sensitive currents recorded from individual WT FDB fibers exhibited several hallmarks of CLCN1 currents. First, these 9-AC-sensitive currents recorded from individual WT FDB fibers isolated from a 19-day-old WT mouse. Representative whole cell raw (A), 9-anthracene carboxylic acid (9-AC)-blocked (B), and 9-AC-sensitive (raw − 9-AC blocked; C) CLCN1 currents recorded from a FDB fiber isolated from a 19-day-old WT mouse. D: representative macroscopic 9-AC-sensitive CLCN1 currents recorded from a FDB fiber isolated from a 19-day-old HSA<sup>LR</sup> mouse. A–D: dotted lines represent the zero current level. C, inset: capacitative current recorded from the 19-day-old WT FDB fiber following blockade with 1 mM 9-AC (scale = 3 nA, 4 ms). The time constant of capacitative current relaxation (τ<sub>m</sub> = 435 μs) is well described by a first-order exponential fit to the current decay [thick continuous line: total cell capacitance (C<sub>m</sub>) = 592 pF, uncompensated access resistance (R<sub>a</sub>) = 0.64 MΩ]. Similar values were obtained for the experiment shown in B (C<sub>m</sub> = 592 pF, R<sub>a</sub> = 0.81 MΩ, τ<sub>m</sub> = 480 μs). E: average (±S.E) instantaneous CLCN1 current–voltage relationship for FDB fibers obtained from 18- to 20-day-old WT (solid circles, n = 12) and HSA<sup>LR</sup> mice (open circles, n = 29). F: average (±S.E) peak CLCN1 current density (measured at −140 mV) for FDB fibers obtained from 9- to 20-day-old WT (solid circles) and HSA<sup>LR</sup> mice (open circles). No. of experiments is shown in parentheses. V<sub>m</sub>, test potential; I<sub>cl</sub>, chloride current magnitude.

Figure 5E depicts the mean instantaneous I–V relationship for 9-AC-sensitive CLCN1 currents observed for FDB fibers obtained from 18- to 20-day-old WT (n = 12) and HSA<sup>LR</sup> (n = 29) mice. These data demonstrate that FDB fibers from HSA<sup>LR</sup> mice exhibit a profound reduction in CLCN1 current density at all voltages. Specifically, instantaneous CLCN1 current density measured at −140 mV was reduced ~71% in 18- to 20-day-old HSA<sup>LR</sup> fibers (WT, −48.50 ± 3.59 pA/pF; HSA<sup>LR</sup>, −13.97 ± 1.62 pA/pF), and EMG recordings from hindlimb muscle at this age demonstrated robust myotonic discharges (not shown). HSA<sup>LR</sup> fibers exhibited a similar relative reduction in CLCN1 current density compared with age-matched control WT fibers at each postnatal age studied (Fig. 5F). Moreover, relative CLCN1 current density actually increased in parallel for both WT and HSA<sup>LR</sup> fibers during this developmental period.

DISCUSSION

Results of the present study are consistent with a developmental mechanism in which CLCN1 is regulated by transcriptional and posttranscriptional controls. Levels of CLCN1 mRNA increase ~10<sup>3</sup>-fold in the transition from myoblasts to mature muscle (2). However, CLCN1 transcripts in late fetal and neonatal muscle are mainly reeled by alternative splicing to a “discard” pathway. These splice products contain PTCs, they undergo accelerated decay, and they encode truncated proteins that do not form functional chloride channels. During postnatal development, the transition to splice isoforms encoding full-length channel protein is associated with greater stability and accumulation of CLCN1 mRNA and increased Cl⁻ channel activity. Developmental regulation of CLCN1, therefore, is an example of regulated unproductive splicing and translation, or RUST (24). Bioinformatic analysis suggested that RUST was a common mechanism for regulating mammalian gene expression and that >1,000 human genes were candidates for posttranscriptional regulation in this manner (17, 24). However, global analysis using exon junction microarrays failed to confirm widespread coupling of alternative splicing to NMD (34), and physiological regulation by RUST has been clearly shown for only a small number of genes (23, 41). Our study is the first to show developmental regulation of a mammalian ion channel by this mechanism.

On the basis of observations in muscle cell cultures, Ebralidze et al. (13) proposed that decreased CLCN1 expression in DM1 resulted from sequestration of transcription factors Sp1 and retinoic acid receptor-γ (RARγ) in nuclear foci of CUG<sup>exp</sup> RNA, leading to reduced transcription of the CLCN1 gene. However, our findings argue against this mechanism for CUG<sup>exp</sup>-induced chloride channelopathy in muscle fibers. First, the level of CLCN1 pre-mRNA in the HSA<sup>LR</sup> transgenic mouse model was not reduced (Fig. 2A), indicating that expression of CUG<sup>exp</sup> RNA did not inhibit CLCN1 transcription. Second, by combining fluorescence in situ hybridization for CUG<sup>exp</sup> RNA with immunofluorescence for nuclear proteins, a method that clearly visualized recruitment of RNA binding proteins into ribonuclear foci, we saw no recruitment of Sp1 or RARγ into nuclear foci in DM1 cortical neurons (20) or muscle fibers (H. Jiang and C. A. Thornton, unpublished observation). Third, ablation of MBNL1, a factor that regulates splicing but that is not known to regulate transcription, repro-
duced the effects of DM1 on CLCN1 expression and muscle excitability (21, 25). Finally, the results of the present study indicate that effects on alternative splicing, when coupled with accelerated decay of ex7a+ splice products, can explain the modest reduction of CLCN1 mRNA observed in HSA1LR mice and DM1 patients, without needing to invoke an independent effect on transcription. Taken together, these results indicate that CUG.exp RNA evokes myotonia by compromising the posttranscriptional component of CLCN1 control. Moreover, the loss of postnatal splicing transition for CLCN1 is similar to that observed for other DM1 target transcripts (25), except that CLCN1 is currently the only such transition in which alternative splicing is coupled with NMD. At present, these effects on CLCN1 provide the clearest evidence that symptoms of DM1 can result directly from effects on splicing regulation.

CLCN1 accounts for >90% of the resting Cl conductance in skeletal muscle (10). Several lines of evidence, including experiments with Cl channel blockers, replacement of chloride by impermeant ions, observations in heterozygous carriers of mutations in CLCN1 (15). While the failure to execute the splicing switch is executed properly during postnatal development but that later it reverts to the immature pattern of splicing. Alternatively, factors other than CLCN1 splicing may condition the onset of myotonia in human DM1 (32, 36).

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REFERENCES