Abnormal Distribution of Calcium-Handling Proteins: A Novel Distinctive Marker in Core Myopathies

Muriel Herasse, PhD, Karine Parain, MSc, Isabelle Marty, PhD, Nicole Monnier, PhD, Angela M. Kaindl, MD, Jean-Paul Leroy, MD, Pascale Richard, PhD, Jöel Lunardi, PhD, Norma B. Romero, MD, PhD, and Ana Ferreiro, MD, PhD

Abstract

Central core disease (CCD) and multi-minicore disease (MmD) are muscle disorders characterized by foci of mitochondria depletion and sarcomere disorganization (“cores”) in muscle fibers. Although core myopathies are the most frequent congenital myopathies, their pathogenesis remains elusive and specific diagnostic markers are lacking. Core myopathies are mostly caused by mutations in 2 sarcoplasmic reticulum proteins: the Ca$^{2+}$-release channel RyR1 or the selenoprotein N (SelN) of unknown function. To search for distinctive markers and to obtain further pathophysiological insight, we identified the molecular defects in 12 core myopathy patients and analyzed the immunolocalization of 6 proteins of the Ca$^{2+}$-release complex in their muscle biopsies. In 7 cases with RyR1 mutations (6 CCD, one MmD), RyR1 was depleted from the cores; in contrast, the other proteins of the sarcoplasmic reticulum (calsequestrin, SERCA1/2, and triadin) and the T-tubule (dihydropyridine receptor-$\alpha$,subunit) accumulated within or around the lesions, suggesting an original modification of the Ca$^{2+}$-release complex protein arrangement. Conversely, all Ca$^{2+}$-related proteins were distributed normally in 5 MmD cases with SelN mutations. Our results provide an appropriate tool to orientate the differential and molecular diagnosis of core myopathies and suggest that different pathophysiological mechanisms lead to core formation in SelN- and in RyR1-related core myopathies.

Key Words: Calcium-release proteins, Core myopathies, RyR1, SelN.

INTRODUCTION

Core myopathies (CM) are the most prevalent congenital myopathies (1). They manifest clinically with early-onset muscle weakness and are defined by characteristic histopathologic changes of the muscle fiber structure, termed “cores.” Core lesions are localized areas of mitochondria depletion and sarcomere disorganization. Their presence in muscle fibers characterizes 2 congenital myopathies: central core disease (CCD) (2) and multi-minicore disease (MmD) (3).

Classically, CCD and MmD were considered independent entities. CCD was defined as an autosomal-dominant disorder characterized by central, well-delimited cores spanning the entire fiber length. Most CCD cases carry heterozygous mutations of the ryanodine receptor type 1 gene (RyR1) (4–6). In contrast, MmD is an autosomal-recessive disorder whose hallmarks are multiple, poorly defined cores that spread only a few sarcomeres in the longitudinal fiber axis. Four different clinical phenotypes have been distinguished in MmD (7, 8). The most prevalent one, termed “classical MmD,” is associated in most but not all cases with mutations in the selenoprotein N gene (SEPN1) (9–11).

Despite these classic differences between CCD and MmD, recent progress in the molecular characterization of CM has disclosed an unexpected overlap between both disorders. In RyR1-related CCD, the spectrum of morphologic manifestations can be highly pleomorphic, including multiple cores (5) or presence of only minicores (12, 13). Besides, homozygous or compound heterozygous RyR1 defects are responsible for 2 MmD forms (moderate MmD and MmD with ophthalmoplegia) (12, 14–16). In some of these cases, an age-related evolution of the morphologic lesions, from minicores to cores, has been observed (14, 17). Additionally, other known or unknown genes can be more rarely involved in CM (18); RyR1 and/or SEPN1 implication has been excluded in a number of patients, and mutations of the ACTA1 gene have been identified in 2 families with a dominant CM (19).

Therefore, establishing a precise diagnosis in CM is frequently challenging, particularly in young and/or sporadic cases. These difficulties are exacerbated by the lack of specific morphologic markers that could help selecting the most appropriate genetic test (20). The massive size of RyR1...
(160 kb, 106 exons) (21) precludes systematic whole-gene screen. Consequently, many CM cases remain molecularly undefined, which prevents genetic counseling and accurate assessment of their risks regarding respiratory failure and orthopedic complications.

This lack of diagnostic markers relates to our incomplete understanding of the pathophysiology of CM. *RYR1* encodes the skeletal muscle isoform of a sarcoplasmic reticulum (SR) channel (RyR1), which mediates Ca$^{2+}$ release during excitation–contraction coupling (E-C coupling) and interacts with other proteins to form the triadic junction (Fig. 1). Yet, the pathophysiological consequences of *RYR1* mutations remain controversial (22). Moreover, selenoprotein N (SelN) function is unknown (23). SelN contains a potential Ca$^{2+}$ binding domain (EF-hand) and, like RyR1, is localized in the SR membrane and associated with core lesions. These common features allow hypothesizing a potential functional link between RyR1 and SelN.

To our knowledge, the distribution of the major proteins implicated in Ca$^{2+}$ homeostasis and E-C coupling has not been ascertained in CM (except for sarco/endoplasmic reticulum Ca$^{2+}$-ATPase SERCA [13]). This prompted us to study the immunolocalization of 6 of these proteins (RyR1, the dihydropyridine receptor DHPR-α1 subunit, SERCA isoforms 1 and 2, triadin, and calsequestrin) in skeletal muscles from genetically characterized CCD and MmD patients carrying *RYR1* or *SEPN1* mutations.

**MATERIALS AND METHODS**

**Patients**

Open diagnostic muscle biopsies from 12 ambulant patients with a clinical, histologic, and molecular diagnosis of *SEPN1*- or *RYR1*-related MmD or CCD were included in this study.

Histologic criteria in the 6 MmD cases included type I fiber predominance and relative hypotrophy as well as the presence of short cores in most type I and type II fibers. Five of these cases had a classical MmD phenotype (9): congenital weakness predominantly of axial muscles, scoliosis, and respiratory failure requiring nighttime ventilation. The sixth patient presented in infancy with the moderate form of MmD (pelvic girdle weakness, no ophthalmoplegia).

The 6 CCD patients showed long, well-delimited cores in 90% to 100% of type I fibers. All showed early-onset muscle weakness, mainly involving the pelvic girdle. One patient (CCD6) belongs to a previously reported family with recessive CCD (14) in which the affected siblings showed minicores in the muscle biopsies taken in childhood (no longer available) but long cores with rods in those taken in adulthood.

To validate our results, the 12 genetically characterized patients were compared with 6 CM patients (MmD7–MmD9, CCD7–CCD9) without *SEPN1* or *RYR1* mutations selected using the same clinical and morphologic criteria. *SEPN1* mutations were excluded in the 3 MmD cases; *RYR1* mutations were excluded in the 6 patients after screening of the whole *RYR1* cDNA (in 5 cases) or the C-terminal encoding exons (in MmD7). Also, we excluded *ACTA1* mutations in MmD8, CCD7, and CCD8 (the latter belonging to the same dominant family as CCD9).

**Linkage Analysis and Mutation Screening**

*SEPN1* and *RYR1* linkage studies were performed in the genetically informative families as described (9, 12). *SEPN1* mutation screening was performed by direct sequencing as described (9). Because of its large size, the whole *RYR1* coding sequence was screened when possible using complementary DNA (cDNA) obtained from a skeletal muscle biopsy (12). When muscle samples were unavailable, we screened *RYR1* using genomic DNA and focused on the 15 3′-terminal exons containing most of the known CCD mutations (5). All samples were obtained after informed consent according to local ethics committees.

**Immunohistochemical and Ultrastructural Procedures**

Muscle samples were frozen immediately in isopentane cooled in liquid N$_2$. Histologic and histochemical stainings were performed according to standard procedures using 10-μm cryosections (24). For immunohistochemistry, we used the following primary antibodies: polyclonal antibodies developed by one of the authors (IM) and directed...
against purified pig skeletal muscle RyR1 (anti-RyR, 1/500) (12) and the N-terminal domain of the rabbit triadin (anti-

TNter, 1/20) (25, 26); commercial antibodies directed
against purified alpha1 subunit of rabbit skeletal muscle
DHPR (monoclonal anti-DHPRα1; ABCAM, Cambridge,

UK; 1:300), rabbit caldeslestrin (polyclonal anti-Calsq;
Affinity BioReagents, Golden, CO; 1:200), and mouse
SERCA 1 and 2 isoforms (monoclonal anti-SERCA1/2;
Novocastra, Newcastle, UK; 1:100). Serial 7-μm cryosec-
tions were fixed with paraformaldehyde 4% in phosphate-
buffered saline (PBS). After washing and incubation in PBS
with 3% bovine serum albumin, labeling with primary
antibodies was performed overnight at 4°C. Sections were
then washed in PBS with Tween 0.1% and incubated 1 hour
at room temperature with the following secondary anti-
bodies: fluorescein isothiocyanate-conjugated (FITC) swine
antibodies (DAKO; 1:300); FITC mouse anti-rabbit (DAKO;
1:300); or CY3-

anti-rabbit immunoglobulins (DAKO, Carpinteria, CA;
bodies: fluorescein isothiocyanate-conjugated (FITC) swine
at room temperature with the following secondary anti-
In all cases and with all the antibodies used, the
preserved areas of the muscle fibers showed a labeling of the
intermyofibrillar network indistinguishable from that
observed in control muscle.

Multi-Minicore Disease Patients With
SEPN1 Mutations
In these cases, both fiber types were well represented;
type 1 fibers were slightly more numerous. Classic histo-
chemical techniques (Fig. 2) showed minicores in a variable
percentage of fibers, which was lowest (around 50%) in
MmD3, maximum (100%) in MmD1 and MmD2, and intermediate in MmD4 and MmD5. However, these lesions
were not visible by immunohistochemistry, because there
was no focal modification of immunolabeling with any of
the antibodies analyzed. The expression patterns of all the
Ca²⁺-related proteins studied were normal and identical to
those observed in normal controls (Fig. 3; Table 2).

RESULTS

Mutational Analysis
The mutations identified are shown in Table 1. The five
patients with classical MmD carried SEPN1 mutations. Three
of them were compound heterozygous for a missense
mutation associated with either a splicing or a nonsense
mutation (out-of-frame deletion or insertion). The 2 remain-
ing patients were homozygous; MmD2 carried a common
missense mutation, whereas in MmD3, an out-of-frame
nucleotide insertion in exon 5 led to an absence of SerN
protein verified by Western blot on fibroblast cultures (data
not shown).

The 6 CCD patients and the moderate MmD case
(MmD6) had RYR1 mutations. Five of them carried missense
heterozygous changes in the C-terminal coding region of the
gene (exons 100 and 102), a hot spot where most of the
known CCD mutations cluster. The remaining 2 patients
showed more uncommon genetic defects. Patient CCD5 had
an in-frame heterozygous deletion of 3 bases in exon 91,
predicting loss of one amino-acid residue. Patient CCD6
belonged to a consanguineous family with recessive CCD; she
carried a homozygous missense change in exon 71, resulting
in the replacement of a proline by serine (p.P3527S).

Histologic and Immunohistochemical Results

In these cases, both fiber types were well represented;
type 1 fibers were slightly more numerous. Classic histo-
chemical techniques (Fig. 2) showed minicores in a variable
percentage of fibers, which was lowest (around 50%) in
MmD3, maximum (100%) in MmD1 and MmD2, and intermediate in MmD4 and MmD5. However, these lesions
were not visible by immunohistochemistry, because there
was no focal modification of immunolabeling with any of
the antibodies analyzed. The expression patterns of all the
Ca²⁺-related proteins studied were normal and identical to
those observed in normal controls (Fig. 3; Table 2).

<table>
<thead>
<tr>
<th>Cases</th>
<th>Genes</th>
<th>Exons</th>
<th>Mutations</th>
<th>Pattern of Inheritance</th>
<th>Muscle Analyzed</th>
<th>Age at Muscle Biopsy</th>
</tr>
</thead>
<tbody>
<tr>
<td>MmD1</td>
<td>SEPN1</td>
<td>6/12</td>
<td>p.H293R/g.IVS11-2:A&gt;G</td>
<td>AR</td>
<td>Deltoïd</td>
<td>9 years</td>
</tr>
<tr>
<td>MmD2</td>
<td>SEPN1</td>
<td>5</td>
<td>p.G273R Ho</td>
<td>AR</td>
<td>Deltoïd</td>
<td>11 years</td>
</tr>
<tr>
<td>MmD3</td>
<td>SEPN1</td>
<td>4</td>
<td>c.713_714insA Ho</td>
<td>AR</td>
<td>Deltoïd</td>
<td>12 years</td>
</tr>
<tr>
<td>MmD4</td>
<td>SEPN1</td>
<td>5/10</td>
<td>c.863-864 delTG/p.W490L</td>
<td>AR</td>
<td>Deltoïd</td>
<td>12 years</td>
</tr>
<tr>
<td>MmD5</td>
<td>SEPN1</td>
<td>4/6</td>
<td>c.713_714insA/p.G315S</td>
<td>AR</td>
<td>Deltoïd</td>
<td>35 years</td>
</tr>
<tr>
<td>MmD6</td>
<td>RYR1</td>
<td>100</td>
<td>p.H4803Y</td>
<td>Sporadic</td>
<td>Deltoïd</td>
<td>25 years</td>
</tr>
<tr>
<td>CCD1</td>
<td>RYR1</td>
<td>102</td>
<td>p.H4887Y</td>
<td>AD</td>
<td>Deltoïd</td>
<td>33 years</td>
</tr>
<tr>
<td>CCD2</td>
<td>RYR1</td>
<td>100</td>
<td>p.R4825C</td>
<td>AD</td>
<td>Quadriceps</td>
<td>37 years</td>
</tr>
<tr>
<td>CCD3</td>
<td>RYR1</td>
<td>100</td>
<td>p.Y4796C</td>
<td>AD</td>
<td>Deltoïd</td>
<td>31 years</td>
</tr>
<tr>
<td>CCD4</td>
<td>RYR1</td>
<td>100</td>
<td>p.L4793P</td>
<td>Sporadic</td>
<td>Deltoïd</td>
<td>37 years</td>
</tr>
<tr>
<td>CCD5</td>
<td>RYR1</td>
<td>91</td>
<td>c.del4214-16</td>
<td>AD</td>
<td>Quadriceps</td>
<td>30 years</td>
</tr>
<tr>
<td>CCD6</td>
<td>RYR1</td>
<td>71</td>
<td>p.P3527S Ho</td>
<td>AR</td>
<td>Deltoïd</td>
<td>21 years</td>
</tr>
</tbody>
</table>

 Mutations are designed according to the published reference sequences.
Ho, homozygous; AD, autosomal-dominant; AR, autosomal-recessive.
Central Core Disease Patients With RYR1 Mutations

In all CCD samples, myosin ATPase reactions disclosed an extreme predominance of type I fibers (approximately 90–100%), all expressing SERCA2. Oxidative enzyme stainings revealed long cores, which were multiple and peripheral in all cases but one (Fig. 2D–H). Although the archetypal cores in CCD are central, sharply delimited, unique lesions, only one CCD biopsy (CCD4) showed this pattern (D); all other CCD samples disclosed multiple cores that were often subsarcolemmal and less well-defined (E). Thus, core length as evidenced by longitudinal muscle fiber sections is the most reliable criterion to differentiate minicores (C) from cores (F). The dark rim surrounding some cores ([G, H], arrows) has often been considered a sign of mitochondria accumulation. However, this rim is more intense with NADH-TR (G), reflecting both mitochondrial and sarcoplasmic reticulum (SR) oxidative activity, than with SDH (H), which is exclusively mitochondrial. This suggests a perilesional accumulation of SR (and possibly mitochondria). NADH-TR-stained transverse muscle sections from MmD5 ([A], 40×), MmD1 ([B], 40×), CCD4 ([D], 20×; [G, H], 40×), and CCD1 ([E], 25×); longitudinal electron microscopy sections from MmD2 (C), and CCD1 (F). Scale bar = 2.5 μm.

Independent of the core distribution and associated lesions, all samples displayed focal immunostaining abnormalities with all the antibodies. These abnormalities were consistent and restricted to the core lesions (Fig. 4). Strikingly, RyR1 immunolabeling was virtually absent from the cores, suggesting a focal depletion of this protein. In contrast, most cores were strongly immunolabeled for DHPRα1-3, triadin, SERCA1/2 and, particularly, calsequestrin, indicating a focal accumulation of these proteins within and/or around the cores (Table 2).

Some cores were diffusely and homogeneously labeled with the 5 latter antibodies (“homogeneous pattern”), suggesting a focal accumulation of SR and triads...
devoid of RyR1. Conversely, other lesions showed a peripheral rim of immunocytochemical protein accumulation, which contrasted with a variable degree of labeling reduction in their center ("perilesional/halo pattern") (Figs. 4, 5A). Both patterns of immunocytochemical protein accumulation could coexist in the same patient (Fig. 5B) or even in the same fiber, but never in the same core (Fig. 4). However, one of these patterns tended to predominate in a single patient. There was no correlation between the immunocytochemical pattern and the type of \textit{RYR1} mutation or the degree of sarcomere disorganization observed by EM (structured vs. unstructured cores, presence or absence of rods). No alteration in the distribution of SR or T-tubules within or around the cores was apparent on ultrastructural sections.

Interestingly, in 3 CCD patients (CCD1, CCD3, and CCD4), NADH-TR staining showed sparse fibers with only small, poorly defined cores, virtually identical to the minicores in MmD. All the labeling abnormalities described previously were retrieved in these \textit{RYR1}-related minicores (Fig. 6A).

**Multi-Minicore Disease Patient With \textit{RYR1} Mutation**

Muscle from MmD6 showed short cores associated with centrally located nuclei and multiple foci of increased oxidative activity, staining dark blue with NADH-TR (Fig. 6B). The minicores showed a labeling pattern identical to that observed in CCD with \textit{RYR1} mutations (Fig. 6Ba–c, f, g, arrows). Noticeably, the dark oxidative-positive areas were often labeled for triadin and, occasionally, for DHPRs and RyR1, suggesting focal accumulation of these proteins outside the cores (Fig. 6Bf–h, asterisk).
Multi-Minicore Disease and Central Core Disease Patients Without SEPN1 or RYR1 Mutations

Labeling in these nonmutated cases was relatively variable, but none of them showed a pattern identical to either of those in SEPN1- or in RYR1-mutated patients (Fig. 7).

DISCUSSION

Recent progress in the molecular characterization of CM has shown that the classic diagnostic criteria based on core morphology alone are not sufficient for an exact diagnosis, stressing the necessity of novel markers. Previous studies demonstrated that all types of core lesions show increased immunoreactivity for several proteins such as filamin C, αB-crystallin, actin, dystrophin, gelsolin, desmin, α1-antichymotrypsin, β-amyloid precursor protein, β2-microglobulin, NCAM, and myotillin (10, 13, 20, 27–30). Filamin C and αB-crystallin have been considered the strongest immunohistochecmical markers of core lesions (13, 20). However, the described immunocytochemical alterations are nonspecific; they are present in minicores, cores, and in other structural muscle defects such as target lesions (20, 28). Thus, they probably represent a secondary, stereotyped cellular response to sarcomere disorganization, nonindicative of the primary molecular defect.

In contrast, our study revealed a particular gene-related immunohistochemical pattern in CM. The distribution of Ca²⁺-handling proteins was normal in SEPN1-related MmD but was consistently altered in CCD and MmD with RYR1 mutations. Within or around the cores, we observed a virtual absence of RyR1 and a focal accumulation of calsequestrin, SERCA1/2, triadin, and DHPRα1s. This pattern was present in RYR1-related minicores as well as in cores; therefore, the immunohistochemical differences between RYR1- and SEPN1-related myopathies cannot be fully explained by the distinct core sizes but inform on the different molecular defects.

These distinctive immunohistochemical patterns represent a useful marker for differential diagnosis and may help choosing the appropriate genetic test for disease confirmation, especially in young CCD patients whose biopsies do not show the classic core structures. Cores showing the described immunolabeling abnormalities are not indicative of SEPN1 mutations, but advocate RYR1 screening. In our experience, RyR1 depletion and calsequestrin accumulation were the most conspicuous markers in RYR1-mutated cases. Therefore, we recommend the use of these 2 antibodies as a first immunohistochemical screening in CM. Calsequestrin accumulation within the cores is particularly noticeable as a result of the low level of labeling in normal fiber areas. In contrast, SERCA focal abnormalities are frequently inconspicuous as a result of the strong basal labeling for this protein in muscle fibers; actually, no modification in SERCA immunolabeling was observed in a previous study of 3 families with RYR1 mutations (13). Noticeably, in 5 CM cases without RYR1 or SEPN1 mutations, we observed dark oxidative-positive areas that were immunolabeled for calsequestrin, triadin, and DHPRα1s, whereas the cores showed
no labeling abnormality. Thus, identification of immunolabeled spots on a CM biopsy is not reliable in itself; comparison with serial NADH-TR or SDH-stained sections is necessary to verify whether they correspond to the cores. This could partly explain the RyR1 accumulation described in a previous $\text{RYR1}$-mutated case in which correlation with cores or serial sections are not illustrated (31).

Aside from its diagnostic applications, our results can provide some prospective indications about the pathophysiology of CM. It has been hypothesized that SelN could be implicated in skeletal muscle $\text{Ca}^{2+}$ handling and directly related with the SR $\text{Ca}^{2+}$-release structures (9). Our results do not support this hypothesis; on the contrary, they suggest that SelN is not directly involved in maintaining the structural integrity of the $\text{Ca}^{2+}$-release complex. Thus, different mechanisms could lead to core formation in muscles lacking normal SelN and in those carrying RyR1 defects.

Two models have been proposed to explain the functional consequences of $\text{RYR1}$ mutations (22) based on data obtained using nonhuman and/or nonmuscular cells. According to the first model, RyR1 mutations would lead to a sustained calcium leak. The second model suggests that the mutated RyR1 would lose its functional connection with DHPR, leading to E-C uncoupling. Alternatively, protein accumulation in muscle fibers can be a nonspecific phenomenon. However, neither this possibility nor any of the 2 former pathophysiological models can explain the focal RyR1 immunocytochemical depletion that we observed in human
muscle expressing RYR1 missense mutations. Our results point to a focal accumulation of SR virtually depleted of RyR1 but not of the other Ca²⁺ handling proteins. This can be best understood according with a novel, hypothetical pathophysiological mechanism that we tentatively propose for core generation: some RYR1 mutations would lead to a relative and focal RyR1 depletion, thereby modifying the stoichiometry of proteins in the Ca²⁺-release complex. This could cause initially a focal compensatory increase in SR and T-tubules; the absence of RyR1, and thus of a correct functional bridging between SR and T-tubules, would eventually provoke a loss of the normal SR distribution and its accumulation around the lesions, whereas T-tubules remain present within the cores. This evolving character of the cores is difficult to document and cannot be proven by this study, but would explain why 2 different patterns of protein accumulation (“homogeneous” and “perilesional”) may coexist in the same biopsy.

So far, definition of cores has been based on focal mitochondria and sarcomere abnormalities. Our results suggest that, in cases with RYR1 mutations, SR and T-tubule abnormalities are a more distinctive change than the conventional EM defects in mitochondria and contractile apparatus. Based on the central role of SR and T-tubules in muscle cells, it is tempting to speculate that their pathologic modifications would lead to E-C coupling dysfunction, thereby causing muscle weakness. Along these lines, the mitochondrial and sarcomere modifications would represent secondary morphologic changes whose functional relevance remains to be proven.

FIGURE 7. Immunolabeling patterns in multi-minicore disease (MmD) and central core disease (CCD) patients without SEPN1 or RYR1 mutations. Serial transverse muscle sections from MmD9 (A–C), CCD8 (D–F), CCD7 (G–I), MmD 7 (J, K), and CCD9 (L, M). NADH-TR (A, D, G, J, L); immunolabeling for DHPRβ1s (B), RyR1 (E–H), and triadin (C, F, I, K, M). In 5 of the 6 nonmutated patients (MmD7–MmD9, CCD8, and CCD9), most cores showed no labeling abnormality ([A–F], arrowheads). Yet, these cases differed from those with SEPN1 mutations by the presence of rare, small areas positively labeled for calsequestrin, triadin, DHPRβ1s and occasionally for RyR1 ([A–F], arrows). Some of these areas colocalized partially with the cores (D–F), but most corresponded to oxidative-positive dark areas adjacent to the cores ([J–M], arrows). An exception to this pattern was CCD7 (G–I), whose cores were labeled for DHPRβ1s, triadin, SERCA1/2, and calsequestrin but tended to have a halo of perilesional RyR1 accumulation (H) instead of the RyR1 depletion observed in RYR1-mutated cases. Original magnifications: (A–C) 25×; (D–M) 40×.
In conclusion, our findings provide an appropriate tool to discriminate between RYR1- and SEPN1-related CM and suggest some novel pathophysiological indications. Further studies, including additional mutations and Western blot analysis, are needed to extend our results and gain a deeper insight into the generation of core lesions and muscle weakness in CM.

ACKNOWLEDGMENTS

The authors thank Emmanuelle Lacène, Melanie Pacelle, and Céline Ledueil for technical assistance. The authors also thank Prof. Michel Fardeau and Dr. Frédéric Chevessier for useful advice and discussions.

AMK is a member of the German Network on Muscular Dystrophies (MD-NET). AF is the recipient of an Avenir Career Development Award.

REFERENCES