Novel LAMA2 Gene Mutations Associated with Merosin-Deficient Congenital Muscular Dystrophy

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ABSTRACT

Background: Merosin-deficient congenital muscular dystrophy (MDC1A) is a rare autosomal recessive genetic disease occurred due to mutations in the LAMA2 gene. This study investigated the molecular genetics of three Iranian MDC1A patients who manifested hypotonia, muscle weakness at birth, elevated levels of creatine kinase, and normal magnetic resonance imaging before the age of six months. Methods: Peripheral blood samples were collected from three unrelated patients and their families after obtaining informed written consents. Genomic DNA was extracted and sequenced using next-generation sequencing, followed by Sanger confirmation. Results: Sequencing results revealed a known missense mutation, c.8665G>A, and two novel heterozygous sequencing variants affecting splicing, c.397-4_c.478del and c.7452-1G>A, in the LAMA2 gene. Reverse transcriptase-PCR analysis showed that a new intronic variant, c.7452-1G>A, produced aberrant splicing pattern in the patient. Conclusion: This study expands the mutation spectrum of LAMA2 and assists in the diagnosis, genetic counseling, and prenatal diagnosis of the affected families. DOI: 10.29252/22.6.408

Keywords: Creatine Kinase, Genetic counseling, Mutation, Reverse transcriptase polymerase chain reaction

INTRODUCTION

Merosin-deficient congenital muscular dystrophy (MDCMD, CMD, MDC1A) is a rare autosomal recessive genetic disease involving the central and peripheral nervous system in the childhood (OMIM: 607855)[1]. MDC1A is common in China and Western countries[2,3]. Affected infants present with muscle weakness, hypotonia, failure to thrive, poor suck and cry, and delayed motor development[4,5]. A previous study has shown a correlation between the levels of merosin expression and clinical severity[6]. The disorder is caused by the mutations in the LAMA2 (Gene ID: 3908, OMIM: 156225) on chromosome 6q22, which encodes the α2 chain subunit of laminin 2 (merosin) and laminin 4 (s-merosin)[7]. A recessive mutation in this gene also causes a wide phenotypic spectrum of LAMA2-related muscular dystrophy from a severe early-onset CMD to a mild later childhood-onset limb-girdle type muscular dystrophy[8-10]. Signs and symptoms in early-onset LAMA2-related muscular dystrophy (early-onset LAMA2 MD) appears at birth or within the first few months of life, including contractures of the large joints, profound hypotonia, poor spontaneous movement, and severe muscle weakness. Diagnosis of early-onset LAMA2 MD is based on clinical examination, high serum creatine kinase (CK) concentrations, merosin deficiency detected by immunohistochemical staining of muscle or skin biopsy, and white matter changes on brain MRI. Clinical manifestation in late-onset LAMA2 MD are similar to a group of muscle disorders classified as limb-girdle muscular dystrophies and are milder than
in the early-onset type. Late-onset LAMA2 MD has clinical overlap with Emery-Dreifuss myopathy due to elbow contractures, high serum CK concentrations, and prominent spinal rigidity; however, major cardiac involvement is absent in LAMA2 MD\[11\]. Muscular dystrophies are a group of heterogeneous disorders that have overlapping clinical symptoms, which may lead to misdiagnosis. The efficiency of the next-generation sequencing (NGS) had previously been reported for the molecular diagnosis of the CMD, based on clinical and laboratory findings\[12,14\]. It has been shown that NGS-targeted panels of 40 genes can be a useful approach to identify causative variants in CMDs\[13\]. However, this method is not cost-effective when there is a clinical overlap. A previous report from Iran showed an improved diagnostic yield of neuromuscular disorders applying clinical exome sequencing\[16\]. In this study, we aimed to investigate the molecular genetics of three unrelated Iranian MDC1A patients using whole exome sequencing (WES) method, followed by data analysis of known CMD genes.

MATERIALS AND METHODS

This study was approved by the Ethics Committee of the Deputy of Research Affairs, Shahid Beheshti University of Medical Sciences (Tehran, Iran). Three patients who participated in this study were from unrelated Iranian families upon previous diagnosis/suspicion of merosin deficiency. Blood samples were collected from the patients and the parents after obtaining their informed written consents. Genomic DNA was extracted using conventional salting-out protocol\[15\]. WES was performed by Macrogen Inc. (Seoul, Korea) and sequenced on illumine HiSeq 4000 at the mean coverage of 100x. The DNA samples were prepared according to an Agilent SureSelect Target Enrichment Kit preparation guide. The SureSelect Target Enrichment workflow was used to capture the regions of interest, enriching them out of an NGS genomic fragment library guide, followed by paired-end sequencing. The sequencing read was aligned and mapped to hg19 from UCSC Genome Browser (https://genome.ucsc.edu), and the variants were annotated and filtered using a custom bioinformatics pipeline for LAMA2 gene in first step and 62 genes in the next step, as previously described in detail\[14\]. In this study, variants with minimum allele frequency (MAF > 0.001) were excluded. Only, rare variants (MAF < 0.001 or new) with nonsense, nonsynonymous, splice site, and insertion and deletion variants in known or related genes to merosin deficiency disorders were selected for interpretation.

Identified pathogenic variants were confirmed in the patients and segregated within the families using specific primer pairs and Sanger sequencing (Table 1). For analysis of splicing mutation, cDNAs were synthesized using PrimeScript RT reagent kit (TAKARA, Japan) after the extraction of total RNAs from peripheral blood using TRIzol® reagent (Qiagen, USA) following the manufacturer’s protocol. Then the partial-length LAMA2 cDNA was amplified by reverse transcription-PCR (RT-PCR) using one specific primer pair cDNA-F and cDNA-R (Table 1), followed by 2.5% agarose gel electrophoresis. All primers and sequencing results were designed and analyzed using Gene Runner 6.2.07 Beta and Chromas 2.4, respectively. The mutations nomenclature was based on the cDNA nucleotide position, according to the LAMA2 genomic sequence in the GenBank database (NM_000426.3) and Mutalyzer 2.0.21 (https://www.mutalyzer.nl) (Table 2).

Bioinformatics tools were used to test the pathogenicity of the mutations, including PolyPhen-2 (http://genetics.bwh.harvard.edu/pph2/), SIFT (http://sift.jcvi.org), Mutation Taster (http://www.mutationtaster.org), UMD-Predictor (http://umd-predictor.eu), and Combined Annotation Dependent Depletion (CADD) (http://cadd.gs washington.edu/)\[16-20\]. In addition, the protein

<table>
<thead>
<tr>
<th>Primer name</th>
<th>Primer sequence (5’ to 3’)</th>
<th>Annealing temperature (°C)</th>
<th>Extension (s)</th>
<th>Product size (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>LAMA2-F3</td>
<td>TCAGGTGAAATTTGTGCACATAG</td>
<td>60</td>
<td>60</td>
<td>571</td>
</tr>
<tr>
<td>LAMA2-R3</td>
<td>TTTCGACAGGCTTTATTCACC</td>
<td>60</td>
<td>60</td>
<td>571</td>
</tr>
<tr>
<td>LAMA2-F54</td>
<td>GAACATCCATTAGACCAACCCAG</td>
<td>58</td>
<td>60</td>
<td>507</td>
</tr>
<tr>
<td>LAMA2-R54</td>
<td>TGATCACACATCTAGGACTTC</td>
<td>58</td>
<td>60</td>
<td>507</td>
</tr>
<tr>
<td>LAMA2-F61</td>
<td>AGACCTTCGACCTTTAAAACCAG</td>
<td>58</td>
<td>60</td>
<td>523</td>
</tr>
<tr>
<td>LAMA2-R61</td>
<td>TGACCTTCATTACACCTATCG</td>
<td>58</td>
<td>60</td>
<td>523</td>
</tr>
<tr>
<td>cDNA-F</td>
<td>ATATAGCAACGTCTTCGTCTGG</td>
<td>58</td>
<td>40</td>
<td>318-330</td>
</tr>
<tr>
<td>cDNA-R</td>
<td>TCTTGGTGCTGAATGACAGGT</td>
<td>58</td>
<td>40</td>
<td>318-330</td>
</tr>
</tbody>
</table>

Table 1. List of primers and PCR condition for confirmation of mutations
Table 2. A summary of mutation identified in the LAMA2 gene

<table>
<thead>
<tr>
<th>Patient</th>
<th>Nucleic acid alteration</th>
<th>Amino acid alteration</th>
<th>Location</th>
<th>Zygosity</th>
<th>Affected domain</th>
<th>GenBank accession No.</th>
<th>ClinVar accession</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>c.8665G&gt;A</td>
<td>Gly2889Arg</td>
<td>Exon61</td>
<td>Hom.</td>
<td>LamG4</td>
<td>KY054725</td>
<td>SCV000323176.1</td>
</tr>
<tr>
<td>2</td>
<td>c.397-4_c.478del</td>
<td>-</td>
<td>Intron3_Exon4</td>
<td>cHet.</td>
<td>LamG2</td>
<td>KY100117</td>
<td>SCV000590914.1</td>
</tr>
<tr>
<td>3</td>
<td>c.7452-1G&gt;A</td>
<td>-</td>
<td>Intron53</td>
<td>cHet.</td>
<td>LamNT</td>
<td>KY100118</td>
<td>SCV000590915.1</td>
</tr>
</tbody>
</table>

Hom, homozygous; Het, heterozygous; cHet, compound heterozygous; Lam, laminin; LamNT, laminin N-terminal domain

RESULTS

Clinical description

Patient 1, a seven-year-old boy, who belonged to a consanguineous couple, was born by normal delivery. His mother experienced pregnancy with intrauterine fetal death. Initial symptoms arisen in him since birth included muscle weakness, inactivity, and hypotonia. At the age of ten months, concentrations of lactate dehydrogenase, CK, and aldolase were found to be 2005 IU/l (normal range 180–430 U/L), 1248 U/l (normal range 200–400 U/L), and 13.9 IU/l, respectively. At age two years, six months, immunohistochemical (IHC) analysis results showed weak and patchy sarcolemmal labeling with merosin antibody. Muscle biopsy results showed severe myopathic atrophy with endomyos fibrosis, compatible with muscular dystrophy. At age seven, he had kyphosis, short elbow, and contractures of elbow and wrist. The CK and aldolase levels decreased to 523 U/l and 5,5 U/l, respectively (Table 3). He attended a regular school having normal intelligence (with IQ score estimated to be 160). Based on clinical and biochemical finding, merosin deficiency was proposed, and genetic test for the LAMA2 gene was recommended. At the age of six, he had kyphosis, and cognitive function was normal with no history of seizure (Table 3).

Sequencing results

The biochemical analysis showed a high level of the serum CK in both patients. The molecular analysis results revealed pathogenic variants in the LAMA2 gene. In patient 1 and 3, a known missense mutation, c.8665G>A (p.G2889R), was identified, in which was segregated within the families. In patient 2, two novel splice site mutations, c.397-4_c.478del and c.7452-1G>A, were found in LAMA2, as a compound heterozygote (Table 2). The segregation analysis in patient 2 revealed that compound heterozygote mutation was in trans status. He had inherited c.397-4_c.478del from his father and c.7452-1G>A from his mother. The frequencies of identified variants are very low in normal population or absent in databases.
Table 3. A summary of patients under study, including age of onset, biochemical analysis, clinical examination, and muscle biopsy results

<table>
<thead>
<tr>
<th>Patients</th>
<th>Gender</th>
<th>Age (y)</th>
<th>Age at follow-up (months)</th>
<th>Age of onset</th>
<th>Consanguinity</th>
<th>Prominent symptoms</th>
<th>MRI before the age one</th>
<th>CK (U/l) (^a)</th>
<th>LDH (U/l)</th>
<th>Aldolase (U/l)</th>
<th>Muscle biopsy/IHC</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>M</td>
<td>7</td>
<td>10</td>
<td>birth</td>
<td>Yes</td>
<td>Muscle weakness, inactivity, hypotonia, kyphosis</td>
<td>normal</td>
<td>1248</td>
<td>2005</td>
<td>13.9</td>
<td>Merosin positive CMD</td>
</tr>
<tr>
<td>2</td>
<td>M</td>
<td>5</td>
<td>5</td>
<td>birth</td>
<td>No</td>
<td>Hypotonia, myopathic face, kyphoscoliosis</td>
<td>normal</td>
<td>1762</td>
<td>871</td>
<td>21.0</td>
<td>Merosin positive CMD</td>
</tr>
<tr>
<td>3</td>
<td>M</td>
<td>6</td>
<td>5</td>
<td>birth</td>
<td>Yes</td>
<td>Hypotonia, kyphosis</td>
<td>normal</td>
<td>6304</td>
<td>NA</td>
<td>44.0</td>
<td>Merosin positive CMD</td>
</tr>
</tbody>
</table>

\(^a\) CK normal range: 200-400 U/l depending on the laboratory\(^{[11]}\). NA, not assigned
including ExAC, 1000G, dbSNP, gnomAD, Iranome, and an in-house database of nearly 500 WES results. No additional incidental findings were identified in the analysis of other genes related to muscular dystrophy. The result of RT-PCR analysis of c.7452-1G>A mutation in patient 1 showed a different pattern of the LAMA2 mRNA expression in comparison to his parents and a healthy control. Partial LAMA2-cDNA analysis in the patient with heterozygote GA genotype (c.7452-1G>A) demonstrated a reduced LAMA2-mRNA expression (318-330 bp) rather than his mother who was also (lane-3) heterozygote for c.7452-1G>A mutation. It may happen due to nonsense-mediated mRNA decay of another allele with c.397-4_c.478del mutation in the patient. The mother had not c.397-4_c.478del mutation, while the father and the patient were heterozygote for this mutation.

**DISCUSSION**

In this study, we reported biochemical and genetic data obtained from three Iranian patients with MDC1A (Table 2). The patients in this study had a severe phenotype of MDC1A with normal cognitive function. The patients manifested hypotonia, muscle weakness, high levels of CK, and positive results in the muscle biopsy IHC studies. The absence of laminin α2 antibody in muscle fibers, nerves, and skin biopsy is useful for differential diagnosis of LAMA2-related disorder versus αDG disorder versus αDG-related disorder (Alpha dystroglycan-related dystrophies) [3]. The molecular analyses of the patients identified a known mutation, c.8665G>A (p.G2889R), in two patients and a novel compound heterozygous mutation, including c.397-4_c.478del and c.7452-1G>A mutations (Table 2).

In this study, c.8665G>A was found in two affected patients with MDC1A in homozygous state. According to the American College of Medical Genetics and Genomics guideline (ACMG), c.8665G>A variant was first classified as the variant of likely pathogenic mutation in patient 1 and patient 2. This mutation has also been reported for the first time as a pathogenic mutation in an affected patient with MDC1A in homozygote status [14]. c.8665G>A is a missense mutation that results in the substitution of Arg amino acid at conserved position 2889. Its frequency in population databases, including dbSNP (https://www.ncbi.nlm.nih.gov/SNP), ExAC (exac.broadinstitute.org), 1000 genomes (http://www.internationalgenome.org/), gnomAD (gnomad.broadinstitute.org/), Iranome (www.irgenome.info), and in-house database of WES was very low. PolyPhen-2 and SIFT, MutationTaster, and UMD-Predictor predicted that this variant was damaging, causes disease, and is pathogenic, respectively. According to the crystal structure of LG4 domain (pdb 5IK8), protein modeling showed that the p.G2889 is a buried amino acid in the 3D structure of the protein, which is conserved among different species (Fig. 1A), as well as human LG domains (Fig. 1B) [23]. The C-terminus of LAMA2 consists of five laminin G domains that form the globular part of the laminin, which engage in network formation and cell-surface interaction [23-25]. The modeling result showed that the substitution of Arg at position 2889 may affect the α2 laminin G4 structure and calcium-binding site, resulting in the disruption of binding site for heparin and dystroglycan molecules (Fig. 2). The result also suggested that this mutation

![Fig. 1](image-url)  
**Fig. 1.** Conservation analysis of amino acid sequences among different species (A) and LG domains (B). The p.G2889R variant site is located in a highly conserved amino acid position among different species (marked with a black box in A). Figure 1B shows the conservation of p.G2889R among LG domains from LG1 to LG5 domains (highlighted in red).
may be a common mutation among Iranian patients, and/or it may show ancestral relationship among MCD1A patients. Therefore, evidence mentioned above suggested c.8665G>A as a variant of pathogenic mutation. In patient 2, the c.397-4_c.478del splicing mutation is an 86-bp deletion at the DNA level that may cause the skipping of exon-4 or nonsense-mediated mRNA decay, resulting in the disruption of the laminin N-terminal domain (LamNT, domain VI) or the truncated protein. The subsequent RT-PCR analysis suggested that c.7452-1G>A, in patient 2, may cause the skipping of exon-54 (Fig. 3), which affects the α2 laminin G2 domain. This mutation along with c.397-4_c.478del together with c.397-4_c.478del caused the disease in patient 2. Compound heterozygous mutation has previously been reported in a severe form of CMD[26].

Regarding the analysis of known genes in CMDs, we can conclude that WES can be more beneficial and cost-effective than direct sequencing of large genes or NGS-targeted panels for identification of causal variants. The finding of this study demonstrated that the identified mutations were consistent with the diagnosis of MDC1A. The disease is very rare in Iran, and more studies are needed to provide extensive information about the mutation spectra of the LAMA2 gene in this country. Our finding would be helpful in diagnosis, genetic counseling, and prenatal diagnosis.

ACKNOWLEDGMENTS

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CONFLICT OF INTEREST. None declared.

REFERENCES


