Genetic profile for suspected dysferlinopathy identified by targeted next-generation sequencing

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ABSTRACT

Objective: To investigate the genetic causes of suspected dysferlinopathy and to reveal the genetic profile for myopathies with dysferlin deficiency.

Methods: Using next-generation sequencing, we analyzed 42 myopathy-associated genes, including *DYSF*, in 64 patients who were clinically or pathologically suspected of having dysferlinopathy. Putative pathogenic mutations were confirmed by Sanger sequencing. In addition, copy-number variations in *DYSF* were investigated using multiplex ligation-dependent probe amplification. We also analyzed the genetic profile for 90 patients with myopathy with dysferlin deficiency, as indicated by muscle specimen immunohistochemistry, including patients from a previous cohort.

Results: We identified putative pathogenic mutations in 38 patients (59% of all investigated patients). Twenty-three patients had *DYSF* mutations, including 6 novel mutations. The remaining 16 patients, including a single patient who also carried the *DYSF* mutation, harbored putative pathogenic mutations in other genes. The genetic profile for 90 patients with dysferlin deficiency revealed that 70% had *DYSF* mutations (n = 63), 10% had *CAPN3* mutations (n = 9), 2% had *CAV3* mutations (n = 2), 3% had mutations in other genes (in single patients), and 16% did not have any identified mutations (n = 14).

Conclusions: This study clarified the heterogeneous genetic profile for myopathies with dysferlin deficiency. Our results demonstrate the importance of a comprehensive analysis of related genes in improving the genetic diagnosis of dysferlinopathy as one of the most common subtypes of limb-girdle muscular dystrophy. Unresolved diagnoses should be investigated using whole-genome or whole-exome sequencing. ***Neurol Genet*** **2015;1:e36; doi: 10.1212/NXG.0000000000000036**

GLOSSARY

CK = creatine kinase; **DM** = distal myopathy; **HGMD** = Human Gene Mutation Database; **LGMD** = limb-girdle muscular dystrophy; **MLPA** = multiplex ligation-dependent probe amplification; **MMD** = Miyoshi muscular dystrophy; **XHMM** = eXome-Hidden Markov Model.

Dysferlinopathies are a group of autosomal recessive muscular dystrophies caused by mutations in *DYSF*. There are 3 main phenotypes: Miyoshi muscular dystrophy 1 (MMD1; OMIM #254130), limb-girdle muscular dystrophy type 2B (LGMD2B; OMIM #253601), and distal myopathy with anterior tibial onset (OMIM #606768). *DYSF* is located on chromosome 2p13.3-p13.1. It is composed of 55 exons coding for 2,080 amino acid residues, which form the dysferlin protein (approximately 230 kDa).[1] Dysferlin is expressed in the plasma membrane of skeletal muscles[2] and is involved in calcium-mediated membrane fusion events and membrane repair.[3,4] Patients with *DYSF* mutations have very low levels of dysferlin expression in

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skeletal muscle membranes (called primary dysferlinopathy).[2,5,6] Secondary dysferlin deficiency or altered localization due to mutation of the non-*DYSF* gene has also been reported in patients with dystrophinopathy,[7] sarcoglycanopathy,[7] caveolinopathy,[8–10] or calpainopathy[8,11–13] (often classified as secondary dysferlinopathy). Thus, the definitive diagnosis of dysferlinopathy requires identification of the *DYSF* mutation. Since 1998, our group has performed mutation analysis for *DYSF* in more than 160 families suspected of having dysferlinopathy using PCR–single-strand conformational polymorphism analysis or Sanger sequencing.[1,14,15] We previously identified >50 different mutations across the entire *DYSF* gene in approximately 60% of the patients.[1,14,15] We did not find *DYSF* mutations in the remaining approximately 40% of the patients, which suggests that these patients may have mutations in other myopathy-associated genes.

The aim of this study was to conduct targeted next-generation sequencing of myopathy-associated genes to reanalyze the patients with suspected dysferlinopathy who did not previously show *DYSF* mutations. This should enable us to reveal the genetic profile for myopathies with dysferlin deficiency.

METHODS

Standard protocol approvals, registrations, and patient consents. This study was approved by the Ethics Committee of the Tohoku University School of Medicine, and all individuals gave their informed consent before their inclusion.

Patients. ***Cohort for targeted next-generation sequencing (cohort 1).*** PCR–single-strand conformational polymorphism analysis or Sanger sequencing of *DYSF* had previously been performed in 150 probands with suspected dysferlinopathy: 98 of them (65.3%) were diagnosed with *DYSF* mutations and 52 (34.7%) remained undiagnosed, with no pathogenic mutation in 43 and single heterozygous mutations in 9 (table e-1 at Neurology.org/ng). A total of 64 patients, including the above-mentioned prescreened but undiagnosed 52 patients and 12 newly enrolled patients, were analyzed using targeted next-generation sequencing. Of the 64 patients analyzed, a deficiency or reduction in sarcolemmal dysferlin was confirmed in 41 patients using immunohistochemical analysis of dysferlin in muscle samples (classified as "pathologically proven cases"), whereas dysferlin deficiencies were not confirmed in the remaining 23 patients, mainly because muscle biopsies or immunohistochemical analyses for dysferlin had not been performed (classified as "clinically suspected cases") (table 1). All of the 23 patients had teenage-to-adult–onset slowly progressive myopathy without predominant cardiac dysfunction or early-onset respiratory dysfunction with at least 1 of the dysferlinopathy-likely phenotypes: initial or strong involvement of the flexor muscles in distal lower limbs (15 of 23 patients) or a moderate-to-extreme increase (>1,000 IU/L) in serum creatine kinase (CK) levels (12 of 23 patients).

Cohort for analyzing the genetic profile in the pathologically proven cases (cohort 2). To analyze the genetic profile in

Table 1 Constitution and results for 2 cohorts

	Pathologically proven cases (cohort 2)		Clinically suspected cases		Total
Previously diagnosed cases		N = 49		N = 51	N = 100
	DYSF	47	*DYSF*	51	
	non-*DYSF*	2			
	CAPN3	1			
	CAV3	1			
Patients analyzed by targeted next-generation sequencing (cohort 1)		N = 41		N = 23	N = 64
	DYSF	16[a]	*DYSF*	7	23[a] (table 3)
	non-*DYSF*	12[a]	non-*DYSF*	4	16[a] (table 4)
	CAPN3	8	*CAPN3*	2	
	DYSF/MYOT/CAV3	1[a]	*GNE*	1	
	CAV3	1	*MYH2*	1	
	ANO5	1			
	GNE	1			
	Undiagnosed	14	Undiagnosed	12	26
Total		N = 90		N = 74	N = 164

[a] Includes 1 patient (Dys149-1) with putative pathogenic mutations detected in *DYSF*, *MYOT*, and *CAV3*, who was counted in both *DYSF* and non-*DYSF* groups.

the pathologically proven cases, the 47 patients with previously identified *DYSF* mutations[1,14,15] and the 2 patients with *CAPN3* and *CAV3*[10] mutations were combined with the aforementioned 41 undiagnosed but pathologically proven cases, amounting to a total of 90 patients in this cohort (table 1).

Immunohistochemical analysis for dysferlin. Immunohistochemical analysis for dysferlin in muscle samples was performed in the institution or hospital that the patient visited. Although the detailed methods may not have been identical in all cases, most cases were investigated by the avidin–biotin–peroxidase complex immunostaining method using the mouse monoclonal antibody to dysferlin (NCL-Hamlet; Leica Biosystems, Wetzlar, Germany) as the primary antibody.

Targeted next-generation sequencing. We selected 42 genes that have been reported to cause adult-onset myopathy or muscular dystrophy (table 2). The targeted regions were designed using the SureDesign system (Agilent Technologies, Santa Clara, CA) to include all coding exons with 3′ and 5′ intronic 25-bp flanking bases (the regional source for coding exons was extracted from RefSeq, CCDS, Ensemble, Gencode, or Vega databases) and 3′ and 5′ untranslated regions. The targeted region for *DYSF* was designed to include 58 exons (i.e., exon 1–55, the alternative first exon, and exons 5a and 40a) to cover all alternative spliced variants. Of the total targeted region of 498.98 kb, 488.98 kb (98.08% coverage) was expected to be covered by 17,143 amplicons. Genomic DNA from the targeted region was captured using the HaloPlex target-enrichment system (Agilent Technologies). Targeted libraries were sequenced using the MiSeq platform, according to the manufacturer's instructions (Illumina, San Diego, CA). Paired 151-bp reads were aligned to the reference human genome (UCSChg19) using the Burrows–Wheeler Alignment tool.[16] Single-nucleotide variants and indels were identified using the Genome Analysis Toolkit v1.5.[17] Single-nucleotide variants and indels were annotated against the RefSeq and Single Nucleotide Polymorphism databases (dbSNP137) in the ANNOVAR program.[18] We used the PolyPhen-2 polymorphism phenotyping software tool and SIFT[19,20] to predict the functional effects of mutations and eXome-Hidden Markov Model (XHMM, http://atgu.mgh.harvard.edu/xhmm/) to call copy-number variations. We extracted variations that were listed as myopathy-causing mutations in the Human Gene Mutation Database (HGMD; provided by BIOBASE, Waltham, MA). For further analysis, we filtered variations satisfying all of the following conditions: variations located in exon or splice sites that were not detected in the control DNA included in the HaloPlex target enrichment system, variations that were covered by a minimum of 20 reads with a genotype quality score of at least 80, and variations with an altered allele frequency that ranged from 0.3 to 0.7 in the heterozygous state or that was greater than 0.7 in the homozygous state. Among these, nonsynonymous variants that either were absent or had a frequency of $<1\%$ in both the 1000 Genomes Database and the Human Genetic Variation Database (http://www.genome.med.kyoto-u.ac.jp/SnpDB/) were left as rare variants.

Sanger sequencing. We performed Sanger sequencing to confirm that the mutations identified by exome sequencing segregated with the disease. PCR products were purified using a MultiScreen-PCR plate (Millipore, Billerica, MA) followed by sequencing with a 3500xL Genetic Analyzer (Thermo Fisher Scientific, Waltham, MA).

Multiplex ligation-dependent probe amplification. To investigate copy-number variation in *DYSF*, we performed multiplex ligation-dependent probe amplification (MLPA) with SALSA MLPA probemix P268-A1 DYSF (MRC Holland, Amsterdam, the Netherlands) according to the manufacturer's instructions. This MLPA design contains probes to amplify 40 of the 58 exons. Genomic DNA (50–250 ng) was hybridized using the probemix. After ligation and amplification, the PCR products were separated by size using a 3130xL Genetic Analyzer (Thermo Fisher Scientific). Relative peak areas were calculated with GeneMapper software (Thermo Fisher Scientific).

Subcloning. To investigate the allelic condition of multiple heterozygous mutations in a particular gene, we performed subcloning of PCR products. Long-range PCR was performed under optimized long-PCR conditions using LA Taq polymerase (Takara, Shiga, Japan). The PCR products were subcloned into the vector pCR2.1 TOPO (Invitrogen, Waltham, MA). Several clones were randomly picked from each bacterial culture, and DNA was extracted for Sanger sequencing.

RESULTS

Targeted next-generation sequencing. An average of 96.8% (92.6%–98.2%) and 93.7% (84.6%–97.6%) of the overall targeted regions had at least 10- and 30-fold coverage, respectively (table e-2). The average read depth calculated for each gene ranged from 207 (*GFPT1*) to 429 (*CAV3*). An average of 89.7% (*FKRP*) to 99.9% (*CAPN3*) of the targeted regions had at least 10-fold coverage, and 83.1% (*FKRP*) to 99.4% (*TRIM32*) of the targeted regions had at least 30-fold coverage. These regions corresponded to those estimated to have been uncaptured by any amplicon. The sequencing data covered 99.4% and 98.1% of the targeted *DYSF* region with at least 10- and 30-fold coverage, respectively, with an average read depth of 388.

With reference to the HGMD, 0–3 myopathy-causing mutations were extracted per individual. After filtering with the quality-related and frequency thresholds described earlier, 0–17 rare nonsynonymous variants remained per individual. After considering the predicted functional effect, pattern of inheritance, and clinical information, putative pathogenic variants were detected in 38 of 64 patients (26 of 52 prescreened undiagnosed patients and all 12 newly enrolled patients).

Twenty-three of the 38 mutation-positive patients (12 of 52 prescreened undiagnosed patients and 11 of 12 newly enrolled patients) had *DYSF* mutations; these included 6 novel mutations (tables 1 and 3). Novel homozygous deletion of exons 37 and 38 (Dys194-1) and heterozygous deletion of exons 37 to 41 (Dys119-1-2) were predicted by XHMM software and confirmed by MLPA and Sanger sequencing, which revealed deletions of 5,862 and 51,161 bps, respectively.

The remaining 16 patients (15 of 52 prescreened undiagnosed patients and 1 of 12 newly enrolled patients), including a single patient (Dys149-1) in whom the *DYSF* mutation was simultaneously detected, were revealed to harbor known or rare

Table 2 The 42 myopathy-associated genes targeted in this study

Gene symbol	Position	Representative phenotype	OMIM no.	RefSeq no.	No. of coding exons	Transcript length, bp	Protein (aa)
ANO5	11p14.3	LGMD2L	611307	NM_213599	22	6,651	913
BAG3	10q25.2-q26.2	Myopathy, myofibrillar, 6	612954	NM_004281	4	2,571	575
CAPN3	15q15.1-q15.3	LGMD2A	253600	NM_000070	24	3,228	821
CAV3	3q25	LGMD1C	607801	NM_033337	2	1,431	151
COL6A1	21q22.3	Bethlem myopathy	158810	NM_001848	35	4,238	1,028
COL6A2	21q22.3	Bethlem myopathy	158810	NM_001849	28	3,461	1,019
COL6A3	2q37	Bethlem myopathy	158810	NM_004369	44	10,749	3,177
CRYAB	11q22.3-q23.1	Myopathy, myofibrillar, 2	608810	NM_001289807	3	1,017	175
DAG1	3p21.31	LGMD2P	613818	NM_001177634	6	5,829	895
DES	2q35	LGMD2R	615325	NM_001927	9	2,248	470
DNAJB6	7q36.3	LGMD1E	603511	NM_058246	10	2,527	326
DNM2	19q13.2	Myopathy, centronuclear	160150	NM_004945	20	3,588	866
DYSF	2p13.3-p13.1	LGMD2B	253601	NM_003494	55	6,796	2,080
EMD	Xq28	Emery–Dreifuss muscular dystrophy 1, X-linked	310300	NM_000117	6	1,379	254
FHL1	Xq27.2	Emery-Dreifuss muscular dystrophy 6, X-linked	300696	NM_001159704	6	2,888	280
FKRP	19q13.3	LGMD2I	607155	NM_024301	4	3,332	495
FKTN	9q31	LGMD2M	611588	NM_006731	10	7,364	461
FLNC	7q32	Myopathy, myofibrillar, 5	609524	NM_001458	48	9,188	2,725
GFPT1	2p13	Myasthenia, congenital, with tubular aggregates 1	610542	NM_001244710	20	8,703	699
GNE	9p13.3	Inclusion body myopathy, autosomal recessive	600737	NM_001128227	12	5,298	753
KLHL9	9p22	Early-onset distal myopathy	NA	NM_018847	1	5,710	617
LDB3	10q22.2-q23.3	Myopathy, myofibrillar, 4	609452	NM_001171610	14	5,436	732
LMNA	1q21.2	LGMD1B	159001	NM_170707	12	3,190	664
MATR3	5q31.2	Amyotrophic lateral sclerosis 21	606070	NM_001194954	18	5,604	847
MYH2	17p13.1	Inclusion body myopathy 3	605637	NM_017534	40	6,339	1,941
MYH7	14q12	Laing distal myopathy	160500	NM_000257	40	6,087	1,935
NEB	2q22	Nemaline myopathy 2, autosomal recessive	256030	NM_004543	150	20,637	6,669
PLEC1	8q24	LGMD2Q	613723	NM_000445	33	14,787	4,574
POMGNT1	1p34-p33	LGMD2O	613157	NM_001243766	23	2,934	748
POMT1	9q34.1	LGMD2K	609308	NM_001136113	20	3,320	725
POMT2	14q24.3	LGMD2N	613158	NM_013382	21	4,876	750
SGCA	17q12-q21.33	LGMD2D	608099	NM_000023	10	1,432	387
SGCB	4q12	LGMD2E	604286	NM_000232	6	4,431	318
SGCD	5q33	LGMD2F	601287	NM_000337	9	1,606	290
SGCG	13q12	LGMD2C	253700	NM_000231	8	1,624	291
TCAP	17q12	LGMD2G	601954	NM_003673	2	2,123	167
TPM2	9p13.2-p13.1	Nemaline myopathy 4, autosomal dominant	609285	NM_003289	9	1,189	284
TPM3	1q22-q23	Nemaline myopathy 1, autosomal dominant or recessive	609284	NM_001278188	8	3,131	248
TRIM32	9q31-q34.1	LGMD2H	254110	NM_012210	2	3,717	653
TTID	5q31	LGMD 1A	159000	NM_006790	10	2,337	498
TTN	2q31	LGMD2J	608807	NM_001267550	363	109,224	35,991
VCP	9p13-p12	Inclusion body myopathy with early-onset Paget disease and frontotemporal dementia 1	167320	NM_007126	17	4,370	806

Abbreviations: LGMD = limb-girdle muscular dystrophy; NA = not available.

Table 3 Summary of known or putative pathogenic *DYSF* mutations detected in this study

ID	Zygosity	Mutation type	Nucleotide change	Protein change	Listed in HGMD	dbSNP137	MAF in 1000 Genomes	MAF in HGVD	SIFT[a]	PolyPhen-2[b]
Pathologically proven cases										
Dys92-1	Het	Missense	c.356T>C	p.L119P	No		NA	NA	D	D
	Het	Missense	c.2997G>T	p.W999C	Yes	rs28937581	NA	NA	D	D
Dys129-1	Het	Nonsense	c.3444_3445delinsAA	p.Y1148X	Yes		NA	NA		
	Het	Nonsense	c.5903G>A	p.W1968X	Yes		NA	NA		
Dys149-1	Hom	Missense	c.1667T>C	p.L556P	Yes	rs200916654	0.0005	NA	D	P
Dys154-1	Hom	Nonsense	c.6135G>A	p.W2045X	Yes		NA	NA		
Dys166-1	Het	Frameshift	c.4200delC	p.P1400Pfs48X	Yes		NA	NA		
	Het	Missense	c.3118C>T	p.R1040W	Yes		NA	NA	D	D
Dys168-1	Het	Nonsense	c.2494C>T	p.Q832X	Yes	rs199543257	0.0005	NA		
	Het	Missense	c.2974T>C	p.W992R	Yes		NA	NA	D	D
Dys192-1	Hom	Missense	c.5078G>A	p.R1693Q	Yes		NA	NA	D	D
Dys194-1	Hom	Gross deletion	exon37-38del[c]		No		NA	NA		
Dys119-1-2	Het	Gross deletion	exon37-41del[d]		No		NA	NA		
	Het	Nonsense	c.3244G>T	p.E1082X	No		NA	NA		
Dys211-1	Het	Missense	c.2997G>T	p.W999C	Yes	rs28937581	NA	NA	D	D
	Het	Missense	c.5077C>T	p.R1693W	Yes		NA	NA	D	D
Dys213-1	Hom	Splicing	c.2644-2A>G		Yes		NA	0.001166		
Dys215-1	Het	Nonsense	c.1566C>G	p.Y522X	Yes		NA	NA		
	Het	Nonsense	c.2494C>T	p.Q832X	Yes	rs199543257	0.0005	NA		
Dys216-1	Hom	Missense	c.2974T>C	p.W992R	Yes		NA	NA	D	D
Dys218-1	Het	Splicing	c.663+1G>C		Yes		NA	NA		
	Het	Missense	c.2997G>T	p.W999C	Yes	rs28937581	NA	NA	D	D
Dys219-1	Het	Missense	c.2974T>C	p.W992R	Yes		NA	NA	D	D
	Het	Frameshift	c.3373delG	p.E1125Kfs9X	Yes		NA	NA		
Dys220-1	Hom	Nonsense	c.1566C>G	p.Y522X	Yes		NA	NA		
Clinically suspected cases										
Dys71-1	Het	Missense	c.356T>C	p.L119P	No		NA	NA	D	D
	Het	Missense	c.2997G>T	p.W999C	Yes	rs28937581	NA	NA	D	D
Dys116-1	Het	Missense	c.565C>G	p.L189V	Yes	rs13407355	0.02	0.020276	T	B
	Het	Missense	c.5873C>T	p.S1958F	No		NA	0.001166	D	D
	Het	Nonsense	c.6135G>A	p.W2045X	Yes		NA	NA		

Continued

Table 3 Continued

ID	Zygosity	Mutation type	Nucleotide change	Protein change	Listed in HGMD	dbSNP137	MAF in 1000 Genomes	MAF in HGVD	SIFT[a]	PolyPhen-2[b]
Dys132-1	Hom	Missense	c.1667T>C	p.L556P	Yes	rs200916654	0.0005	NA	D	P
Dys155-1	Hom	Nonsense	c.5713C>T	p.R1905X	Yes	rs121908959	NA	NA		
Dys207-1	Hom	Splicing	c.2643+1G>A		Yes	rs140108514	NA	NA		
Dys208-1	Hom	Missense	c.1663C>T	p.R555W	Yes		NA	NA	D	D
Dys210-1	Het	Missense	c.6196G>A	p.A2066T	Yes		NA	NA	T	B
	Het	Frameshift	c.5900delG	p.G1967Afs6X	No		NA	NA		

Abbreviations: HGMD = Human Gene Mutation Database; HGVD = Human Genetic Variation Database; Het = heterozygous; Hom = homozygous; MAF = minor allele frequency; NA = not available.
[a] SIFT scores are described as D = deleterious (SIFT ≤ 0.05); T = tolerated (SIFT >0.05).
[b] PolyPhen-2 (pp2_hvar) scores are described as D = probably damaging (≥0.909); P = possibly damaging (0.447 ≤ pp2_hdiv ≤ 0.909); B = benign (pp2_hdiv ≤ 0.446).
[c] Mutations are described according to NM_003494.3: c.3903+3532_c.4167+572del5862.
[d] Mutations are described according to NM_003494.3: c.3903+1161_c.4510-1036del51161.

mutations in non-*DYSF* genes (tables 1 and 4). Of these, novel or known mutations in *CAPN3* were detected in 10 patients, accounting for the majority of non-*DYSF* genes. The heterozygous p.V805A mutation in *MYH2*, which is a known mutation leading to inclusion body myositis,[21] was detected in Dys86-1. The pathogenicity of this mutation remained uncertain because of the lack of relevant information in muscle pathology.

Subsequently, MLPA was performed for the remaining 27 patients (table e-1), including all 14 patients who were undiagnosed after targeted sequencing but were pathologically proven, through targeted next-generation sequencing. We detected no additional duplications or deletions in *DYSF* (table e-1).

Genetic profile for pathologically proven cases. Figure 1 shows the genetic profile of the 90 pathologically proven cases (patients who showed sarcolemmal dysferlin deficiency in immunohistochemical analyses). Intriguingly, the 63 patients (47 previously diagnosed patients and 16 newly diagnosed patients) with *DYSF* mutations accounted for only 70% of cases, *CAPN* mutations accounted for 10% of cases (9/90), and *CAV3* mutations accounted for 2% of cases (2/90). The other genetic profile included mutations in *ANO5*, *GNE*, and *MYOT* (together with *CAV3* and *DYSF*), each of which was detected in a single individual. Clinical information for the remaining 14 patients who showed secondary dysferlin deficiency due to putative pathogenic mutations in non-*DSYF* genes is summarized in table 5.

DISCUSSION We performed targeted next-generation sequencing of 42 myopathy-associated genes in 64 patients with clinically or pathologically suspected dysferlinopathy. We found possible pathogenic mutations in *DYSF* or other genes in 38 patients (59.4%). The use of this targeted resequencing technique improved positive genetic detection from 65.3% (98/150 patients) to 82.7% (124/150 patients) overall, owing to (1) the detection of previously unrevealed *DYSF* mutations, including gross deletions, and (2) the comprehensive sequencing of non-*DYSF* genes and the detection of novel or known mutations in these genes.

Although secondary dysferlin deficiency can be caused by *CAPN3* mutations,[11–13] the exact frequency of *CAPN3* mutations in patients with dysferlin deficiency has not been reported previously. Human *CAPN3* is located on chromosome 15q15.1-15.3, comprises 24 exons, and codes a Ca^{2+}-dependent cysteine protease called calpain 3 (p94). Across the entire *CAPN3* gene, nearly 300 mutations have been reported to be pathogenic and the cause of LGMD2A (OMIM #253600),[22] which is estimated to be the most frequent type of LGMD in the Japanese

Table 4 Summary of known or putative pathogenic non-*DYSF* mutations detected in this study

ID	Gene	Zygosity	Mutation type	Nucleotide change	Protein change	Listed in HGMD	dbSNP137	MAF in 1000 genomes	MAF in HGVD	SIFT[a]	PolyPhen-2[b]
Pathologically proven cases											
Dys76-1	*CAPN3*	Het	Missense	c.2105C>T	p.A702V	Yes		NA	NA	D	D
			Missense	c.2120A>G	p.D707G	Yes	rs200379491	0.0005	0.005	D	D
Dys79-1	*CAPN3*	C/H	Missense	c.992T>A	p.V331D	No		NA	NA	D	D
			Splicing	c.1194-9A>G		Yes		NA	0.001166		
Dys81-1	*CAPN3*	Hom	Missense	c.1524+1G>T		Yes		NA	NA		
Dys88-1	*CAPN3*	C/H	Missense	c.1435A>G	p.S479G	Yes	rs201736037	NA	NA	D	P
			Nonsense	c.1786A>T	p.K596X	No		NA	NA		
Dys91-1	*GNE*	Hom	Missense	c.1714G>C	p.V572L	Yes	rs121908632	0.0005	0.004283	D	D
Dys112-1	*CAPN3*	Hom	Missense	c.1381C>T	p.R461C	Yes		NA	0.002232	D	D
Dys149-1	*MYOT*	Het	Missense	c.1214G>A	p.R405K	Yes		NA	NA	T	B
	CAV3	Het	Missense	c.40G>A	p.V14I	No	rs121909281	0.0014	0.001255	T	B
Dys185-1	*PLEC*	Hom	Splicing	c.4126-4A>G		Yes	rs7002152	0.25	0.188366		
Dys189-1	*CAPN3*	C/H	Missense	c.2120A>G	p.D707G	Yes	rs200379491	0.0005	0.005	D	D
			Frameshift	c.2287_2288del	p.Y763X	No		NA	NA		
Dys195-1	*CAPN3*	Hom	Frameshift	c.7delA	p.T3Pfs54X	No		NA	NA		
Dys201-1	*ANO5*	Hom	Splicing	c.180+2T>C		No		NA	NA		
Dys203-1	*CAV3*	Het	Missense	c.122T>C	p.F41S	No		NA	NA	D	D
Dys214-1	*CAPN3*	C/H	Splicing	c.1194-9A>G		Yes		NA	0.001166		
			Missense	c.1742C>G	p.S581C	Yes		NA	0.013158	D	D
Clinically suspected cases											
Dys45-1	*GNE*	Het	Missense	c.1714G>C	p.V572L	Yes	rs121908632	0.0005	0.004283	D	D
			Del/ins	c.907_908delinsGT	p.C303V	Yes	rs121908633	NA	NA	D	P
Dys53-1	*CAPN3*	Het	Missense	c.1202A>G	p.Y401C	Yes		NA	0.001166	D	D
			Missense	c.1892A>G	p.D631G	No		NA	NA	D	B
Dys86-1	*MYH2*	Het	Missense	c.2414T>C	p.V805A	Yes	rs200662973	0.0018	0.009337	T	B
Dys188-1	*CAPN3*	Het	Missense	c.1465C>T	p.R489W	Yes		NA	NA	D	D
			Missense	c.1892A>G	p.D631G	No		NA	NA	D	B

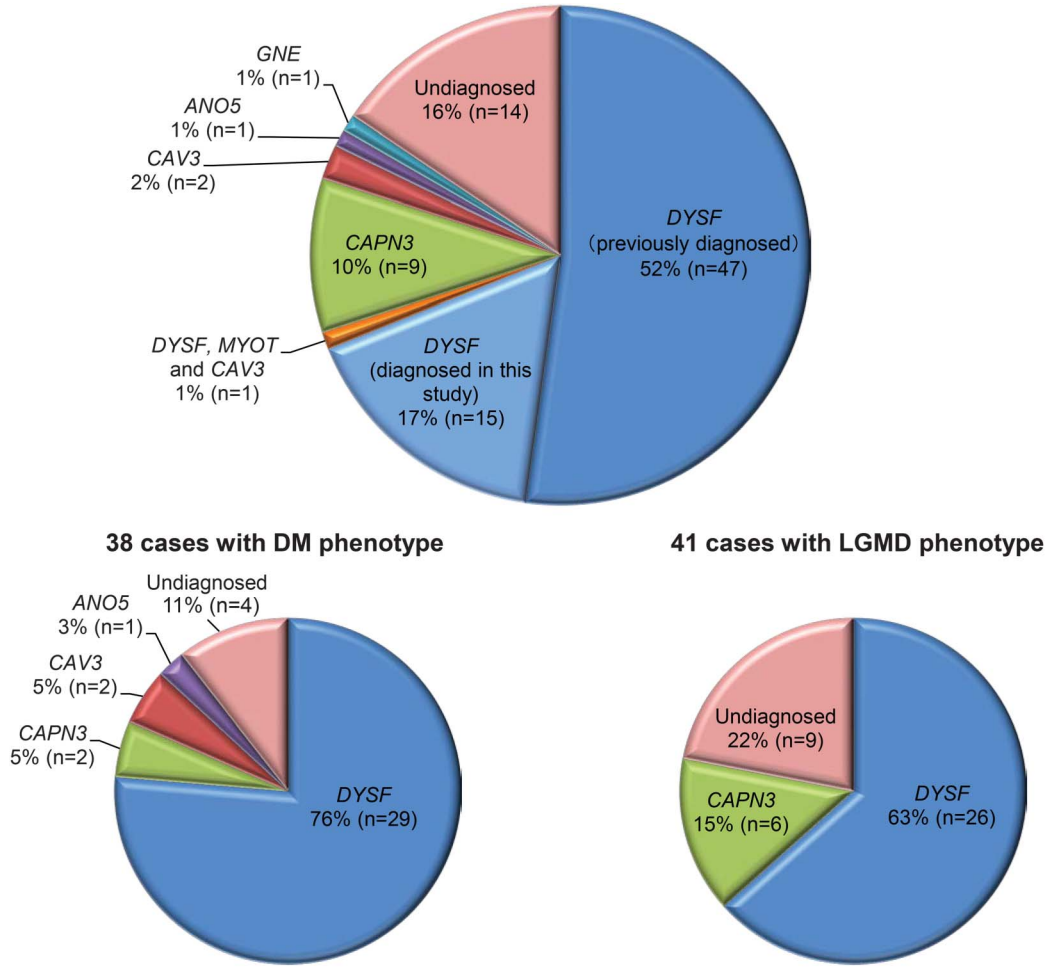
Abbreviations: C/H = compound heterozygous; HGMD = Human Gene Mutation Database; HGVD = Human Genetic Variation Database; Het = heterozygous; Hom = homozygous; MAF = minor allele frequency; NA = not available.

Mutations are described according to the following RefSeq numbers. *ANO5*: NM_213599, *BAG3*: NM_004281.3, *CAPN3*: NM_000070, *CAV3*: NM_033337, *FKRP*: NM_024301.4, *GNE*: NM_005476, *MYOT*: NM_006790, *MYH2*: NM_017534, *PLEC*: NM_000445.3.

[a] SIFT scores are described as D = deleterious (SIFT ≤ 0.05); T = tolerated (SIFT > 0.05).

[b] PolyPhen-2 (pp2_hvar) scores are described as D = probably damaging (≥0.909); P = possibly damaging (0.447 ≤ pp2_hdiv ≤ 0.909); B = benign (pp2_hdiv ≤ 0.446).

Figure 1 Genetic profile of 90 patients with dysferlin deficiency



DYSF mutations were identified in a total of 63 patients (70%). Nine patients (10%) were diagnosed with *CAPN3* mutations. Of the 90 patients, 38 and 41 manifested as distal myopathy (DM) and limb-girdle muscular dystrophy (LGMD), respectively, and the remaining 11 were unclassifiable. The genetic profiles for each manifestation are also shown. The proportion of *DYSF* mutations was more frequent for the DM phenotype (76%) than for the LGMD phenotype (63%), whereas *CAPN3* mutations were more frequent in the LGMD phenotype (15%) than in the DM phenotype (5%).

population.[8] In this study, although mutations in *CAPN3* were essentially distributed sporadically, thus not suggesting a specific genotype to associate with dysferlin deficiency, our result of 10% frequency in *CAPN3* mutations with dysferlin deficiency emphasizes the necessity for genetic analysis of both genes.

Clinically, 2 of the 9 patients with *CAPN3* mutations manifested atypically with a distal myopathy (DM) phenotype rather than LGMD (figure 1, table 5). One of the patients with DM (Dys189-1) had weakness of the tibialis anterior muscle as an initial symptom and showed gastrocnemius muscle atrophy, closely resembling MMD1 (table 5).

Immunohistochemistry for calpain 3 revealed reduced expression in this patient. The other patient (Dys88-1) also had distal weakness with wasting, particularly in the tibialis anterior muscle. Although immunohistochemistry for calpain 3 was rarely investigated in our cases of dysferlinopathy, a secondary reduction in calpain 3 with *DYSF* mutations has also been reported.[23] These findings indicate that it is difficult to distinguish calpainopathy from dysferlinopathy, even when considering clinical information together with immunohistochemical analysis of both proteins. Genetic analysis of both genes would be valuable for genetic counseling, clinical management,[24] and possible specific genetic therapies in the future.

Non-*DYSF* and non-*CAPN3* genes were responsible for 5% of patients with dysferlin deficiencies (figure 1, table 5). A novel *CAV3* mutation was identified in Dys203-1, and immunohistochemical analyses in this patient showed reduced expression of both dysferlin and caveolin, confirming the diagnosis. Together with the known homozygous p.L556P mutation in *DYSF*, a known heterozygous p.R405K mutation in *MYOT* and a rare mutation of p.V14I in *CAV3* were detected in 1 patient (Dys149-1). This

Table 5 Clinical characteristics for the 14 patients who showed secondary dysferlin deficiency

ID	Gene	Mutation	Sex, population, family history	Initial manifestation	Phenotype	Distribution of affected muscles	Serum CK, IU/L	Muscle pathology	Immunohistochemical detection of dysferlin
Dys201-1	*ANO5*	Hom, c.180+2T>C	Male, Japanese, sporadic	54 y, walking disability	DM	GC, BF, AM	4,489	Inflammation and degeneration	Reduced expression (figure e-1)
Dys70-1	*CAV3*	Het, p.R27Q	Female, Japanese, sporadic	12 y, hyperCK	DM	Small muscles of hands and feet	2,092	Mild myopathic change and type 1 fiber predominance	Reduced expression (not shown)
Dys203-1	*CAV3*	Het, p.F41S	Male, Japanese, sporadic	43 y, hyperCK	DM	GC, RF, Ham	2,295	Degeneration with RVs and neuropathic change	Reduced expression (figure e-1)
Dys189-1	*CAPN3*	C/H, p.D707G, p.763_763del	Male, Japanese, sister	19 y, walking disability	DM	TA, IP (weakness); GC, BF (atrophy)	3,695	Mild myopathic change	Reduced expression (figure e-1)
Dys195-1	*CAPN3*	Hom, p.T3fs	Female, Egyptian, brother	NA	NA	NA	NA	Inflammation	Absent (not shown)
Dys214-1	*CAPN3*	C/H, c.1194-9A>G, p.S581C	Female, Japanese, sporadic	Childhood, walking disability	LGMD	Proximal and lower limb dominant	3,324	NA	Reduced expression (not shown)
Dys76-1	*CAPN3*	Possible C/H, p.A702V, p.D707G	Female, Japanese, sporadic	28 y, walking disability	LGMD	Diffuse	1,000–3,000	Degeneration	Reduced expression (not shown)
Dys79-1	*CAPN3*	C/H, c.1194-9A>G, p.V331D	Male, Japanese, sporadic	18 y, walking disability	LGMD	Proximal dominant with scapular wing	1,992	Degeneration with lobulated fibers	Reduced expression (not shown)
Dys81-1	*CAPN3*	Hom, c.1524+1G>T	Female, Japanese, brother	18 y, walking disability	LGMD	Proximal dominant	115	Degeneration	Reduced and mosaic expression (not shown)
Dys88-1	*CAPN3*	Possible C/H, p.S479G, p.K596X	Female, Australian, cousin	NA	DM	TA	NA	NA	Reduced expression (not shown)
Dys112-1	*CAPN3*	Hom, p.R461C	Male, Japanese, sporadic	43 y, grip weakness	Unclassifiable	BB	1,500	Dystrophic change	Reduced expression (not shown)
Dys209-1	*CAPN3*	Hom, c.1194-9A>G	Female, Japanese, sporadic	Childhood, walking disability	LGMD	Proximal dominant	261	Mild degeneration	Reduced expression (not shown)
Dys91-1	*GNE*	Hom, p.V572L	Male, Japanese, NA	NA	NA	NA	NA	RVs	Partial reduction (not shown)
Dys149-1	*MYOT*, *CAV3*	Het, p.R405K Het, p.V14I	Male, Japanese, sporadic	18 y, hyperCK	NA	No weakness or atrophy	>20,000	NA	Absent (figure e-1)

Abbreviations: AM = adductor magnus; BB = biceps brachii; BF = biceps femoris; C/H = compound heterozygous; CK = creatine kinase; DM = distal myopathy; GC = gastrocnemius; GM = gluteus maxim; Ham = hamstrings; Het = heterozygous; Hom = homozygous; IP = iliopsoas; LGMD = limb-girdle muscular dystrophy; NA = not available; RF = rectus femoris; RV = rimmed vacuole; TA = tibialis anterior.

patient was a sporadic case with isolated hyperCKemia. Thus, it is unknown whether the muscle pathology showing absent dysferlin was caused by the *DYSF* mutation or by the associated effects of multiple mutations. A novel homozygous *ANO5* splicing mutation was identified in Dys201-1. *ANO5* encodes the transmembrane protein anoctamin 5 and is the causative gene for MMD3 (OMIM #613319) and LGMD2L (OMIM #611307). Asymmetrical muscle atrophy was predominantly observed in the gastrocnemius, biceps femoris, and adductor magnus in this patient and is a possible distribution in both MMD1 and MMD3.[25] Expression of dysferlin in this patient was diffusely decreased, mimicking MMD1 (figure e-1). A homozygous *GNE* mutation was detected in Dys91-1, compatible with DM with rimmed vacuoles, and this patient had a partial reduction in dysferlin (figure e-1). Secondary dysferlin deficiency from mutations in *ANO5* or *GNE* has not been reported previously. Hence, further investigations are required to clarify the possible association between these mutations and dysferlin deficiency.

Even after the targeted next-generation sequencing, 26 of 64 patients (40.6%) remained undiagnosed. This means that undiagnosed patients accounted for 15.6% of pathologically proven cases (14/90 patients) and 16.2% of clinically suspected cases (12/74 patients), showing nonsignificant difference between the 2 groups (table 1). There are several possible explanations: (1) mutations in subtle unsequenced targeted regions were not detected in this study; (2) intronic *DYSF* mutations that might result in abnormal splicing were not detected because these regions, along with messenger RNA, were not investigated; (3) pathogenic mutations were excluded because of biased filtering or overfiltering; or, most probably; (4) other genes not targeted in this study may be responsible. More than 50 molecules have been reported to interact with dysferlin.[26–32] These molecules are encoded by a fraction of genes such as *CAPN3*, *CAV3*, *DES*, *FLNC*, and *FHL1*, which are already known to cause myopathies. The remaining molecules may well be the next candidates. The identification of novel molecules that cause dysferlin deficiency can help elucidate the mechanisms by which dysferlin achieves membrane repair.

The study had a few limitations. The targeted genes in this study did not include the *DMD* gene, whose mutation is reported to result in secondary dysferlinopathy.[7] The immunoblot assay of muscle samples was not performed because muscle samples were not available. Thus, the quantitative level of dysferlin expression in sarcolemma or cytoplasm remains undetermined. The allelic zygosity of the multiple heterozygous candidate variants was not confirmed in all patients for the following reasons: (1) long-range PCR was unsuccessful if the distance between variants was too long or genomic DNA was estimated to be fragmented, or (2) there was a lack of available genomic parental DNA.

We used targeted next-generation sequencing to effectively and comprehensively analyze mutations in myopathy-associated genes and to clarify the heterogeneous nature of the genetic profile in patients with suspected dysferlinopathy. Our results illustrate the importance of comprehensive analysis of related genes when performing genetic diagnosis for dysferlinopathy. We believe that the genes and molecules responsible for the cases in which diagnosis remained unresolved will be identified by future whole-exome sequencing projects.

AUTHOR CONTRIBUTIONS

Rumiko Izumi: principal author, designed the study, analyzed and interpreted the data, drafted the manuscript. Tetsuya Niihori and Yoko Aoki: designed the study, analyzed and interpreted the data, and revised the manuscript. Toshiaki Takahashi: acquired and provided data, performed the Sanger sequencing, and revised the manuscript. Naoki Suzuki, Masaaki Kato, and Hitoshi Warita: revised the manuscript. Maki Tateyama: performed the immunohistochemical analysis of the biopsied muscles and revised the manuscript. Chigusa Watanabe, Kazuma Sugie, Hirotaka Nakanishi, and Gen Sobue: acquired and provided data. Masashi Aoki: designed the study, revised the manuscript, and acquired funding.

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Genetic profile for suspected dysferlinopathy identified by targeted next-generation sequencing

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