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Journal of Human Genetics (2013) 58, 259–266

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ORIGINAL ARTICLE

Exome sequencing identifies a novel *TTN* mutation in a family with hereditary myopathy with early respiratory failure

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Myofibrillar myopathy (MFM) is a group of chronic muscular disorders that show the focal dissolution of myofibrils and accumulation of degradation products. The major genetic basis of MFMs is unknown. In 1993, our group reported a Japanese family with dominantly inherited cytoplasmic body myopathy, which is now included in MFM, characterized by late-onset chronic progressive distal muscle weakness and early respiratory failure. In this study, we performed linkage analysis and exome sequencing on these patients and identified a novel c.90263G>T mutation in the *TTN* gene (NM_001256850). During the course of our study, another groups reported three mutations in *TTN* in patients with hereditary myopathy with early respiratory failure (HMERF, MIM #603689), which is characterized by overlapping pathologic findings with MFMs. Our patients were clinically compatible with HMERF. The mutation identified in this study and the three mutations in patients with HMERF were located on the A-band domain of titin, suggesting a strong relationship between mutations in the A-band domain of titin and HMERF. Mutation screening of *TTN* has been rarely carried out because of its huge size, consisting of 363 exons. It is possible that focused analysis of *TTN* may detect more mutations in patients with MFMs, especially in those with early respiratory failure.
Journal of Human Genetics (2013) **58,** 259–266; doi:10.1038/jhg.2013.9; published online 28 February 2013

Keywords: A-band; cytoplasmic body; Fn3 domain; hereditary myopathy with early respiratory failure; HMERF; myofibrillar myopathy; titin; *TTN*

INTRODUCTION

Myofibrillar myopathies (MFMs) were proposed in 1996 as a group of chronic muscular disorders characterized by common morphologic features observed on muscle histology, which showed the focal dissolution of myofibrils followed by the accumulation of products of the degradative process.[1] The clinical phenotype of MFM is characterized by slowly progressive muscle weakness that can involve proximal or distal muscles, with onset in adulthood in most cases. However, other phenotypes are highly variable. Although 20% of patients with MFMs have been revealed to have mutations in *DES*, *CRYAB*, *MYOT*, *LDB* (*ZASP*), *FLNC* or *BAG3*, the major genetic basis of MFMs remains to be elucidated.

Respiratory weakness is one of the symptoms of MFMs. The early or initial presentation of respiratory failure is not a common manifestation of MFMs as a whole, and there are limited reports regarding a fraction of patients with *DES*,[2] *MYOT*[3] or *CRYAB*[4] mutation. In 1993, our group reported a Japanese family with dominantly inherited cytoplasmic body (CB) myopathy,[5] which is now included in MFM. Currently, this family includes 20 patients in five successive generations who show almost homogeneous clinical features characterized by chronic progressive distal muscle weakness and early respiratory failure. However, the underlying genetic etiology in this family was unknown. The aim of this study was to determine the genetic cause in this family. To identify the responsible genetic mutation, we performed linkage analysis and whole-exome sequencing.

MATERIALS AND METHODS

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 in the study.

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Received 23 October 2012; revised 9 January 2013; accepted 10 January 2013; published online 28 February 2013

Clinical information on the family

This family includes 20 patients (13 males and 7 females) in five successive generations (Figure 1). The family is of Japanese ancestry, and no consanguineous or international mating was found. Of all patients, seven underwent a muscle biopsy, and two were autopsied. All of the histological findings were compatible with MFM (see clinical data).

The age of onset ranged from 27–45 years. The most common presenting symptom was foot drop. At the initial evaluations, muscle weakness was primarily distributed in the ankle dorsiflexors and finger extensors. The patients were generally built and showed no other extramuscular abnormalities. In addition to this chronic progressive distal muscle weakness, respiratory distress occurred between 0 and 7 years from the initial onset (average 3.8 years) in seven patients (IV-9, V-2, A, B, E, H, and J) with adequate clinical information. Two patients who had not had any respiratory care died of respiratory failure approximately a decade from the initial onset. The other patients have been alive for more than 10 years (maximum 18 years) but require nocturnal non-invasive positive pressure ventilation. They were 37–58 years of age as of 2012 and able to walk independently with or without a simple walking aid. Although the time at which patients recognized dysphagia or dysarthria varied between 1 to more than 10 years from the initial onset, decreased bulbar functions had been noted at the initial evaluation in most cases. Cardiac function was normally maintained in all patients of the family.

Clinical data

The level of serum creatine kinase was normal or mildly elevated. Electromyography of affected muscles showed a chronic myogenic pattern, and the nerve conduction study did not suggest any neuropathic involvement. Muscle imaging showed focal atrophy in the tibialis anterior, tibialis posterior, extensor hallucis and digitorum longus, peroneal and semitendinosus muscle on initial assessment (Figure 2A), and atrophy became clear in cervical muscles, shoulder girdles, intercostals and proximal limb muscles in the following several years. Upon muscle biopsy, the most common finding was numerous cytoplasmic bodies (CBs), which were found on 7.3% of myofibers in the tibialis anterior of individual E (Figure 2B (a–c)) and 50–80% of intercostals in other cases.[5] Other nonspecific findings were increased variability in the size of myofibers, central nuclei and rimmed vacuoles observed on a few fibers. No strong immunoreaction of desmin was seen in the CBs (Figure 2B (d, e)). An electron microscope examination showed that the regular sarcoplasmic pattern was replaced by abnormal fine filamentous structures, which seemed to attach to the Z-band. CBs were also found in almost all skeletal muscles and some smooth muscles in autopsied cases.[5] Cardiac myofibers also contained numerous CBs in one of the autopsied cases (V-2),[5] although the patient did not present any cardiac complication. The sequence analysis of the coding regions and flanking introns of *DES* and *MYOT* showed no pathogenic mutation in individual E. An array comparative genomic hybridization performed with the Agilent SurePrint G3 Human CGH 1M microarray format in individual A did not reveal any aberrations of genomic copy number.

Linkage analysis

DNA was extracted by standard methods. Linkage analysis was performed on nine family members (A–I in Figure 1; four of them were affected, and the others were unaffected) through genotyping using an Illumina Human Omni 2.5 BeadChip (Illumina, San Diego, CA, USA). We chose single-nucleotide polymorphisms (SNPs) that satisfied all of the following criteria: (1) autosomal SNPs whose allele frequencies were available from the HapMap project (http://hapmap.ncbi.nlm.nih.gov/), (2) SNPs that were not monomorphic among members and (3) SNPs that were not in strong linkage disequilibrium with neighboring SNPs (r2 values <0.9). Then, we selected the first five SNPs from each position of integer genetic distance from SNPs that met the above criteria for the initial analysis. The details were as follows; we chose a SNP closest to 0 cM and the neighboring four SNPs. If the genetic distance of a SNP was the same as that of the next SNP, we considered the genomic position to determine their order. We repeated this process at 1 cM, 2 cM and so on.

We performed a multipoint linkage analysis of the data set (17 613 SNPs) using MERLIN[6] 1.1.2 under the autosomal dominant mode with the following parameters: 0.0001 for disease allele frequency, 1.00 for individuals heterozygous and homozygous for the disease allele and 0.00 for individuals

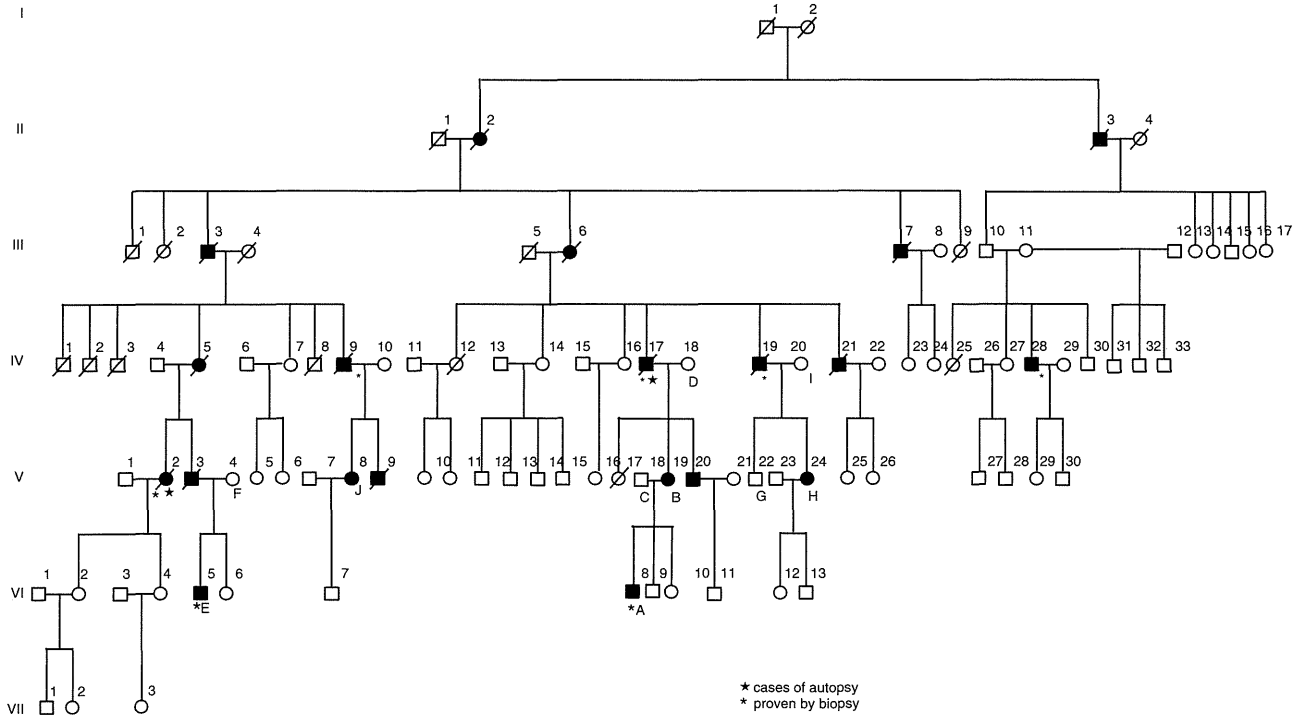


Figure 1 Family pedigree. Filled-in symbols indicate individuals with MFM. Empty symbols indicate unaffected individuals. A star and asterisk indicate autopsy-proven and muscle biopsy-proven cases, respectively. (A–J) indicates individuals whose DNA was used for this study.

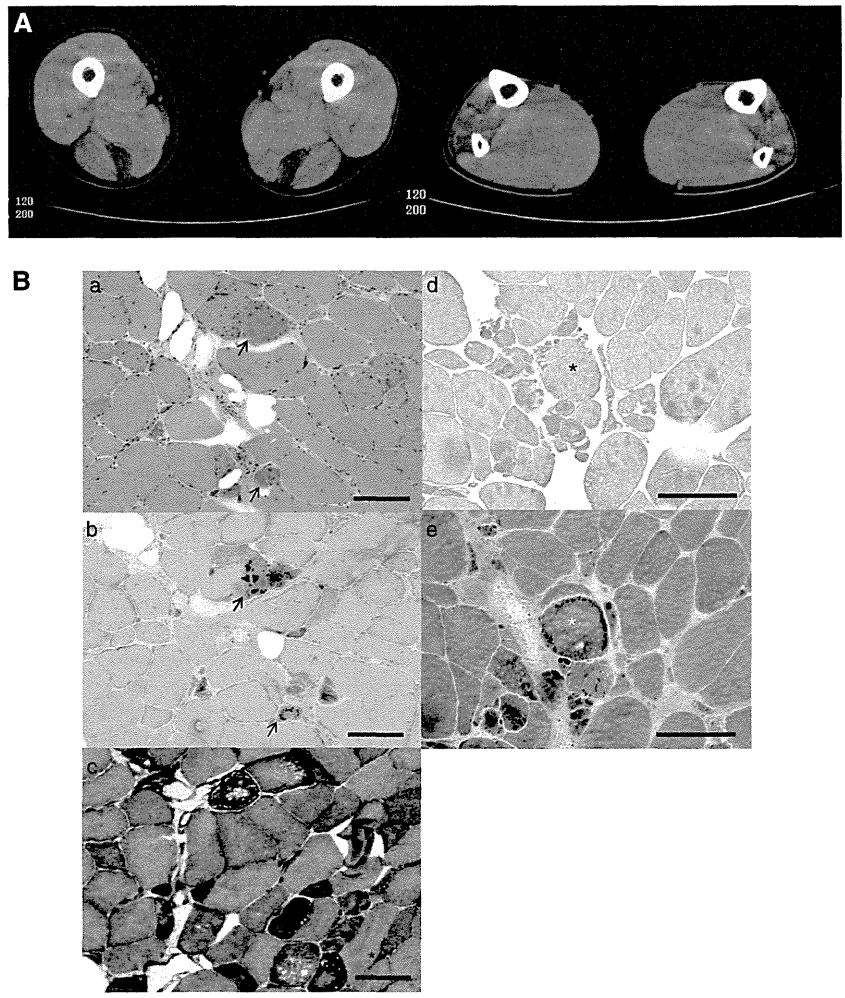


Figure 2 Family clinical data. (**A**) Muscle computed tomography of affected lower extremity. The imaging in the initial assessment of individual A showed symmetrical atrophy and fatty replacement of the semitendinosus in the proximal lower extremities (left) and the tibialis anterior, tibialis posterior, extensor hallucis and digitorum longus, and peroneal muscle in the distal (right) lower extremities. (**B**) Pathology of muscle biopsy. Hematoxylin-eosin (a), Gomori-trichrome (b) and NADH (nicotinamide adenine dinucleotide)-tetrazolium reductase (c) staining of the muscle biopsy sample from the tibialis anterior of individual E are shown. CBs are indicated by arrows. CBs were round or oval, 5–10 μm in diameter and predominantly located in the periphery of type 1 fibers, which stained eosinophilic with hematoxylin-eosin and blue–purple with Gomori-trichrome. NADH-tetrazolium reductase staining showed disorganization of the myofibrillar network. Immunostaining for desmin (d) and Gomori-trichrome staining (e) are serial sections of the muscle biopsy from individual E. Stars indicate corresponding fibers. No strong immunoreaction of desmin was seen in the CBs. Scale bars = 100 μm

homozygous for the alternative allele. After this first analysis, a second analysis was performed with all SNPs fulfilling the above criteria around the peaks identified in the first analysis.

Exome sequencing

Exome sequencing was performed on seven family members in three generations (A–E, H and I in Figure 1), four of whom were affected. Exon capture was performed with the SureSelect Human All Exon kit v2 (individuals E, H and I) or v4 (A–D) (Agilent Technologies, Santa Clara, CA, USA). Exon libraries were sequenced with the Illumina Hiseq 2000 platform according to the manufacturer's instructions (Illumina). Paired 101-base pair reads were aligned to the reference human genome (UCSChg19) using the Burrows-Wheeler Alignment tool.[7] Likely PCR duplicates were removed with the Picard program (http://picard.sourceforge.net/). Single-nucleotide variants and indels were identified using the Genome Analysis Tool Kit (GATK) v1.5 software.[8] SNVs and indels were annotated against the RefSeq database and dbSNP135 with the ANNOVAR program.[9] We used the PolyPhen2 polymorphism phenotyping software tool[10] to predict the functional effects of mutations.

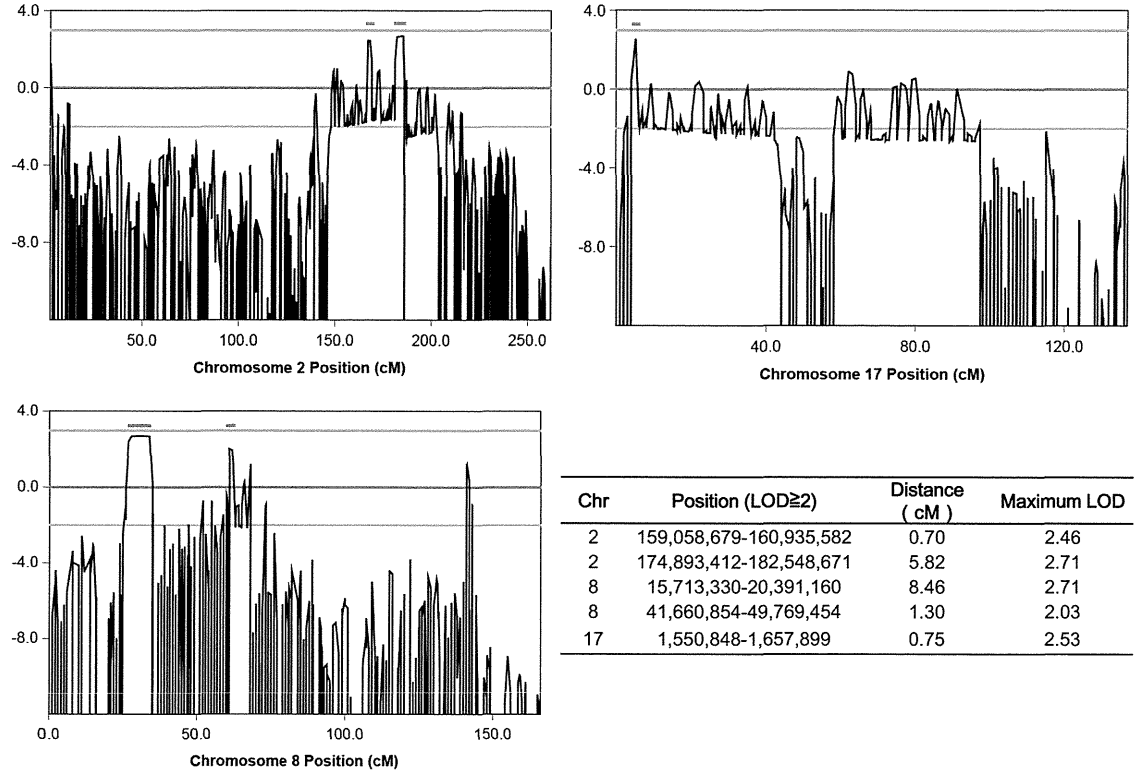
Sanger sequencing

To confirm that mutations identified by exome sequencing segregated with the disease, we performed direct sequencing. PCR was performed with the primers shown in Supplementary Table 1. PCR products were purified with a MultiScreen PCR plate (Millipore, Billerica, MA, USA) and sequenced using BigDye terminator v1.1 and a 3500xL genetic analyzer (Applied Biosystems, Carlsbad, CA, USA).

RESULTS

Linkage analysis

The first linkage analysis identified five regions across autosomes with a logarithm of odds (LOD) score greater than 2 (Figure 3). Of the five regions, two were on chromosome 2 (from 167 cM to 168 cM, with a maximum LOD score of 2.46 and from 182 cM to 185 cM, with a maximum LOD score of 2.71), the other two were on chromosome 8 (from 27 cM to 34 cM, with a maximum LOD score of 2.71 and at 61 cM, with a maximum LOD score of 2.03), and one was on



Chr	Position (LOD≧2)	Distance (cM)	Maximum LOD
2	159,058,679-160,935,582	0.70	2.46
2	174,893,412-182,548,671	5.82	2.71
8	15,713,330-20,391,160	8.46	2.71
8	41,660,854-49,769,454	1.30	2.03
17	1,550,848-1,657,899	0.75	2.53

Figure 3 Linkage analysis. Linkage analysis was performed on nine family members (four of them were affected, the others were unaffected) using an Illumina Human Omni 2.5 BeadChip. Five regions with an LOD score greater than 2 (indicated by bar) were identified. A full color version of this figure is available at the *Journal of Human Genetics* journal online.

Table 1 Summary of detected variants by exome sequencing

Individual *Morbidity*	*A* *Affected*	*B* *Affected*	*C* *Unaffected*	*D* *Unaffected*	*E* *Affected*	*H* *Affected*	*I* *Unaffected*	*Segregated in seven family members*
Exonic, splicing	10089	10064	10079	10065	10230	10194	10216	64
Nonsynonymous, splicing, indel, nonsense	4987	5020	5055	5038	5143	5234	5200	32
Allele frequency not available	577	600	536	555	671	794	786	2

chromosome 17 (at 5 cM, with a maximum LOD score of 2.53). In the second detailed linkage analysis, these peaks were determined to range from 167.49 cM at rs4233674 at position 159 058 679 to 168.19 cM at rs7598162 at position 160 935 582, and from 181.23 cM at rs4402725 at position 174 893 412 to 187.05 cM at rs7420169 at position 182 548 671 on chromosome 2; from 26.42 cM at rs2736043 at position 15 713 330 to 34.88 cM at rs9325871 at position 20 391 160, and from 61.02 cM at rs6999814 at position 41 660 854 to 62.32 cM at rs10957281 at position 49 769 454 on chromosome 8; and from 4.7 cM at rs11078552 at position 1 550 848 to 5.45 cM at rs1057355 at position 1 657 899 on chromosome 17. Haplotypes shared by affected individuals in these regions were confirmed by visual inspection. There were a few incompatible SNPs in these regions, presumably due to genotyping error.

Exome sequencing and segregation analysis

In exome sequencing, an average of 215 million reads enriched by SureSelect v4 (SSv4) and 319 million reads enriched by SureSelect v2 (SSv2) were generated, and 99% of reads were mapped to the reference genome by Burrows-Wheeler Alignment tool. An average of 57% (SSv4) and 61% (SSv2) of those reads were duplicated and removed, and an average of 80% (SSv4) and 66% (SSv2) of mapped reads without duplicates were in target regions. The average coverage of each exome was 163-fold (SSv4) and 130-fold (SSv2). An average of 85% (SSv4) and 69% (SSv2) of target regions were covered at least 50-fold (Supplementary Table 2). On average, 10 133 SNVs or indels, which are located within coding exons or splice sites, were identified per individual (Table 1). A total of 64 variants were common among patients and not present in unaffected individuals, and 32 of those were left after excluding synonymous SNVs. In these variants, only the heterozygous mutation c.90263G>T (NM_001256850) at position 179 410 777 of chromosome 2, which was predicted to p.W30088L in *TTN*, was novel (that is, not present in dbSNP v135 or 1000 genomes). Polyphen2 predicted this mutation as probably damaging. This mutation was located in a candidate region suggested by the linkage analysis in the present study. The other variants were registered with dbSNP135, and the allele frequencies, except for one SNV, rs138183879, in *IKBKB*, ranged from 0.0023 to 0.62.

a

Gene	Chr	Position	Variant type	Reference	Variant	dbSNP v135	Coding change	Prediction	Segregaion analysis
TTN	2	179 410777	Missense	G	T	Not present	W30088L	Probably damaging	Segregating
IKBKB	8	42 188 457	Missense	C	T	rs138183879	T742M	Benign	Non-segregating

b

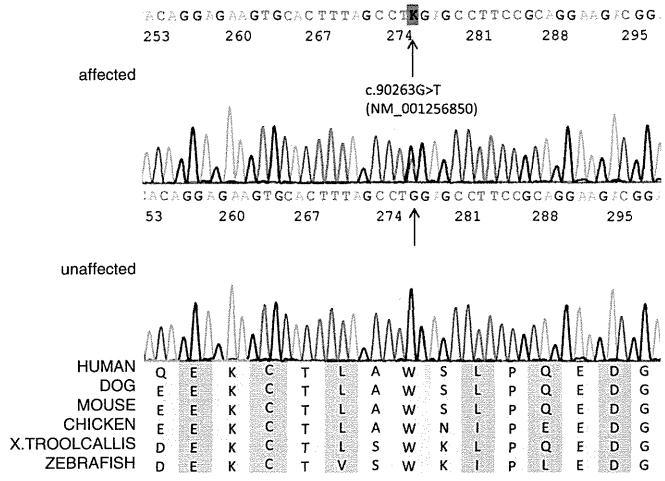


Figure 4 Identified mutations by exome sequencing. (**a**) We performed segregation analysis of two candidates. (**b**) The identified *TTN* mutation and its conservation among species. Sanger sequencing confirmed the heterozygous G to T substitution (indicated by the arrow) at the position chr2;179 410 777, which corresponds to c.90263G>T in exon 293 (NM_001256850.1). The substitution leads to p.W30088L (NP_001243779.1), and this amino acid is conserved among species.

These values were not compatible with the assumption that MFM was a rare disease and showed complete penetrance in this family. The allele frequency of rs138183879 was not available in dbSNP135, and this SNV was in the candidate region on chromosome 8 based on linkage analysis.

We then performed a segregation analysis on the two candidates, the novel mutation c.90263G>T in *TTN* and rs138183879 in *IKBKB*, through Sanger sequencing in 10 family members (A–J in Figure 1; Figure 4a). The rs138183879 SNP was not found in individual J, that is, it was not segregated with the disease in this family. In contrast, the novel mutation c.90263G>T in *TTN* was detected in all patients ($n=5$) and not detected in any of the unaffected family members ($n=5$) or 191 ethnically matched control subjects (382 chromosomes). These results suggested that this rare mutation in *TTN* segregated with the disease in this family.

DISCUSSION

In this study, we found that a novel missense mutation in *TTN* segregated with MFM in a large Japanese family. The identified c.90263G>T mutation in *TTN* (NM_001256850) was considered to be the genetic cause of MFM in our family, because (1) exome sequencing revealed that this was the best candidate mutation after filtering SNPs and indels, (2) this mutation is located in a region on chromosome 2 shared by affected family members, (3) the segregation with MFM was confirmed by Sanger sequencing, (4) this mutation was not detected in 191 control individuals, (5) this mutation was predicted to alter highly conserved amino acids (Figure 4b) and (6) *TTN* encodes a Z-disc-binding molecule called titin, which is similar to all of the previously identified causative genes for MFMs, which also encode Z-disc-associated molecules.

Recently, three mutations in *TTN* have been reported as the causes of hereditary myopathy with early respiratory failure (HMERF, MIM #603689),[11–16] which has similar muscle pathology to MFMs. The identified novel missense mutation c.90263G>T in our study was located on the same exon as recently reported HMERF mutations: c.90272C>T in a Portuguese family[16] and c.90315T>C in Swedish and English families[14,15] (Table 2). This finding suggests the possibility that our family can be recognized as having HMERF from a clinical aspect.

Compared with symptoms described in the past three reports on HMERF (also see Table 2), our patients have common features, such as autosomal dominant inheritance, early respiratory failure, the absence of clinically apparent cardiomyopathy, normal to mild elevation of serum CK and histological findings compatible with MFM. Early involvement of the tibialis anterior is also common, except for the Portuguese family, who reported isolated respiratory insufficiency and a milder presentation of HMERF. Thus, our family shares major clinical manifestations with patients with HMERF, suggesting that the identified mutation is novel for MFM and HMERF.

To date, mutations in *TTN* have been identified in skeletal myopathy and cardiomyopathy.[17,18] The relationship between the variant positions on *TTN* and phenotypes accompanied by skeletal or respiratory muscle involvement is summarized in Table 2. Titin is a large protein (4.20 MDa) that extends from the Z-disk to the M-line within the sarcomere, and it is composed of four major domains: Z-disc, I-band, A-band and M-line (Figure 5). All four HMERF mutations detected by other groups and our study were consistently located in the A-band domain, while mutations in tibial muscular dystrophy (TMD) (MIM #600334),[19–24] limb-girdle muscular dystrophy type 2J (LGMD2J) (#608807)[19,25] and early-onset myopathy with fatal cardiomyopathy (#611705)[26] were located in the M-line domain. HMERF and TMD have some common clinical characteristics, such as autosomal dominant inheritance with onset in adulthood and strong involvement of the tibialis anterior muscle.

Table 2 Previously reported TTN mutations with skeletal and/or respiratory muscle involvement

Phenotype	*LGMD*	*HMERF*	*Our family*	*HMERF*	*HMERF*	*TMD*	*TMD*	*LGMD2J*	*TMD*	*TMD*	*TMD*	*TMD*	*TMD*	*Early-onset myopathy with fatal cardiomyopathy*	*Early-onset myopathy with fatal cardiomyopathy*
Reported by	Vasli *et al.*[16]	Ohlsson *et al.*,[14] Pfeffer *et al.*[15]	Abe *et al.*[5]	Vasli *et al.*[16]	Edstrom *et al.*,[12] Nicolao, *et al.*[11] Lang e *et al.*[13]	Hackman *et al.*[23]	Udd *et al.*,[20] Hackman *et al.*[19]	Udd *et al.*,[25] Hackman *et al.*[19]	Pollazzon *et al.*[24]	Van den Bergh *et al.*[22]	Seze *et al.*,[21] Hackman *et al.*[19]	Hackman *et al.*[23]	Hackman *et al.*[23]	Carmignac *et al.*[26]	Carmignac *et al.*[26]
Mutation identified in Nucleotide (NM_001256850.1)	2012 c.3100G>A, c.52024G>A	2012 c.90315T>C	2012 c.90263G>T	2012 c.90272C>T	2005 c.97348C>T	2008 c.102724delT	2002 102857_ 102867 del11ins11	2002 102857_ 102867 del11ins11	2010 c.102914A>C	2003 c.102917T>A	2002 c.102944T>C	2008 c.102966delA	2008 c.102967C>T	2007 g.289385del ACCAAGTG	2007 g.291297delA
Protein (NP_001243779.1)	p.V1034M, p.A17342T	p.C30071R	p.W30088L	p.P30091L	p.R32450W				p.H34305P	p.I34306N	p.L34315P		p.Q34323X		
Domain	I-band, A-band	A-band (Fn3)	A-band (Fn3)	A-band (Fn3)	A-band (kinase)	M-line	M-line	M-line	M-line	M-line	M-line	M-line	M-line	M-line	M-line
Population	French	Swedish English	Japanese	Portuguese	Swedish	French	Finnish	Finnish	Italian	Belgian	French	Spanish	French	Sudanese	Moroccan
Inheritance	AR	AD	AD	AD	AD	AD	AD	AR	AD	AD	AD	AD	AD	Consanguineous siblings	Consanguineous siblings
Onset	35	33–71	27–45	46	20–50s	20–30s	35–55	20–30s	50–60s	47	45	40–50s	30s	Neonatal	Infant-early childhood
Skeletal muscles															
Major	Proximal UL and LL	TA, PL, EDL, ST	TA, ST	No	TA, neck flexor, proximals	TA, GA,HAM, pelvic	TA	All proximals	TA	TA	TA	TA	TA, HAM, pelvic	General muscle weakness and hypotonia	Psoas, TA, GA, peroneus
Minor		Neck flexor	Cervical, shoulder girdles, intercostals, proximal limb			QF				EDL, peroneal, TP	GA, femoral, scapular	HAM, GA	GA, distal UL		QF, proximal UL, neck, facial, trunk flexor
Spared			Facial			Proximal UL	Facial, UL, proximals	Facial		UL, proximal LL	Facial	UL	Proximal UL, QF		
Cardiac muscles	ND	No	No	ND	ND	ND	No	No	ND	ND	ND	ND	ND	DCM, onset; in the first decade	DCM, onset; 5–12 years old
Respiratory failure	ND	Yes, within 5–8 years	Yes, within 7 years	Isolated respiratory failure	Yes, as first presentation	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Muscle pathologic features	ND	Inclusion bodies (major) and RVs (minor)	Cytoplasmic bodies (major) and RVs (minor)	Cytoplasmic bodies	Cytoplasmic bodies, positive for rhodamine-conjugated phalloidin	Dystrophic pattern without vacuoles	Nonspecific dystrophic change	Nonspecific dystrophic change, loss of calpain-3	Dystrophic pattern with RVs	Nonspecific, RV	Nonspecific	Dystrophic pattern with RVs	Nonspecific	Minicore-like lesions and abundant central nuclei	Minicore-like lesions and abundant central nuclei

Abbreviations: AD, autosomal dominant; AR, autosomal recessive; DCM, dilated cardiomyopathy; EDL, extensor digitorum longus; GA, gastrocnemius; HAM, hamstrings; LL, lower limb; ND, not described; no, no involvement; PL, peroneus longus; QF, quadriceps femoris; RV, rimmed vacuole;
ST, semitendinosus; TA, tibialis anterior; TMD, tibial muscular dystrophy; TP, tibialis posterior; UL, upper limb.

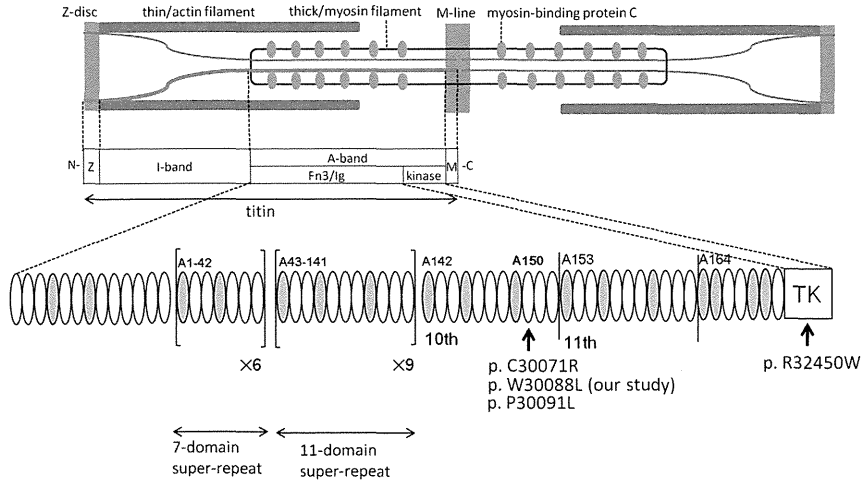


Figure 5 Structure of titin and mutation distribution in the A-band domain. Human *TTN* was mapped to 2q31.2. *TTN* is 294 kb and is composed of 363 exons that code for a maximum of 38 138 amino-acid residues and a 4.20-MDa protein[32] called titin. Titin is expressed in the cardiac and skeletal muscles and spans half the sarcomere, with its N-terminal at the Z-disc and the C-terminal at the M-line.[33] Titin is composed of four major domains: Z-disc, I-band, A-band and M-line. I-band regions of titin are thought to make elastic connections between the thick filament (that is, myosin filament) and the Z-disc within the sarcomere, whereas the A-band domain of titin seems to be bound to the thick filament, where it may regulate filament length and assembly.[34] The gray and white ellipses indicate an Ig-like domain and fibronectin type 3 domain, respectively. Our mutation (p.W30088L) and the neighboring two mutations (that is, p.C30071R and p.P30091L) were all located in the 6th Fn3 domain in the 10th domain of large super-repeats. A full color version of this figure is available at the *Journal of Human Genetics* journal online.

In contrast, one of the distinctive features of TMD is that early respiratory failure has not been observed in patients with TMD. Histological findings of TMD usually do not include CBs but show nonspecific dystrophic change. The underlying pathogenic processes explaining why mutations on these neighboring domains share some similarities but also some differences are unknown.

Three of four HMERF mutations in the A-band domain are located in the fibronectin type 3 and Ig-like (Fn3/Ig) domain, and one of four HMERF mutations is located in the kinase domain (Table 2, also see Figure 5). The missense mutation c.97348C>T in the kinase domain was the first reported HMERF mutation. It has been shown that the kinase domain has an important role in controlling muscle gene expression and protein turnover via the neighbor of BRCA1 gene-1-muscle-specific RING finger protein-serum response transcription factor pathway.[13] Moreover, the Fn3/Ig domain is composed of two types of super-repeats: six consecutive copies of 7-domain super-repeat at the N-terminus and 11 consecutive copies of 11-domain super-repeat at the C-terminus.[27–29] These super-repeats are highly conserved among species and muscles. Our identified mutation (c.90263G>T) and the neighboring two mutations (that is, c.90272C>T and c.90315T>C shown in Table 2) were all located on the 6th Fn3 domain in the 10th copy of 11-domain super-repeat (that is, A150 domain[30]) (Figure 5). Although some Fn3 domains are proposed to be the putative binding site for myosin,[31] the role with the majority of Fn3 domains, how it supports the structure of each repeat architecture, and the identity of its binding partner have not been fully elucidated. Our findings suggested that the Fn3 domain, in which mutations clustered, has critical roles in the pathogenesis of HMERF, although detailed mechanisms of pathogenesis remain unknown.

In conclusion, we have identified a novel disease-causing mutation in *TTN* in a family with MFM that was clinically compatible with HMERF. Because of its large size, global mutation screening of *TTN* has been difficult. Mutations in *TTN* may be detected by massively parallel sequencing in more patients with MFMs, especially in patients with early respiratory failure. Further studies are needed to understand the genotype–phenotype correlations in patients with mutations in *TTN* and the molecular function of titin.

ACKNOWLEDGEMENTS

We thank the patients and their family. We are grateful to Yoko Tateda, Kumi Kato, Naoko Shimakura, Risa Ando, Riyo Takahashi, Miyuki Tsuda, Nozomi Koshita, Mami Kikuchi and Kiyotaka Kuroda for their technical assistance. We also acknowledge the support of the Biomedical Research Core of Tohoku University Graduate School of Medicine. This work was supported by a grant of Research on Applying Health Technology provided by the Ministry of Health, Labor and Welfare to YM, an Intramural Research Grant (23-5) for Neurological and Psychiatric Disorders of NCNP and JSPS KAKENHI Grant number 24659421.

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Supplementary Information accompanies the paper on Journal of Human Genetics website (http://www.nature.com/jhg)

CLINICAL REPORT

AMERICAN JOURNAL OF medical genetics PART A

A Transient Myelodysplastic/Myeloproliferative Neoplasm in a Patient With Cardio-Facio-Cutaneous Syndrome and a Germline *BRAF* Mutation

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Manuscript Received: 4 March 2013; Manuscript Accepted: 26 May 2013

A male infant, born at 32 weeks gestation by cesarean because of hydrops fetalis, presented with multiple anomalies, such as sparse and curly scalp hair, absent eyebrows, frontal bossing, an atrial septal defect, pulmonary artery stenosis, and whole myocardial thickening. He was clinically diagnosed with cardio-facio-cutaneous (CFC) syndrome, and was confirmed to have a germline V-raf murine sarcoma viral oncogene homologue B1 (*BRAF*) c.721 A>C mutation. At 1 month of age, he presented with a transient myelodysplastic/myeloproliferative neoplasm (MDS/MPN), which improved within a month without the administration of antineoplastic agents. This is the first report of CFC syndrome with MDS/MPN. The coexistence of MDS/MPN may be related to this *BRAF* c.721 A>C mutation. © 2013 Wiley Periodicals, Inc.

Key words: cardio-facio-cutaneous syndrome; myelodysplastic/myeloproliferative neoplasm; BRAF; RAS/MAPK syndromes; juvenile myelomonocytic leukemia

How to Cite this Article:
Sekiguchi K, Maeda T, Suenobu S-I, Kunisaki N, Shimizu M, Kiyota K, Handa Y-S, Akiyoshi K, Korematsu S, Aoki Y, Matsubara Y, Izumi T. 2013. A transient myelodysplastic/myeloproliferative neoplasm in a patient with cardio-facio-cutaneous syndrome and a germline BRAF mutation.
Am J Med Genet Part A 161A:2600–2603.

INTRODUCTION

Cardio-facio-cutaneous (CFC) syndrome is genetic disorder characterized by clinical features such as congenital heart defects, a characteristic facial appearance, ectodermal abnormalities and growth failure [Reynolds et al., 1986]. V-raf murine sarcoma viral oncogene homolog B1 (*BRAF*) is one of rat sarcoma viral oncogene homolog/mitogen activated protein kinase (RAS/MAPK) signaling pathway genes, and has been identified as a causative gene of CFC syndrome [reviewed in Aoki et al., 2008 and Denayer and Legius, 2007]. We report on a male infant with CFC syndrome, who was confirmed to have a germline *BRAF* mutation, and then presented with a myelodysplastic/myeloproliferative neoplasm (MDS/MPN) at 1 month of age.

CLINICAL REPORT

A male was born through cesarean at 32 weeks gestation as the first product of healthy nonconsanguineous Japanese parents. His birth weight, length and head circumference were 2,370 g (−0.8 SD), 40.0 cm (+2.3 SD), 34.2 cm (+3.2 SD), respectively. Due to hydrops fetalis and neonatal asphyxia, he required immediate resuscitation. Mechanical ventilation was needed until age 3 months. He presented with multiple anomalies, such as sparse and curly scalp hair, absent eyebrows, frontal bossing with temporal narrowing, ocular hypertelorism, low set ears, a short and webbed neck, and cryptorchidism (Fig. 1). His complete blood counts at age 1 day revealed the following: WBC 12,770/μl (neutrophils 80%,

Conflict of interest: none.

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Article first published online in Wiley Online Library (wileyonlinelibrary.com): 15 August 2013
DOI 10.1002/ajmg.a.36107

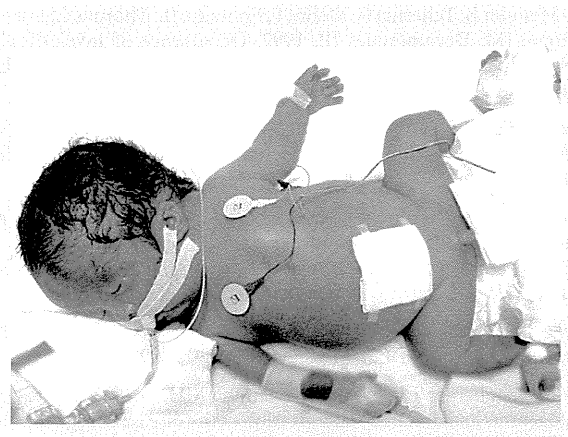

FIG. 1. Full-body image of the patient at birth and his facial features at 3 hours of age. The patient showed severe generalized edema at birth. He presented with sparse and curly hair, frontal bossing, hypertelorism, low-set ears, a short and webbed neck, and cryptorchidism.

lymphocytes 12%, monocytes 6%, myelocytes 2%), RBC 343 × 10^4/μl, erythroblasts 2,430/μl, hemoglobin 14.2g/dl, and platelets 3.2 × 10^4/μl. A chromosome analysis of his peripheral blood lymphocytes showed a 46, XY karyotype. He had an atrial septal defect (ASD), pulmonary artery stenosis (PS), whole myocardial thickening, a pulmonary arteriovenous fistula, an intrahepatic portal systemic shunt, hepatosplenomegaly, right cryptorchidism, a right double renal pelvis, and ureter and agenesis of the corpus callosum. These clinical features were all compatible with CFC syndrome.

At age 1 month, a peripheral blood examination indicated monocytosis of 17% (2,370/μl), with WBC 13,930/μl, RBC 295 × 10^4/μl, and platelets 11.2 × 10^4/μl, with giant platelets. Bone marrow aspiration revealed a nucleated cell count of 9.4 × 10^4/μl, megakaryocyte count 56.2/μl, and did not contain pathologic blasts. The karyotype of the bone marrow cells was 46, XY. The granulocyte-macrophage colony-forming unit (CFU-GM) assay using a semi-solid methylcellulose method showed spontaneous CFU-GM formation of bone marrow (5/5 × 10^4 mononuclear cells) and peripheral blood (35/5 × 10^4 mononuclear cell), without growth factors. Based on these laboratory findings, this patient was diagnosed with MDS/MPN. However, the peripheral blood monocytosis improved without the administration of antineoplastic agents after 1 month with 13% monocytes (1,140/μl), WBC of 8,780/μl, RBC 314 × 10^4/μl, and platelets 26.3 × 10^4/μl. At age 3 years, his complete blood counts revealed 11% monocytes (903/μl), WBC 8,210/μl, RBC 428 × 10^4/μl, and platelets 31.1 × 10^4/μl (Table I). He smiled normally. He demonstrated generalized hypotonia without normal head control and was unable to produce meaningful speech.

CYTOGENETIC AND GENOMIC ANALYSIS

The *BRAF* sequencing analysis showed a heterozygous A>C change at nucleotide 721, resulting in a p.T241P amino acid change in exon 6, which was a previously known mutation in CFC syndrome [Schulz et al., 2008]. No mutations were noted in the Kirsten rat sarcoma viral oncogene homologue (*KRAS*) or protein-tyrosine phosphatase, nonreceptor-type11 (*PTPN11*).

DISCUSSION

A male infant, born via cesarean section because of hydrops fetalis, presented with multiple anomalies suggestive of CFC syndrome. A pulmonary arteriovenous fistula, an intrahepatic portal systemic shunt, hepatosplenomegaly, cryptorchidism, a double renal pelvis, and ureter have been reported as rare complications in CFC syndrome [Narumi et al., 2007]. At 1 month of age, he presented with MDS/MPN, which improved within a month. He showed a germline mutation of *BRAF* c.721 A>C, resulting in a p.T241P amino acid change in exon 6, within a cysteine-rich domain. This mutation was previously described in CFC syndrome [Schulz et al., 2008].

The clinical findings of CFC syndrome are similar to those of other RAS/MAPK or neuro-cardio-facial-cutaneous syndromes, such as Noonan and Costello syndrome [reviewed in Aoki et al., 2008; Denayer and Legius, 2007]. The RAS/MAPK signaling pathway genes, not only *BRAF*, but also *KRAS*, MAPK kinase/ERK kinase 1 (*MEK1*), and MAPK kinase/ERK kinase2 (*MEK2*) have been reported as causative genes for CFC syndrome [Niihori et al., 2006; Rodriguez-Viciana et al., 2006]. CFC syndrome had been considered to have a low risk of malignancy among the various RAS/MAPK syndromes, but a few patients with CFC syndrome due to *BRAF* mutation have presented with malignancies, such as acute lymphoblastic leukemia [van Den Berg and Hennekam, 1999; Makita et al., 2007], and precursor T-lymphoblastic lymphoma [Ohtake et al., 2011].

MDS/MPNs include clonal myeloid neoplasms that at the time of initial presentation have clinical, laboratory or morphologic findings supporting a diagnosis of MDS, and other findings more consistent with MPN. They are usually characterized by hypercellularity of the

TABLE I. Peripheral Blood Examinations of This Patient

Age (months)	0	1	2	12	21	38
WBC (/μl)	12,770	13,930	8,730	8,660	9,040	8,210
Monocytes (/μl)	766	2,370	1,140	866	633	903
RBC (×10^4/μl)	343	295	314	396	404	428
Platelets (×10^4/μl)	3.2	11.2	26.3	24.2	38.6	31.1

bone marrow due to proliferation in one or more of the myeloid lineages [Swerdlow et al., 2008]. Juvenile myelomonocytic leukemia (JMML) is one type of MDS/MPN. Peripheral blood and bone marrow from JMML patients demonstrate spontaneous proliferation according to a CFU-GM assay [Estrov et al., 1986]. Transient monocytosis is not rare in preterm infants [Rajadurai et al., 1992]. Monocytosis in preterm infants is not usually considered a sign of MPD/MPN. In this case, the monocytes proliferation independent of growth factors was noticed according to a CFU-GM assay. The spontaneous proliferation was in favor of MPN. In RAS/MAPK syndromes, occasionally young infants with Noonan syndrome develop a JMML-like disorder which spontaneously resolves without treatment in some, and behaves more aggressively in others [Bader-Meunier et al., 1997; reviewed in Choong et al., 1999]. These children carried germline mutations in *PTPN11* [Tartaglia et al., 2003] or in *KRAS* [Kratz et al., 2005]. *BRAF* mutations had not previously been detected in patients with JMML [de Vries et al., 2007]. This is the first report of a germline *BRAF* mutation and MDS/MPN in a patient with CFC syndrome. The MDS/MPN improved without the administration of antineoplastic agents. This clinical course is similar to the JMML-like disorder observed in Noonan syndrome. This suggests a common mechanism for the development and progression of MDS/MPN in patients with RAS/MAPK syndromes. The MDS/MPN in RAS/MAPK syndrome patients has parallels with the transient leukemia of newborns with Down syndrome. However, the transient leukemia associated with Down syndrome has a high concentration of blasts in the peripheral blood and a GATA binding protein 1 (*GATA1*) mutation as somatic molecular marker [Xu et al., 2003].

The germline *BRAF* mutation site of this patient, c.721 A>C in exon 6, had been reported in two previous patients. One had CFC syndrome [Schulz et al., 2008], and the other had Noonan syndrome with multiple lentigines, previously referred to as LEOPARD syndrome [Sarkozy et al., 2009]. These two patients did not present with malignancies. Garnett and Marais [2004] reviewed the *BRAF* mutations in various adult cancers, and showed that up to 90% of mutations occurred in exon 12. The *BRAF* mutation site of this patient, exon 6, may be related to the spontaneous improvement of his MDS/MPN. A long-term follow-up and additional bone marrow assays might be needed if the patient demonstrates suspicious symptoms with or without peripheral blood monocytosis, because of the risk that MDS/MPN may recur. Further accumulated data about CFC syndrome with a *BRAF* mutation may help to elucidate the basic mechanisms of malignancy, and may suggest a therapeutic strategy.

ACKNOWLEDGMENTS

The authors are grateful to Drs. Hideki Muramatsu and Seiji Kojima, Department of Pediatrics/Developmental Pediatrics, Nagoya University Graduate School of Medicine, Nagoya, for providing important data from the colony assay.

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RESEARCH PAPER

Clinical features and a mutation with late onset of limb girdle muscular dystrophy 2B

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► Additional supplementary files are published online only. To view these files please visit the journal online (http://dx.doi.org/10.1136/jnnp-2011-301339).

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Received 2 September 2011
Revised 18 April 2012
Accepted 13 May 2012
Published Online First 15 December 2012

ABSTRACT

Objective and methods Dysferlin encoded by *DYSF* deficiency leads to two main phenotypes, limb girdle muscular dystrophy (LGMD) 2B and Miyoshi myopathy. To reveal in detail the mutational and clinical features of LGMD2B in Japan, we observed 40 Japanese patients in 36 families with LGMD2B in whom dysferlin mutations were confirmed.

Results and conclusions Three mutations (c.1566C>G, c.2997G>T and c.4497delT) were relatively more prevalent. The c.2997G>T mutation was associated with late onset, proximal dominant forms of dysferlinopathy, a high probability that muscle weakness started in an upper limb and lower serum creatine kinase (CK) levels. The clinical features of LGMD2B are as follows: (1) onset in the late teens or early adulthood, except patients homozygous for the c.2997G>T mutation; (2) lower limb weakness at onset; (3) distal change of lower limbs on muscle CT at an early stage; (4) impairment of lumbar erector spinal muscles on muscle CT at an early stage; (5) predominant involvement of proximal upper limbs; (6) preservation of function of the hands at late stage; (7) preservation of strength in neck muscles at late stage; (8) lack of facial weakness or dysphagia; (9) avoidance of scoliosis; (10) hyperCkaemia; (11) preservation of cardiac function; and (12) a tendency for respiratory function to decline with disease duration. It is important that the late onset phenotype is found with prevalent mutations.

INTRODUCTION

Dysferlinopathies are autosomal recessive muscular dystrophies caused by mutations in the dysferlin gene (*DYSF*, MIM# 603009). Dysferlin deficiency leads to two main phenotypes: limb girdle muscular dystrophy (LGMD) 2B and Miyoshi myopathy (MM).[1 2] Dysferlin is located on the plasma membrane of skeletal muscle and is deficient in patients with MM and LGMD2B.[3 4] However, atypical immunostaining in muscle from patients with dysferlin mutations occurs,[5 6] and dysferlin expression is not normal in sarcoglycanopathy, dystrophinopathy,[7] caveolinopathy[8 9] or calpainopathy[6] muscles. Therefore, the final diagnosis of dysferlinopathy requires identification of mutations in the dysferlin gene. We first reported dysferlin mutations in Japanese patients with MM[10] and in a patient from a non-European ethnic group with distal anterior compartment myopathy (DACM),[11] a relatively new phenotype of dysferlinopathy.[12] Furthermore, we revealed that, in MM, four mutations (c.1566C>G, c.2997G>T, c.3373delG and c.4497delT) were relatively more prevalent in the Japanese population and the c.2997G>T mutation was associated with late onset.[13] Although mutation analysis of the dysferlin gene is a time consuming task because of the large size of the gene,[14] large series of patients with dysferlin gene mutations have been studied.[6 15–24] However, few detailed analyses of the clinical features of LGMD2B, especially in relation to various types of mutations, have been reported. Here we report the clinical features of a series of 40 patients in 36 families with LGMD2B in whom dysferlin mutations were confirmed, and cardiac and respiratory functions were involved. In particular, we took into account the duration that had elapsed since onset when the clinical data were examined.

MATERIALS AND METHODS

We retrospectively observed 40 Japanese patients in 36 families with LGMD2B in whom dysferlin mutations were confirmed. LGMD was defined as symptomatic myopathy excluding MM and DACM at the first visit to a neurologist. Mutational analysis was performed by single strand conformation polymorphism analysis and sequencing on genomic DNA using our previously reported method,[13 14 25] with minor modifications (Ref Seq NM_003494.2), and with informed consent and approval of our local ethics committee. We retrospectively reassessed the history of onset and progression of the disease. The clinical examination included manual muscle testing using the Medical Research Council (MRC) Scale and assignment of scales for the proximal limb muscles, as proposed by Brooke *et al*.[26] Clinical examination was carried out by neurologists from the study groups for muscular dystrophy in Japan.

Most patients had undergone muscle CT scans at some stage of the disease. Serum creatine kinase (CK) activity was measured. Cardiac and respiratory functions were evaluated. We selected the first and last manual muscle testing data and the last data on the scales for the proximal limb muscles, CK activity, cardiac function and respiratory function. We used all muscle CT scans. Patients were divided into three groups according to whether they had the homozygous c.2997G>T (p.Trp999Cys) mutation, the heterozygous c.2997G>T (p.Trp999Cys) mutation or other mutations. Difference in age at onset among the groups was evaluated by the Kruskal–Wallis test. Multiple comparison of age at onset between each group was assessed by Scheffé's F test. Difference in the first symptom among the groups was evaluated by the χ^2 for independence test. Kaplan–Meier curves with log rank test were used to examine survival at each milestone of progression in the groups. Pearson's correlation coefficient test was used to identify significant associations in ejection fraction (EF) (n=21), atrial natriuretic peptide (n=9), brain natriuretic peptide (n=7), per cent vital capacity (%VC) (n=23), carbon dioxide partial pressure (pCO_2) (n=16) and oxygen partial pressure (pO_2) (n=16) with disease duration. Because supine and standing position chest x-rays were mingled, Pearson's correlation coefficient test was not used for the cardiothoracic ratio (n=22).

RESULTS

Mutations

We identified 17 different mutations in 36 families (table 1). Two mutations (c.2974T>C (p.Trp992Arg) and c.2997G>T (p.Trp999Cys)) were missense mutations and four mutations (c.342+1G>A, c.937+1G>A, c.2643+1G>A and c.4794 +1G>A) were splice site mutations. The others were nonsense mutations. The c.2997G>T (p.Trp999Cys) mutation was present in 26 alleles (36.1%). The c.1566C>G (p.Tyr522X) mutation and the c.4497delT mutation were both present in eight alleles (11.1%). We identified the c.3373delG mutation that has high frequency in Japanese patients with MM[13] in only one allele.

Clinical course

Mean age at onset of all patients was 26.6±9.9 years (range 14–58): the group homozygous for the c.2997G>T (p.Trp999Cys) mutation, 37.9±10.2 years (19–58); the group heterozygous for the c.2997G>T (p.Trp999Cys) mutation, 26.8 ±7.6 years (14–35); and the group without the c.2997G>T (p.Trp999Cys) mutation, 21.8±5.8 years (14–41). The difference between the group homozygous for the c.2997G>T (p.Trp999Cys) mutation and the group heterozygous for the c.2997G>T (p.Trp999Cys) mutation was significant ($p<0.05$). The difference between the group homozygous for the c.2997G>T (p.Trp999Cys) mutation and the group without the c.2997G>T (p.Trp999Cys) mutation was significant ($p<0.01$) (figure 1). The first symptom in most patients was lower limb weakness. Walking on tiptoe was the first sign in one patient. In three patients with the homozygous c.2997G>T (p.Trp999Cys) mutation, the first symptom was upper limb weakness. In two patients, one of them carrying the homozygous c.2997G>T (p.Trp999Cys) mutation, upper limb weakness was concomitant with lower limb weakness. There was a significant difference ($p<0.01$) in the probability that the first symptom was upper limb weakness among these three groups. The first symptom in one patient was left brachial pain and in another patient it was limitation of the elbow, hip, knee and spine.[27] In the early stage of the clinical course, hypertrophy of the calves was noticed in three patients. Winged scapula, rigid spine[27] and hollow foot were observed in one patient each. Lordosis was observed in two patients. Weakness of the face, dysphagia, scoliosis and kyphosis were not found. Choreic movements and pollakisuria were found in one patient.[28] Mean duration at difficulty in running was 1.3 years from disease onset (range 0–10), 3.1 years (0–14) for difficulty in climbing stairs, 5.5 years (0–16) for stumbling, 6.0 years (0–10) for difficulty in standing on tiptoe, 6.7 years (0–15) for rising from the floor, 8.7 years (0–25) for noticing weakness in a proximal upper limb, 12.5 years (3–23) for walking with a cane, 20.4 years (9–35) for noticing weakness in a distal upper limb, 21.6 years (13–29) for using a wheelchair and 31.0 years (16–45) for using an electric wheelchair. There was a significant difference ($p<0.05$) in the survival ratio only at the stage of difficulty in standing on tiptoe among these three groups (figure 2). There were no significant differences in survival at the stage of the other symptoms between these three groups. According to the scales for the proximal limb muscles, only two patients each reached the severest stage of arms and shoulders (cannot raise hands to mouth and have no useful function) and hips and legs (confined to bed).

Manual muscle testing

In the first decade of the disease, the muscles of the lower limbs were predominantly involved. In the upper limbs, the deltoid muscle was predominantly involved. In the second decade of the disease, the biceps and triceps brachii muscles became weak. Later on, the flexor and extensor of the hand became weak. Muscle weakness progressed and, in the fifth decade of the disease, the muscles of the lower limbs were very weak (1 on the MRC Scale). In the patient with 52 years of disease duration, although the muscles of the upper and the lower limbs were 0 on the MRC scale, the flexor and extensor of the neck were relatively preserved (2 on the MRC Scale).

Muscle CT scans

The CT scans revealed low density changes in the gastrocnemius, especially in the medial heads, soleus, hamstrings and the erector spinal group, which was mainly affected in the lateral parts in the early disease stage. Low density abnormalities in the quadriceps femoris and the adductor magnus muscles were observed at close to 10 years after disease onset. The tibialis anterior, the peroneal group, the gluteal group, the quadrates lumborum and the deltoid muscles were involved at 10 years after onset. The gracilis and sarcorius muscles were preserved and had hypertrophied during the second decade of disease duration. Approximately 20 years after disease onset, low density changes in the dorsal muscles occurred in the neck region, particularly in the transversospinal group, except for the semispinalis capitis muscle. All muscles were replaced by low density tissue or were atrophied at 30 years after disease onset. The gluteal group, the psoas major muscle, the lateral abdominal group and the levator scapulae muscle were preserved in the late stage. There were exceptional cases. In one patient, low density changes in the dorsal muscles in the neck region occurred at an early stage. In another patient, the quadriceps femoris muscles were more severely damaged than the hamstrings at 14 years of disease duration.

Serum CK levels

Although serum CK levels were very high, there was a tendency for levels to decrease with disease duration (figure 3). There was a trend in the distribution of the levels by

Table 1 Summary of dysferlin gene mutations of patients in this study

Patient	Sex	Age (years)	Disease duration (years)	Exon	Nucleotide change	Protein change	State
Dys48-1	M	54	23	28	c.2997G>T	p.Trp999Cys	Homozygous
Dys58-1	F	51	8	28	c.2997G>T	p.Trp999Cys	Homozygous
Dys64-1	M	58	19	28	c.2997G>T	p.Trp999Cys	Homozygous
Dys93-1	F	57	17	28	c.2997G>T	p.Trp999Cys	Homozygous
Dys99-1	F	55	11	28	c.2997G>T	p.Trp999Cys	Homozygous
Dys106-1	F	22	3	28	c.2997G>T	p.Trp999Cys	Homozygous
Dys113-1	M	57	17	28	c.2997G>T	p.Trp999Cys	Homozygous
Dys123-1	F	59	25	28	c.2997G>T	p.Trp999Cys	Homozygous
Dys133-1	M	66	8	28	c.2997G>T	p.Trp999Cys	Homozygous
Dys170-1	F	38	7	28	c.2997G>T	p.Trp999Cys	Homozygous
Dys13-1	M	43	29	28 34	c.2997G>T c.3771G>A	p.Trp999Cys p.Trp1257X	Compound heterozygous
Dys55-1	F	47	22	28 37	c.2997G>T c.3959_3960insA	p.Trp999Cys p.Met1320IlefsX26	Compound heterozygous
Dys114-1	M	50	15	Intron 25 28	c.2643+1G>A c.2997G>T	Splice site p.Trp999Cys	Compound heterozygous
Dys120-1	M	55	25	18 28	c.1566C>G c.2997G>T	p.Tyr522X p.Trp999Cys	Compound heterozygous
Dys124-1	F	36	12	18 28	c.1566C>G c.2997G>T	p.Tyr522X p.Trp999Cys	Compound heterozygous
Dys127-1	F	56	23	18 28	c.1566C>G c.2997G>T	p.Tyr522X p.Trp999Cys	Compound heterozygous
4	M	75	49	Intron 25 41	c.2643+1G>A c.4497delT	Splice site p.Phe1499LeufsX4	Compound heterozygous
5	M	Died at 59	Died at 42	21	c.1958delG	p.Gly653ValfsX3	Homozygous
15	F	50	34	37	c.3959_3960insA	p.Met1320IlefsX26	Homozygous
39	F	74	52	Intron 25	c.2643+1G>A	Splice site	Homozygous
44	M	41	14	29 41	c.3112C>T c.4497delT	p.Arg1038X p.Phe1499LeufsX4	Compound heterozygous
47	M	55	37	37	c.3959_3960insA	p.Met1320IlefsX26	Homozygous
Dys37-1	M	60	40	Intron 10	c.937+1G>A	Splice site	Homozygous
Dys37-2	F	51	24	Sister of Dys37-1			
Dys43-1	F	36	19	18	c.1566C>G	p.Tyr522X	Homozygous
Dys43-2	F	35	21	Sister of Dys43-1			
Dys46-1	F	67	48	41	c.4497delT	p.Phe1499LeufsX4	Homozygous
Dys50-2	M	70	29	41	c.4497delT	p.Phe1499LeufsX4	Homozygous
Dys59-1	F	49	27	28	c.2974T>C	p.Trp992Arg	Homozygous
Dys61-1	F	43	21	41	c.4497delT	p.Phe1499LeufsX4	Homozygous
Dys78-1	F	54	30	Intron 10	c.937+1G>A	Splice site	Homozygous
Dys84-1	F	64	45	14	c.1321C>T	p.Gln441X	Homozygous
Dys84-2	M	52	32	Brother of Dys84-1			
Dys89-1	F	68	40	18 28	c.1566C>G c.2974T>C	p.Tyr522X p.Trp992Arg	Compound heterozygous
Dys117-1	M	32	9	18	c.1566C>G	p.Tyr522X	Homozygous
Dys117-2	M	30	16	Brother of Dys117-1			
Dys126-1	M	23	2	Intron 4 54	c.342+1G>A c.6135G>A	Splice site p.Trp2045X	Compound heterozygous
Dys145-1	F	27	10	6	c.610C>T	p.Arg204X	Homozygous
Dys146-1	F	58	34	31 Intron 43	c.3373delG c.4794+1G>A	p.Glu1125LysfsX9 splice site	Compound heterozygous
Dys163-1	M	36	11	6	c.493delC	p.Leu165SerfsX48	Homozygous

c.2997G>T (p.Trp999Cys) mutation. Levels in the group homozygous for the c.2997G>T (p.Trp999Cys) mutation were lower than those of the other two groups.

Cardiac function

Although supine and standing position chest x-rays were mingled, in half of the patients the cardiothoracic ratio was >50%. No significant correlation was observed between EF and disease duration. Except for two patients, levels of EF were >50%. In all the patients, concentrations of atrial natriuretic peptide were within the normal range. Except for one patient, concentrations of brain natriuretic peptide were within the normal range. No significant correlation was observed between these peptides and disease duration. Although 19 patients

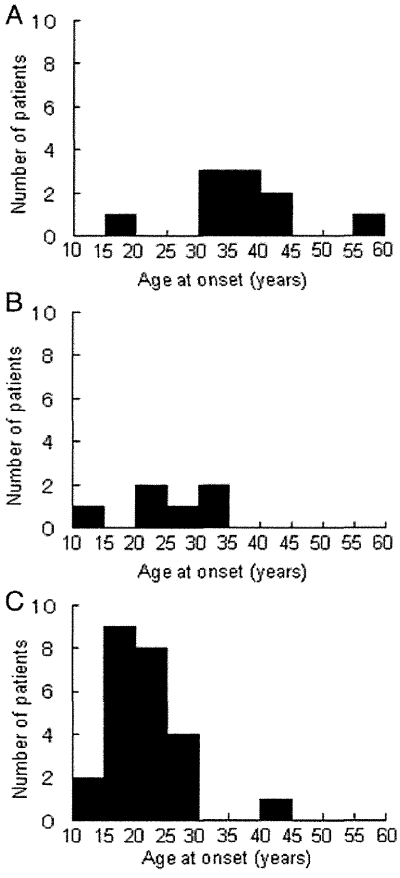

Figure 1 Histogram by age at onset. (A) Patients homozygous for the c.2997G>T mutation. (B) Patients heterozygous for the c.2997G>T mutation. (C) Patients without the c.2997G>T mutation.

exhibited normal findings on ECG, abnormalities were found in nine patients. The ECG showed premature ventricular contraction in one patient, one degree atrioventricular block in two patients, incomplete right bundle branch block in two patients, left axis deviation in two patients, left atrial hypertrophy in one patient, right ventricular hypertrophy in three patients, left ventricular hypertrophy in three patients, ST change in two patients and negative T in one patient.

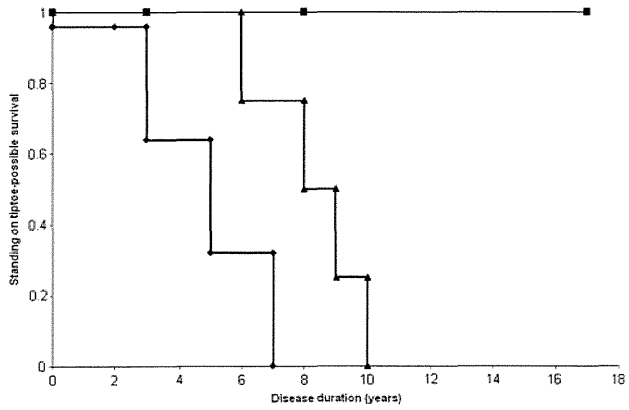

Figure 2 Standing on tiptoe—possible survival curve. Survival curve of patients homozygous for the c.2997G>T mutation (line with squares), those heterozygous for the c.2997G>T mutation (line with triangles) and those without the c.2997G>T mutations (line with diamonds).

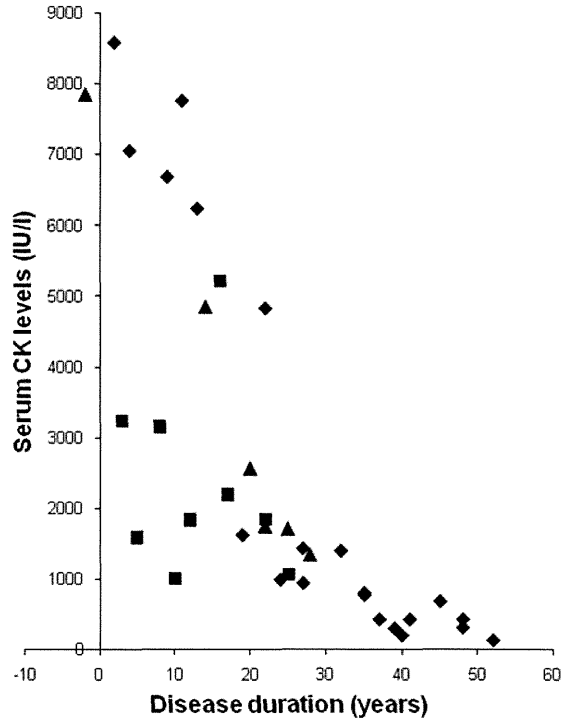

Figure 3 Serum creatine kinase (CK) levels during the disease course. Levels of serum CK in patients homozygous for the c.2997G>T mutation (squares), heterozygous for the c.2997G>T mutation (triangles) and those without the c.2997G>T mutations (diamonds).

Respiratory function

A statistically significant ($p<0.01$) correlation ($r=-0.545$) was observed between %VC and disease duration (figure 4). In 48% of patients, %VC was <80%. Although no significant correlation was observed between pCO_2 and disease duration, in 44% of patients, levels of pCO_2 were >45 mm Hg. In most patients, levels of pO_2 were >70 mm Hg. No significant correlation was observed between pO_2 and disease duration. Four patients had

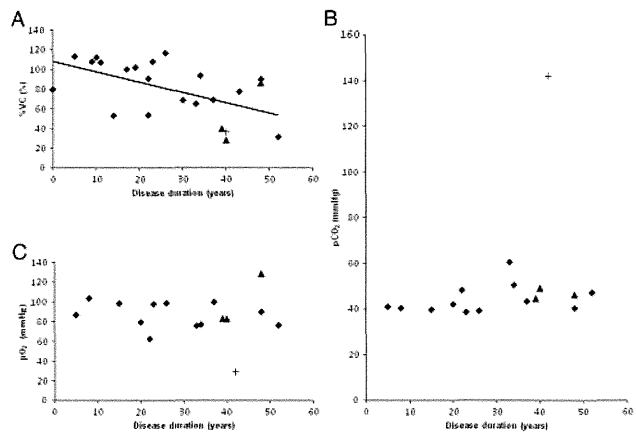

Figure 4 Respiratory function. (A) Per cent vital capacity (%VC) according to disease duration. The line is the regression line of %VC and disease duration. (B) Carbon dioxide partial pressure (pCO_2) according to disease duration. (C) Oxygen partial pressure (pO_2) according to disease duration. The triangles indicate levels in patients who had used non-invasive positive pressure ventilation. The cross (+) indicates the level in a patient who died after 42 years of disease duration of respiratory failure.

used non-invasive positive pressure ventilation (NIPPV). One patient who used NIPPV died after 42 years of disease duration from respiratory failure.

DISCUSSION

Three mutations (c.2997G>T (p.Trp999Cys), c.1566C>G (p.Tyr522X) and c.4497delT) were relatively more prevalent in the present Japanese patients with LGMD2B. Also, in Japanese patients with MM, these three mutations were relatively more prevalent in our previous study.[13] We identified the c.3373delG mutation that occurred with high frequency in Japanese patients with MM, as well as these three mutations,[13] in only one allele in Japanese patients with LGMD2B.

In MM, patients with the c.2997G>T (p.Trp999Cys) mutation had a significantly late onset.[13] Tagawa *et al*[6] reported that age of onset in patients homozygous for the c.2997G>T (p.Trp999Cys) mutation was later than the third decade of life. In this study, especially in patients homozygous for the c.2997G>T (p.Trp999Cys) mutation, onset was significantly late. Only 10% of patients homozygous for the c.2997G>T (p.Trp999Cys) mutation developed muscle symptoms by 30 years. In contrast, 90% of patients without this mutation developed muscle symptoms by the same age. However, it is difficult to explain why the c.2997G>T (p.Trp999Cys) mutation is related to late onset forms. In an immunohistochemical analysis by Tagawa *et al*,[6] although one patient with the homozygous c.2997G>T mutation (p.Trp999Cys) showed an 'abnormal' pattern, cytoplasmic accumulation of immunopositive material with deficiency of membrane staining or positive/negative mosaic membrane staining, three patients with the same mutation showed a negative pattern. Guglieri *et al*[21] reported that patients carrying two truncating mutations showed the first muscular symptoms earlier in life than subjects harbouring double missense substitutions. Indeed, the c.2997G>T mutation is theoretically deduced to be a missense mutation (p.Trp999Cys). Meanwhile, in this study, there were only two patients carrying missense mutations other than the c.2997G>T (p.Trp999Cys) mutation. Thus it is difficult to discuss statistically whether an association between the c.2997G>T (p.Trp999Cys) mutation and late onset forms is due to a missense mutation or other inherent characteristics. Nonetheless, it is important that the late onset phenotype is found with prevalent mutations.

Although patients homozygous for the c.2997G>T (p.Trp999Cys) mutation had late onset, no difference in progression was observed in those harbouring the c.2997G>T (p.Trp999Cys) mutation, except for difficulty in standing on tiptoe. This suggests that the c.2997G>T (p.Trp999Cys) mutation is related to late onset but not to the slow progression of the disease. Furthermore, the c.2997G>T (p.Trp999Cys) mutation may be relevant to the proximal dominant impairment in dysferlinopathy, diagnosed as the limb girdle type. Interestingly, there was only one patient homozygous for the c.2997G>T (p.Trp999Cys) mutation in 27 families with MM.[13] Moreover, patients homozygous for the c.2997G>T (p.Trp999Cys) mutation had a high probability that the muscle weakness started in the upper limbs. In addition, serum CK levels in patients homozygous for the c.2997G>T (p.Trp999Cys) mutation were lower than those in the other two groups.

We investigated the clinical features of 40 patients in 36 families with LGMD2B in whom dysferlin mutations were confirmed. Disease duration was long (26.6±9.9 years) in this study. The clinical features of LGMD2B in this study were as follows: (1) onset in the late teens or early adulthood except in patients homozygous for the c.2997G>T (p.Trp999Cys) mutation; (2) lower limb weakness at onset in most patients; (3) distal change of lower limbs on muscle CT in the early stage; (4) impairment of lumbar erector spinal muscles on muscle CT in the early stage; (5) predominant involvement of the proximal upper limbs; (6) preservation of function of the hands in late stage; (7) preservation of strength in the neck muscles in late stage; (8) lack of facial weakness or dysphagia; (9) avoidance of scoliosis; (10) hyper-Ckaemia; (11) preservation of cardiac function; and (12) tendency for respiratory function to decline with disease duration and occasional necessity for ventilatory assistance.

Age at onset was similar to that reported for various types of mutations.[18 19 21] However, patients with disease onset at 73 years[24 29] or congenital onset[30] have been reported. Clinicians may not have taken into account analyses of the dysferlin gene for such patients.

Nishida *et al* proposed the name 'distal limb girdle type muscular dystrophy' for patients with MM that develop proximal muscle involvement relatively early.[31 32] Nguyen *et al*[17] classified patients for whom it was not possible to distinguish between a distal phenotype of MM and a limb girdle phenotype, even when examined at onset, as a distinct 'proximodistal' phenotype group. Although patients with the typical features of MM[13 33] or asymptomatic hyper-CKaemia were excluded from the present study, variable patterns of weakness in the lower limbs were observed, as in previous studies.[17 19 20 22 24] However, the predominant muscle weakness was in proximal sites of the upper limbs in the present study.

The results of muscle CT scan in this study were similar to those of detailed imaging studies in LGMD2B at a relatively early stage.[23 34 35] In this study, we had only one case in whom a low density change in the dorsal muscle in the neck region occurred in the early stage. In contrast, two patients showed fatty muscle degeneration of the cervical elector spinae muscles after 9 or 10 years of disease duration, in a study performed using 3.0 T MRI.[35] Another exceptional finding was a case in which the quadriceps femoris muscles were more severely damaged than the hamstrings, which was reported in two of five patients.[34]

In the present study, only two patients showed levels of EF that were <50% and the patient who showed the lowest EF (32.7%) had no symptoms or signs of cardiomyopathy.[36] Guglieri *et al*[21] reported cardiac rhythm changes in three patients and left ventricular hypertrophy in four patients from a total of 22 LGMD2B patients. Wenzel *et al*[37] reported ECG abnormalities (repolarisation abnormalities or left ventricular hypertrophy) in four patients and pathological echocardiographic parameters in five of seven LGMD2B patients. Furthermore, two patients had symptoms and signs of dilated cardiomyopathy. Choi *et al*[38] reported left ventricular hypertrophy on ECG in two patients, no cardiac signs in one patient and mildly decreased EF (45%) in one patient among five MM patients. Therefore, we think that in most patients with LGMD2B, in spite of the existence of laboratorial abnormalities, cardiac function was clinically preserved.

Mahjneh *et al*[16] reported that patients with LGMD2B with disease durations of up to 7 years might show slight restrictive lung disease. Cagliani *et al*[39] reported that respiratory tests showed mild obstructive signs at the small airways in a 20-year-old man with LGMD2B. Illa *et al*[12] reported that pulmonary function tests revealed a mild reduction in VC in two

patients with DACM. In this study, many patients showed pathological levels of respiratory parameters and levels of %VC decreased with disease duration. Furthermore, some patients needed NIPPV and one patient died of respiratory failure. The change in muscles related to respiratory function worsens with disease duration. Therefore, it is important to pay attention to respiratory function in patients with dysferlinopathy.

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Acknowledgements The authors thank the patients for participating in the study, Dr Mitsuru Kawai, National Hospital Organisation East Saitama National Hospital, for providing advice and Mr Brent Bell for reading the manuscript.

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Funding This work was supported by Intramural Research Grants (20B-12, 20B-13, 23-4 and 23-5) for Neurological and Psychiatric Disorders of NCNP.

Competing interests None.

Patient consent Obtained.

Ethics approval The study was approved by the National Hospital Organisation Nishitaga National Hospital and Tohoku University School of Medicine.

Provenance and peer review Not commissioned; externally peer reviewed.

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