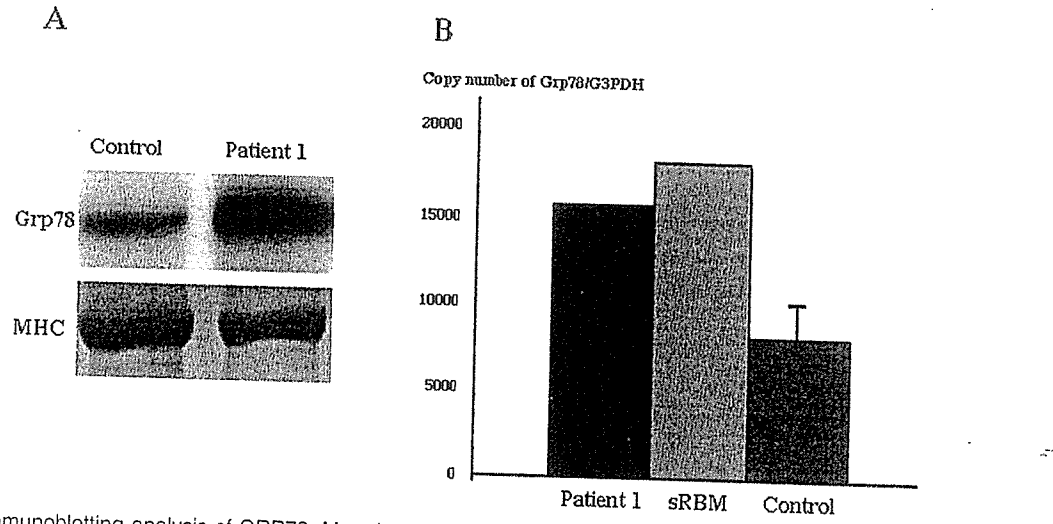

FIGURE 2. (A) Immunoblotting analysis of GRP78. More intense immunoreactive band for GRP78 is seen in patient 1. MHC: myosin heavy chain. (B) Histogram represents the results of quantitative RT-PCR for GRP78 on muscle biopsies. GRP78 in patient 1 and a sporadic reducing-body myopathy (sRBM) patient is upregulated compared to the control samples.

GRP78 expression in muscle from patient 1 compared to the control muscle (Fig. 2A).

Quantitative RT-PCR. The expression of GRP78 mRNA was much higher in the muscles from both patient 1 and one sRBM than the control muscles (Fig. 2B).

Mutation Analysis. No mutation was identified in the *VCP* gene in either patient 1 or 2.

DISCUSSION

Recently, aggresomal features of the inclusion bodies have been reported in several neurodegenerative disorders including Huntington's and Parkinson's diseases. Inclusions observed in Huntington's disease are specifically composed of mutant huntingtin together with ER chaperones and ubiquitin, whereas α-synuclein is the major component in Lewy bodies observed in Parkinson's disease.[9]

In this study, we demonstrated that RBs observed in hRBM patients contained virtually all membrane-associated proteins examined including those of nuclei, sarcoplasmic reticulum, Golgi apparatus, lysosome, and plasma membrane. RBs also had aggresomal features; i.e., positive immunoreaction for ubiquitin and ER chaperones, and positive central immunoreaction for γ-tubulin, and were surrounded by desmin, a major intermediate filament protein of skeletal muscle. Furthermore, increased mRNA and protein levels of GRP78 were observed in the muscle from the hRBM patient. GRP78 is a molecular chaperone, which is upregulated during UPR. Positive immunoreaction for phosphorylated (activated) pancreatic ER kinase observed in RBs also indicates the activation of UPR. From these results, accumulation of various misfolded membrane proteins in ER could be a primary event in hRBM patients, which results in activation of the UPR and subsequent aggresome formation. γ-Tubulin is a marker of the centrosome. Although postmitotic cells like muscle fibers and neurons normally do not contain a centrosome, γ-tubulin distinctly exists in the cytosol. In neurons, the cytosolic γ-tubulins could be reorganized to form juxtanuclear condensation under ER stress, and this lesion could be the microtubule organization center.[9] Positive immunoreaction for γ-tubulin in the center of RBs also suggests ER stress in hRBM.

Except for the consistency of ubiquitin immunoreactivity, previous reports showed equivocal immunohistochemical results of RBs.[2] To know whether the present results could apply to other patients with RBM, we also examined muscle specimens from two sRBM patients with the severe infantile form of the disease. All RBs found in sRBM patients yielded positive immunoreactivity of GRP78, ubiquitin, and emerin, but only a subset of RBs was highlighted by dystrophin and α-sarcoglycan. A desmin-positive rim was not seen in RBs in the sRBM muscles. Deposition of the proteins associated with UPR and ER-associated degradation, together with upregulation of GRP78 mRNA also indicates the activation of UPR in sRBM muscle samples.

Recently, a mutation in the *VCP* gene, a key molecule in the retrotranslocation step of ER stress-associated degradation, was identified in patients with inclusion-body myopathy associated with Paget's disease of bone and frontotemporal dementia (IBMPFD).[14] Due to the similarity of VCP-positive inclusions observed in the hRBM to that in IBMPFD, sequence analysis of the *VCP* gene was performed. However, no mutation was identified in the patients with hRBM.

In conclusion, our data show the aggresomal features of RBs, which might be induced by accumulation of a battery of membrane-associated proteins, resulting in the activation of UPR. To determine the precise pathomechanism of RBM, detailed analyses on the functions of ER chaperones and proteasomes should be investigated. In animal studies, overexpression of chaperones or application of chaperone-inducing compounds such as radicicol is beneficial for the treatment of neurodegenerative diseases with inclusion bodies.[9] Upregulation of chaperone transcription may be an option for the development of therapy in RBM.

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Characterization of lobulated fibers in limb girdle muscular dystrophy type 2A by gene expression profiling

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Abstract

Limb girdle muscular dystrophy type 2A (LGMD2A) is caused by mutations in *CAPN3*, which encodes an intracellular cysteine protease. To elucidate the fundamental molecular changes that may be responsible for the pathological features of LGMD2A, we employed cDNA microarray analysis. We divided LGMD2A muscles into two groups according to specific pathological features: an early-stage group characterized by the presence of active necrosis and a regeneration process and a later-stage group characterized by the presence of lobulated fibers. After comparing the gene expression profiles of the two groups of LGMD2A muscles with control muscles, we identified 29 genes whose mRNA expression profiles were specifically altered in muscles with lobulated fibers. Interestingly, this group included genes that encode actin filament binding and regulatory proteins, such as gelsolin, PDZ and LIM domain 3 (PDLIM3) and troponin I1. Western blot analysis confirmed the upregulation of these proteins. From these results, we propose that abnormal increased expression of actin filament binding proteins may contribute to the changes of the intramyofiber structures, observed in lobulated fibers in LGMD2A.

Keywords: Actin filament; Calpain 3; cDNA microarray; Limb girdle muscular dystrophy type 2A; Lobulated fiber; Myofibril

1. Introduction

Limb girdle muscular dystrophy (LGMD) is a group of disorders characterized by progressive atrophy and weakness of muscles in proximal limbs, scapular/pelvic girdle and trunk sparing facial muscles (Fardeau et al., 1996). At present, seven autosomal dominant and eleven autosomal recessive forms are known. LGMD2A is the most common form of LGMD and accounts for about 26% in Japan (Chae et al., 2001; Fanin et al., 2005). As with other muscular dystrophies, LGMD2A muscles show active necrotic and regenerating process in earlier stages of the disease. In later stages, however, the muscle pathology is characterized mainly by the presence of lobulated fibers (LF), which are composed of misaligned myofibrils that form a lobular pattern, in addition to fiber size variation and interstitial fibrosis (Guerard et al., 1985).

LGMD2A is caused by mutations in *CAPN3* encoding calpain 3, a skeletal muscle-specific non-lysosomal cysteine protease (Richard et al., 1995). Calpain 3 is present on myofibrils and specifically binds to the N2A and M line of titin, a muscle elastic protein (Sorimachi et al., 1995; Keira et al., 2003), although the *in vivo* substrate(s) of calpain 3 have not yet been well characterized. Most of the identified mutations in *CAPN3* are missense mutations, and are distributed throughout the exons of this gene.

LGMD2A is thought to be due to the loss of calpain 3 activity on myofibrils, nevertheless, the detailed pathomechanism remains to be elucidated. Interestingly, calpain 3 deficiency

Abbreviations: cDNA, complementary deoxyribonucleic acid; DMD, duchenne muscular dystrophy; ECM, extracellular matrix; GAPDH, glyceraldehyde phosphate dehydrogenase; H&E, hematoxylin and eosin staining; LGMD, limb girdle muscular dystrophy; LF, lobulated fiber; NADH-TR, β-nicotinamide adenine dinucleotide–tetrazolium reductase; NRF, necrotic and regenerating fiber; PDLIM3, PDZ and LIM domain 3; SPAG9, sperm-associated antigen 9; TUNEL, TdT-mediated dUTP-biotin nick end labeling

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has been shown to cause myonuclear apoptosis in association with subsarcolemmal localization and accumulation of NF-κB, resulting in perturbations in the IκBα/NF-κB pathway (Baghdiguian et al., 1999; Richard et al., 2000). However, this scenario probably cannot fully explain the pathomechanism of LGMD2A, especially the formation of LF in LGMD2A. To elucidate the pathomechanisms of LGMD2A, we obtained the comprehensive gene expression profiles using a muscle-specific cDNA microarray, and focused our attention on LF, which is a pathological hallmark of LGMD2A muscles in later stage.

2. Materials and methods

2.1. Patients

Muscle specimens from seven patients with genetically confirmed LGMD2A and two healthy controls (21 and 71 years old) were used in this study. A clinical summary of the patients is shown in Table 1. Except for patient 6, all of the patients with calpain 3 mutations were reported in our previous study (Chae et al., 2001). Patient 6 was genetically diagnosed by performing direct sequencing of PCR products amplified from cDNA and genomic DNA.

Genomic DNA analysis showed the presence of a homozygous (c.1524 + 1G > T) mutation, which resulted in the generation of an abnormal product (r.1426_1524del) through the activation of a cryptic splice site in exon 11. The biceps brachii muscle from each patient was biopsied after receiving informed consent and was immediately frozen in liquid nitrogen-cooled isopentane. We performed a battery of histochemical stainings on the biopsy, including hematoxylin and eosin (H&E) staining and β-nicotinamide adenine dinucleotide–tetrazolium reductase (NADH-TR) staining. Muscle samples were categorized into two groups according to their histological characteristics: a group with many necrotic and regenerating fibers (NRF in Fig. 1) and a group with LFs (LF in Fig. 1). Electron microscopic observation confirmed the presence of misaligned myofibrils and accumulation of mitochondria in the subsarcolemmal region, a typical feature of LF (Fig. 1F).

2.2. Gene expression profiling and data analysis

Customized cDNA microarray using 5760 probes for the 4200 genes expressed in human skeletal muscle were used in this study. A modified microarray technique allowing gene expression profiling to be performed even with a small amount of individual biopsied muscle was employed (Noguchi et al., 2003, 2005; Taniguchi et al., 2006). RNA extraction, hybridization, and detection of hybridized probes were done as previously described (Noguchi et al., 2003). Briefly, RNA was extracted from frozen muscles of LGMD2A patients and controls. We used a two-color labeling method in our microarray, because this method gives data with small variance, resulting in greater reproducibility and reliability than the one-colored method. In order to compare data between arrays, we performed competitive hybridization of each patient's RNA with a common RNA as one of probes. The relative expression values of this RNA were used to correct the hybridization efficiency in each array. The microarray was hybridized competitively with Cy3-labeled cDNA probes obtained from the RNA of each biopsied muscle, and Cy5-labeled cDNA probes from commercially available RNA (Origene, Rochville, MD, USA), which served as reference RNA for per-spot normalization. For each specimen, microarray experiments were carried out at least twice. Analysis of microarray data was performed using Genespring software 4.2.1 (Agilent, Palo Alto, CA, USA) and Microsoft Excel (Microsoft, Redmond, WA, USA). For per-spot normalization, the ratio of Cy3 to Cy5 intensity on each spot was used for the analyses. When the Cy5 intensity of a spot fell below 10.0, the data was not used. In addition, intensity-dependent (Lowess) normalization per chip was performed to minimize for variation in each microarray experiment. By combining repeated experiments, we identified single-fold changes and significance

Table 1
Clinical and molecular data of LGMD2A patient

Patient	Sex	Age at biopsy (years)	Disease duration (years)	Walking ability at biopsy (years)	Number of necrotic fibers in whole section	Regerating fibers (%)	Lobulated fibers (%)	TUNEL (%)	Calpain 3 gene mutation	Predicted protein change	Calpain 3 protein (%) (MWB[a])
1	F	7	Pre	No symptom	>2	>2	0	0.0056	c.1742C > G, c.2050 + 1G > A	p.S581C, p.(r.spl)	37.3
2	M	40	1	Defect of gait	>2	>2	0	0.014	c.2120A > G, c.1795dupA	p.D707G, p.T559fs	13.8
3	M	25	5	Difficulty of climbing stairs, Gowers sign	>5	>10	0	0	c.698G > T, c.2120A > G	p.G233V, p.D707G	4.9
4	M	56	21	Unable to walk without stick, Gowers sign	0	0	>60	n.t.[b]	c.2120A > G (homozygote)	p.D707G	0
5	M	27	15	Waddling gait, Gowers sign	<2	0	>30	0.0004	c.440G < C, c.?	p.R147P, p.0 (r.0)	0
6	M	32	17	Waddling gait, Gowers sign	0	0	>60	n.t.[b]	c.1524 +1G > T (homozygote)	p.V476_E508del[c]	0
7	M	49	11	Unable to climb stairs without banister	<2	<0.5	>60	0.008	C.1381C > T (homozygote)	p.R461C	43

[a] MWB: Multiplex Western Blotting.
[b] n.t.: Not tested.
[c] RT-PCR analysis showed an abberant splicing product (r.1426_1524del) in P6.

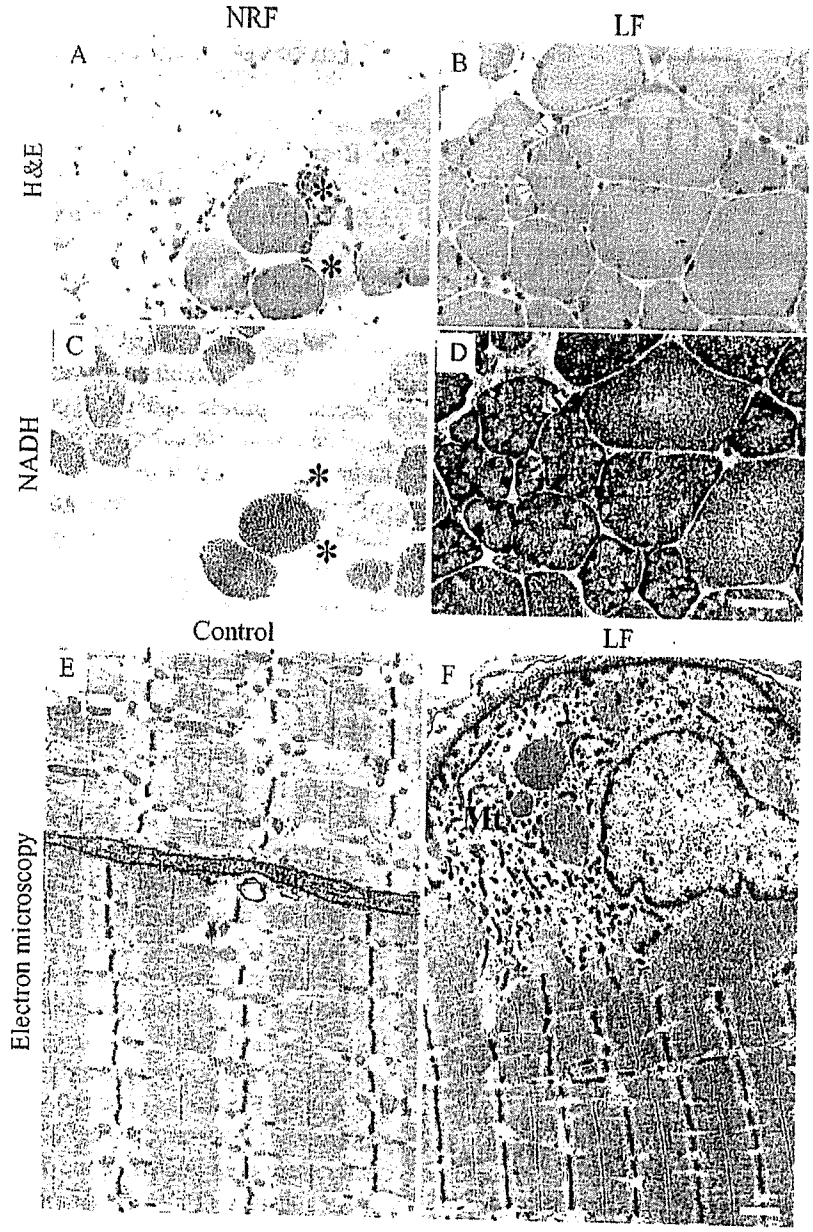

Fig. 1. Two representative muscle pathologies in LGMD2A. Microscopic images of hematoxylin and eosin (H&E) staining (A, B) and nicotinamide adenine dinucleotide tetrazolium reductase (NADH-TR) staining of LGMD2A patients (C, D). Patient 1 was classified into NRF group (A, C), and Patient 7 was classsified into LF group (B, D). Some necrotic (asterisks) and regenerative fibers were observed in the NRF patient and many lobulated fibers (arrowheads) were observed in the LF patient. Bar: 50 μm. Electronmicroscopic images of subsarcolemmal region in control (E) and LGMD2A patients with LF (F), respectively. Note accumulation of mitochondria (Mt) and disruption of myofibrils (F). Bar: 1 μm.

values for data points that were common to multiple microarrays. Hierarchical analyses were performed by using Pearson correlation (Fig. 2 and S1).

2.3. Quantitative RT-PCR

Quantitative RT-PCR was performed with QuantiTect SYBR Green PCR kit (Qiagen GmbH, Hilden, Germany) using iCycler iQ real-time PCR detection system (Bio-Rad, Hercules, CA, USA). We quantitated the amounts of gelsolin and glyceraldehyde phosphate dehydrogenase (GAPDH) transcripts as an internal control. Primer sequences used in this study are as follows. Gelsolin (forward: 5′-GACTTCTGCTAAGCGGTACATCGAG-3′, reverse: 5′-CACAAAGGAGGGAGGCTCAAAG-3′) and GAPDH (forward: 5′-GGTAAAGTGGATATTGTTGCCATCAATG-3′, reverse: 5′-GGAGGGATCTCGCTCCTGGAAGATGGTG-3′).

2.4. Western blotting

Cryosections of muscles were dissolved by heating them in 50 mM Tris–HCl, pH 6.8, 10% glycerol, 2% SDS, 2.5% 2-mercaptoethanol. Equal amounts of protein were separated by Laemmli SDS–PAGE in each lane of a 5–17.5% polyacrylamide gel and then transferred to polyvinyl-difluoride membranes. The membrane was then incubated with antibodies for gelsolin (1:2500 dilution; monoclonal) (clone No. 2, BD Bioscience, San Jose, CA, USA), PDZ and LIM domain 3 (PDLIM3) (1:5000 dilution; polyclonal) (Abcam, Cambridge, UK), and troponin I1 (1:5000 dilution; polyclonal) (Santa Cruz Biotechnology, Inc., Santa Cruz, CA, USA) at room temperature for 1 h. Subsequent incubation with peroxidase-conjugated goat anti-mouse IgG (H + L) (Immunotech, Beckman coulter, Germany), Histofine rabbit anti-goat IgG (Vector Lab. Burlingame, CA, USA) and peroxidase-conjugated goat anti-rabbit IgG (TAGO immunologicals, Camarillo, CA, USA) was performed at

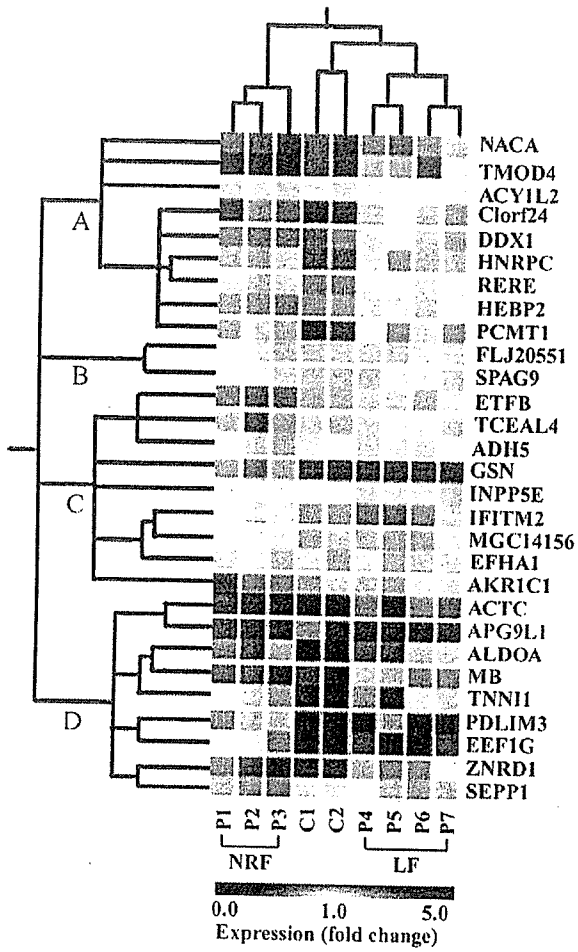

Fig. 2. Hierarchical analysis of the 29 selected genes according to their expression profiles. One block corresponds to one probe, which represents one gene. The expression of each gene relative to that of the reference RNA is shown in graduated colors as a scale to the right. Data for each subject are shown in vertical column in order to categorize the subjects into the NRF, control, or LF group. Color intensities among blocks in a row, which corresponds to a single gene, were compared. For cluster analysis, the 29 genes listed in the right dendrogram were subjected to Pearson correlation and were grouped as branches A–D, as shown on the left dendrogram. The color bar indicates the mRNA expression level of each muscle specimen as estimated from the signal ratio normalized with commercially Origene RNA. P: patient, C: control.

room temperature for 30 min. Membrane was developed using chemiluminescent reagent (Amersham Pharmacia Biotech UK, Buckinghamshire, UK).

2.5. Immunohistochemistry

Immunohistochemical staining was performed as described previously (Keira et al., 2003). We used the same gelsolin, troponin I1, and PDLIM3 antibodies as used in western blot analysis. Appropriate secondary antibodies used were affinity purified goat $(Fab)_2$ anti-rabbit IgG antibody conjugated with fluorescein (Tago, Inc., Burlingame, CA, USA), affinity purified goat anti-mouse IgG (H + L) antibody conjugated with fluorescein (Biosource International, Inc. Camarillo, CA, USA), and rabbit anti-goat IgG Alexa Fluor488 (Molecular probes, Inc., Eugene, OR, USA).

2.6. Apoptosis assay

The TdT-mediated dUTP-biotin nick end labeling (TUNEL) method was performed using an in situ apoptosis detection kit (Takara Co., Ltd., Japan) according to the manufacture's protocol. About 1000 myonuclei on different sections were counted and the percentages of TUNEL-positive myonuclei of each LGMD2A muscle were calculated.

3. Results

3.1. Overview of expression profiling in LGMD2A muscles

We analyzed the expression of more than 4200 genes in skeletal muscles of seven LGMD2A patients and two control individuals. Hierarchical analysis of all 4200 genes was performed to establish an association between the gene expression profile and the type of mutation in *CAPN3*, the residual amount of calpain 3 protein in muscle, and the muscle pathological findings (S1). We found that the pattern of gene expression was well delineated between the three groups, namely NRF, LF and controls. However, clustering analysis of non-selected genes gave results that were difficult to interpret. In order to elucidate the molecular events governing the formation of LFs, we performed further statistical analysis of the association between the expression profiles and the different muscle pathologies. Among the 4200 genes on the cDNA microarray, 207 genes were differentially expressed in LF muscles compared to control using the ANOVA–Welch *t*-test (statistically significant at $P < 0.01$) (S2 and S3). We classified these genes into 17 categories according to their functional characteristics. There were 150 upregulated genes and 57 downregulated genes in LF muscles (Table 2). Among the upregulated genes, genes associated with signal transduction, including calcium signalling-related genes, and cell growth-related genes predominated. In addition, ECM/membrane-related genes were also upregulated in LF muscles. On the other hand, genes related to energy metabolism comprised the majority of the downregulated genes. Similarly, by comparing LF and NRF muscles ($P < 0.01$), 423 genes were found to be differently expressed (S4 and S5). Among the 423 genes, 252 genes were upregulated, while 171 genes were downregulated in LF muscles (Table 3). Among the upregulated genes, the largest category was composed of transcription-related genes, while among downregulated genes, transport and sarcomere-related genes were predominant. Ubiquitin–proteasome-related genes, were also upregulated in LF muscles compared to other types of muscles. We also evaluated the changes in expression of genes related to apoptosis, since it has been reported that the apoptotic pathway is involved in the pathogenesis of LGMD2A (Baghdiguian et al., 1999). Among the 33 apoptosis-related genes in our microarray, eight genes (24%) showed altered expression in LGMD2A muscles (S2–S5). In summary, 207 genes were differentially expressed between LF and control muscles and 423 genes were differentially expressed between LF and NRF muscles. Further analysis revealed that 29 genes were common to both groups (Table 4). In addition, we performed ANOVA–Welch *t*-test with Bonferroni correction ($P < 0.05$) and found that nine genes were differentially expressed between all three groups (S6), although comparisons between NRF and the controls may not be so useful for understanding the pathomechanism of LF.

Table 2
Classification of differentially regulated 207 genes in LF muscles compared to normal muscles

Category	Number of genes with increased expression	Number of genes with decreased expression
Apoptosis	3	0
Catabolism	9	2
Channel/receptor	5	0
Chaperone	0	1
Cytoskeleton	10	3
ECM/membrane	15	0
Energy metabolism	14	8
Enzyme	6	1
Immune response	5	1
Lipid metabolism	3	0
Sarcomere	10	3
Signal transduction	18	7
Transcription	10	8
Translation	4	3
Transport	3	1
Others	13	5
Unknown	22	14
Total	150	57

Total 207 genes were differentially expressed in LF muscles compared to control using ANOVA–Welch t-test (statistically significant at $P < 0.01$). Gene categories are from LocusLink (www.ncbi.nlm.nih.gov/LocusLink).

3.2. Specifically dysregulated genes in LF muscles

We performed hierarchical clustering of the 29 genes using Pearson correlation. By experimental clustering, specimens were largely classified into three groups, which corresponded to NRF, LF and control as shown in the top dendrogram (Fig. 2).

Table 3
Classification of differentially regulated 423 genes in LF muscles compared to NRF muscles

Category	Number of genes with increased expression	Number of genes with decreased expression
Apoptosis	3	2
Catabolism	19	11
Channel/receptor	7	8
Chaperone	4	3
Cytoskeleton	8	3
ECM/membrane	8	5
Energy metabolism	16	12
Enzyme	5	4
Immune response	3	1
Lipid metabolism	3	2
Sarcomere	2	7
Signal transduction	30	28
Transcription	42	16
Translation	14	7
Transport	0	9
Others	32	13
Unknown	56	40
Total	252	171

Total 423 genes were differentially expressed in LF muscles compared to NRF muscles using ANOVA–Welch t-test (statistically significant at $P < 0.01$). Gene categories are from LocusLink (www.ncbi.nlm.nih.gov/LocusLink).

By hierarchical gene clustering, these 29 genes were divided into four branches (branches A–D) (Fig. 2 and Table 4). The genes in branch A were less downregulated in NRF and LF muscles than in the controls, albeit more downregulation was observed in the LF muscles. Branch A was predominantly comprised of transcription-related and RNA-binding protein genes, such as *HNRPC*, *DDX1* and *RERE*, and a gene (*TMOD4*) that encodes an actin regulatory protein, tropomodulin 4. Only two genes, including sperm-associated antigen 9 (*SPAG9*), were found in branch B. Genes in this branch were only mildly downregulated in LF muscles and nearly normally expressed in NRF muscles. The genes in branch C were upregulated in LF muscles but mildly downregulated or normal expressed in NRF muscles. Genes encoding signal-mediating molecules comprised the bulk of this group. Interestingly, of the nine genes in branch C, the expression of *GSN* gene, which encodes gelsolin, an actin depolymerizing or stabilizing plus end protein, was greatly increased about 11-fold in LF muscles compared to NRF muscles (Table 4). The genes in branch D were highly upregulated in NRF muscles and, to a lesser extent, in LF muscles, and primarily included genes that encode sarcomeric proteins such as *TNNI1*, *PDLIM3* and *ACTC*. Based on our previously reported data (Noguchi et al., 2003), the expression of five of the nine genes in branch D was also altered in DMD (Table 4).

3.3. Changes in the expression of actin-associated genes in LF muscles

Of the 29 selected genes, we further focused on the upregulated genes *GSN*, *TNNI1* and *PDLIM3*, which encode

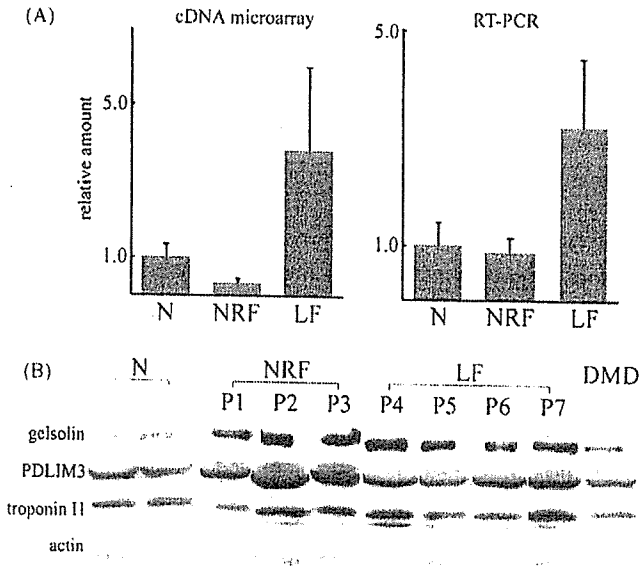

Fig. 3. Validation of cDNA microarray data by quantitative RT-PCR and Western blot analysis. Measurements of mRNA expression of *GSN* using cDNA array analysis or quantitative RT-PCR analysis (A). Western blot analysis of gelsolin, PDLIM3 and troponin I1 using skeletal muscle homogenates from seven LGMD2A patients, two controls, and one DMD patient (B). Note that compared to controls, the expression of these three proteins increases in both NRF and LF patients. The actin band was stained with Coomasie brilliant blue as a control.

Table 4
Specifically regulated 29 genes in patients with lobulated fibers

Accession	Gene	Function	LF/N	LF/NR	DMD	LGMD2B
(A)						
NM_022083	Clorf24	Unknown	−5.7	1.8		
NM_013353	TMOD4	Muscle structure	−4.6	2.6	Down[a]	
NM_005389	PCMT1	Chaperone	−2.8	1.6		
NM_004939	DDX1	Transcription	−2.7	1.5		
NM_031314	HNRPC	Transcription	−2.5	1.4		
NM_012102	RERE	Transcription	−2.1	1.2		
NM_005594	NACA	Others	−2.0	4.3		
NM_014320	HEBP2	Others	−1.8	1.4		
NM_001010853	ACY1L2	Catabolism	−1.1	1.2		
(B)						
NM_003971	SPAG9	Signal transduction	−1.4	−1.2		
NM_017875	FLJ20551	Others	−1.3	−1.2		
(C)						
NM_000177	GSN	Cytoskeletal protein	3.6	10.7	Up[a]	Up[b]
NM_006435	IFITM2	Immune response	3.0	2.0		
NM_032906	MGC14156	Signal transduction	2.0	1.6		
NM_001353	AKR1C1	Catabolism	1.6	2.6	Down[a]	
NM_152726	EFHA1	Signal transduction	1.6	1.6		
NM_001985	ETFB	Lipid metabolism	1.4	1.9	Down[a]	
NM_024863	TCEAL4	Translation	1.3	1.6		
NM_000671	ADH5	Redox	1.2	1.3		
AI026701	INPP5E	Signal transduction	1.2	1.1		
(D)						
NM_005159	ACTC	Muscle structure	14.4	−3.8	Up[a,c,d]	
NM_005368	MB	Energy metabolism	5.7	−2.1		
NM_024085	APG9L1	Catabolism	5.2	−2.1		
NM_014476	PDLIM3	Muscle structure	4.2	−2.1	Down[a]	
NM_000034	ALDOA	Glycolysis	3.9	−3.6	Down[a]	
NM_001404	EEF1G	Translation	3.7	−2.4	Down[a]	
NM_003281	TNNI1	Muscle structure	2.7	−1.9	Down[a]	
NM_170783	ZNRD1	Transcription	2.1	−5.0		
NM_005410	SEPP1	Extracellular matrix	1.5	−1.4		

LF/N represents the fold change in expression in muscles with LF to that in controls. LF/NR represents the fold change in expression in muscles with LF to that with NRF. (−) Denotes down-regulation.
[a]Genes differentially regulated in DMD patients according to Noguchi et al. (2003, 2005).
[b]Genes differentially regulated in LGMD2B patients according to Campanaro et al. (2002).
[c]Genes differentially regulated in DMD patients according to Chen et al. (2000).
[d]Genes differentially regulated in DMD patients according to Haslett et al. (2002).

cytoskeletal and sarcomeric proteins, because myofibrillar structure is greatly altered in LF muscles. We confirmed the upregulation of the *GSN* gene by quantitative RT-PCR (Fig. 3A) and the increase in the expression of its product, gelsolin, by Western blotting (Fig. 3B). Quantitative RT-PCR analysis showed four-fold upregulation of this gene in LF muscles as compared with NRF muscles (Fig. 3A). Moreover, protein expression of gelsolin was increased about 10-fold in LGMD2A muscles when compared with the control. However, there was no difference between LF muscles and NRF muscles (Fig. 3B). Immunohistochemical analysis of LF muscles showed that gelsolin was distributed in the subsarcolemmal regions of LFs (Fig. 4, patient 6, asterisks), and in connective tissue, although it was undetectable in control muscle fibers. In addition, in NRF muscles, gelsolin was diffusely present in the cytoplasm of small regenerating fibers and in the subsarcolemmal region of necrotic fibers and mononuclear cells (Fig. 4).

We also confirmed the upregulation of PDLIM3 and troponin I1 proteins by Western blot analysis both in NRF and LF muscles (Fig. 3B). Immunohistochemistry showed that the sarcomere of LFs and non-LFs was strongly stained with PDLIM3. In contrast, in NRF muscles, immunoreactivity was only mildly increased in apparently unaffected muscle fibers (Fig. 4). Troponin I1 expression was increased in the sarcomere of the small LFs. Fiber typing by anti-myosin heavy chain antibody showed that most of these small muscle fibers were slow-type fibers (data not shown, Chae et al., 2001). In NRF muscles, however, signals were undetectable in either necrotic or regenerating fibers (Fig. 4).

4. Discussion

In our analysis, we have clearly shown that gene expression in LGMD2A can be classified on the basis of differences in muscle pathology (S1), as with other muscular dystrophies

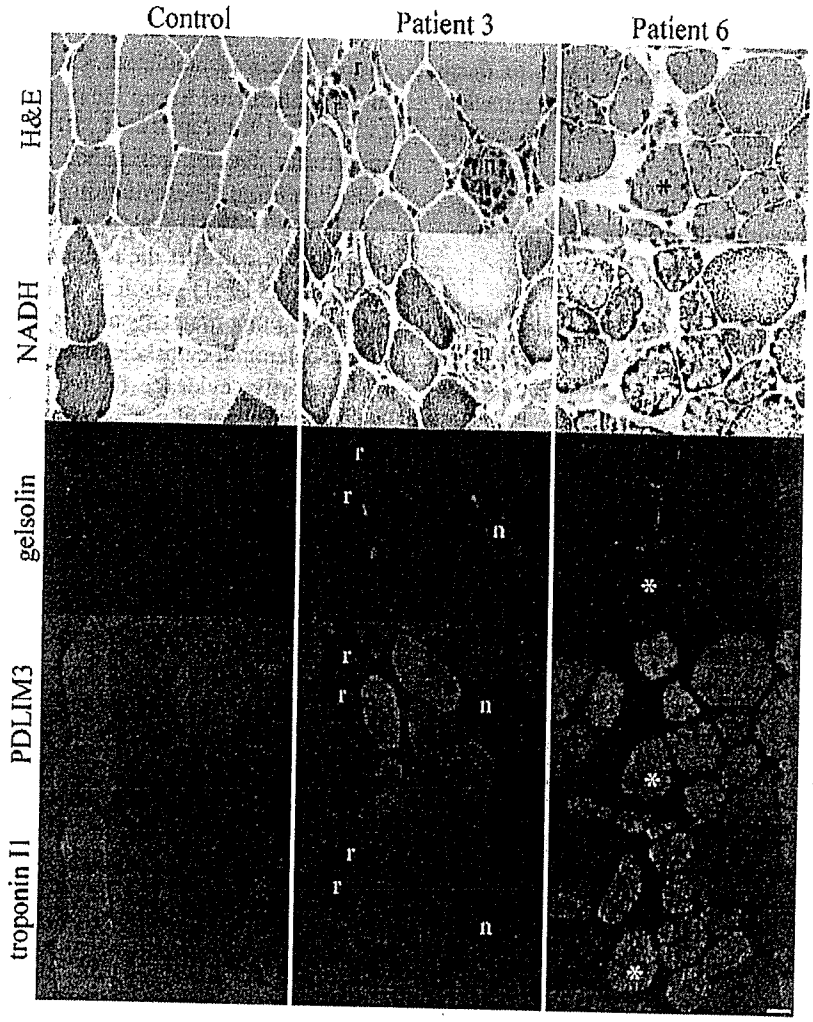

Fig. 4. Immunohistochemical analyses of gelsolin, PDLIM3 and troponin I1 reveal abnormal staining in NRF and LF muscles. Gelsolin, PDLIM3 and troponin I1were stained in control, NRF muscle (Patient 3) and LF muscle (Patient 6). Gelsolin localizes in the cytoplasmic region of regenerating fiber (r) and peripheral region of necrotic fiber (n), and the subsarcolemmal region of LFs (asterisk) and connective tissues. PDLIM3 showed a striation pattern in the control; however, it was not detectable in regenerating (r) or necrotic fibers (n) in NRF muscles (Patient 3). In LF muscle, PDLIM3 is abundantly distributed in the sarcomeric region of LFs (asterisks, Patient 6). Troponin I1 displayed diffuse sarcomeric staining in slow-type fibers in control and NRF muscles (Patient 3), and it localized strongly to the sarcomeric region of many slow-type LFs (white asterisk). Bar: 20 μm.

(Noguchi et al., 2003; Taniguchi et al., 2006). This suggests that the pathological changes seen in LGMD2A muscles might well be caused by molecular events initiated by these differences in gene expression. Since LF is characteristically observed in the later stage of LGMD2A, we therefore divided LGMD2A patients into two groups on the basis of pathological features in order to uncover the characteristic gene expression profiles of LGMD2A.

4.1. Outline of expression profiles in LF muscles

In LF muscles, several genes related to signal transduction and transcription were differentially expressed. These genes encode signaling mediators and transcriptional factors implicated in cell growth, calcium signaling and apoptosis. Interestingly, our results suggested that the genes for cell growth and calcium signaling were upregulated; in contrast, genes involved in apoptosis were rather suppressed in LF muscles. These data suggested that apoptosis signaling might be inactivated at least in LF or the later stage of LGMD2A muscles. In fact, the ratio of TUNEL-positive myonuclei to normal nuclei was less than 0.014% in our series (Table 1).

Genes coding for extracellular matrix (ECM)/membrane-related, cytoskeletal or sarcomeric proteins were also upregulated in LF muscles. These molecular changes could reflect the structural features of LF muscles. For example, upregulation of ECM/membrane-related genes might be associated with interstitial fibrosis observed in LF muscles; likewise, upregulation of cytoskeletal or sarcomeric-related genes might be associated with structural changes of the intramyofibril network in LFs.

The expression changes of some genes in the NRF muscles of LGMD2A patients were similar to those seen in Duchenne muscular dystrophy (DMD) muscles. In our previous study, in muscles from DMD patients, upregulated genes were mostly those related to immune response, sarcomeric, ECM and signal transduction, whereas, downregulated genes were associated with energy metabolism, transcription/translation,

signal transduction and the proteasome (Noguchi et al., 2003). In the present study, however the expression levels of these genes in LF stage were similar to those in control muscles. These results confirm the absence of necrotic and regenerating processes in LF muscles.

4.2. The 29 specifically dysregulated genes in LF muscles

4.2.1. Overview of the 29 genes in LF muscles

As shown in Table 4, we found that the expression of the genes in branch A was comparable between control and LF but was greatly decreased in NRF muscles. On the other hand, the expression of genes in branch D was greatly increased in NRF muscles compared to LF muscles. From these results, we considered that the expression of genes in branches A and D might be closely related to necrosis and regeneration in NRF. In contrast, the expression of genes in branches B and C underwent more extensive downregulation or upregulation in LF than in NRF. The genes in these branches may play specific roles in LF formation, although we were unable to get any conclusive information about, or identify common properties between the genes in these groups.

4.2.2. Apoptosis-associated genes among the 29 genes

Among the 29 genes, genes related to cytoskeletal, sarcomeric, signal transduction and catabolism proteins were upregulated, while genes related to transcription were downregulated in LF muscles. One of the downregulated genes was *SPAG9*, which encodes a scaffold protein that binds to several signaling molecules or transcription factors (Lee et al., 2002). Interestingly, SPAG9 interacts with NF-κB1/p105 but not with NF-κB2/p100, and expression of RNAi for *SPAG9* results in decreased NF-κB activity in response to treatment with tumor necrosis factor-α (Bouwmeester et al., 2004). NF-κB signaling pathway was reported to be downregulated in muscles from LGMD2A patients and calpain 3 knockout mice (Baghdiguian et al., 1999; Richard et al., 2000). The down-regulation of *SPAG9* observed in this study may partly reflect perturbation of the NF-κB signaling pathway as reported by Baghdiguian. Although, as earlier mentioned, other apoptotic signals seemed to be suppressed in LF, a more extensive analysis of the NF-κB pathway in LGMD2A patients is still needed to clarify the role of SPAG9 and other related genes in apoptosis.

4.2.3. Actin-associated genes among the 29 genes

Since the presence of LF is a characteristic structural change observed in LGMD2A muscles, changes in the expression of genes encoding intracellular structural proteins and their regulators should be important. In this study, we focused on upregulated genes for actin-associated proteins in LF muscles, such as gelsolin, troponin I1 and PDLIM3.

4.2.3.1. Gelsolin. A comparison of the present data with our previous data (Noguchi et al., 2003) shows that gelsolin gene expression is more upregulated in LF than in DMD muscles. We found that gelsolin was distributed diffusely in the cytoplasm of regenerating fibers, in contrast to its subsarcolemmal distribution in LFs, which are characterized by deranged myofibrils and mitochondria accumulation. Gelsolin mainly functions to sever actin filament and to cap the plus ends of the severed filaments (Yin et al., 1981; Lamb et al., 1993). In cultured myogenic cells, myofibrils develop resistance to this severing function of gelsolin during differentiation (Huckriede et al., 1988; Gonsior and Hinssen, 1995). Taking all the available information into account, we consider the following roles for gelsolin during its activation in LF:1) gelsolin could scavenge the disrupted actin-containing thin filaments of LFs and 2) gelsolin could sever the subsarcolemmal cytoskeletal actin network. Although we have no supportive evidence for any of these possibilities, the upregulation of gelsolin may be associated with actin derangement in LFs.

4.2.3.2. TroponinI1. Troponin I is a subunit of the actin filament-associated troponin–tropomyosin complex involved in the regulation of skeletal and cardiac muscle contraction (Gordon et al., 2000). In our study, troponin I1, which is a slow-twitch isoform of troponin I family, was highly upregulated in LGMD2A muscles with NRF, and to a lesser extent, in those with LF (Table 4). Other subunit genes in the troponin complex, such as *TNNI2*, *TNNC1*, *TNNC2* and *TNNT3* were also strongly upregulated in LGMD2A muscles with NRF and weakly in those with LF (S1). Expression of each troponin subunit gene seems to be similarly regulated during the progression of muscle pathology in LGMD2A. In LF muscles, troponin I1 immunoreactivity was observed strongly in the small slow-type LFs. Considering the predominance of slow-twitch fibers in LF muscles, the increase in troponin I1 mRNA expression in LF muscles might be due to the increased numbers of slow fibers in LF muscles (Chae et al., 2001). Interestingly, troponin I1 was not observed in the subsarcolemmal region and did not co-localize with gelsolin in LFs. From this result, the intensive expression of troponin I1 might not be directly related to the derangement of myofibrils in subsarcolemmal regions in LFs.

4.2.3.3. PDLIM3. PDLIM3 is known to bind the spectrin-like repeats of α-actinin via its PDZ domain and localize to the Z-lines (Xia et al., 1997; Jo et al., 2001). It has been reported that overexpression of PDLIM3 results in the increased ability of α-actinin to cross-link actin filaments (Pashmforoush et al., 2001). In our study, PDLIM3 showed stronger immunoreactivity in LFs, but did not colocalize with gelsolin accumulation. The upregulation of PDLIM3 observed in LF muscles might have some roles in stabilizing Z-line of myofibril structures.

4.3. Conclusion

Upregulation of the genes associated with actin filament observed in LF muscles is consistent with the markedly disorganized myofibrils in these muscles. Although, further analyses will be needed to explain relationship between calpain 3 and associated molecules whose functions remain unknown, our study shows that gene expression profiling of LGMD2A is a powerful tool that can provide clues to the pathomechanism of this disease.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.neures.2006.12.010.

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