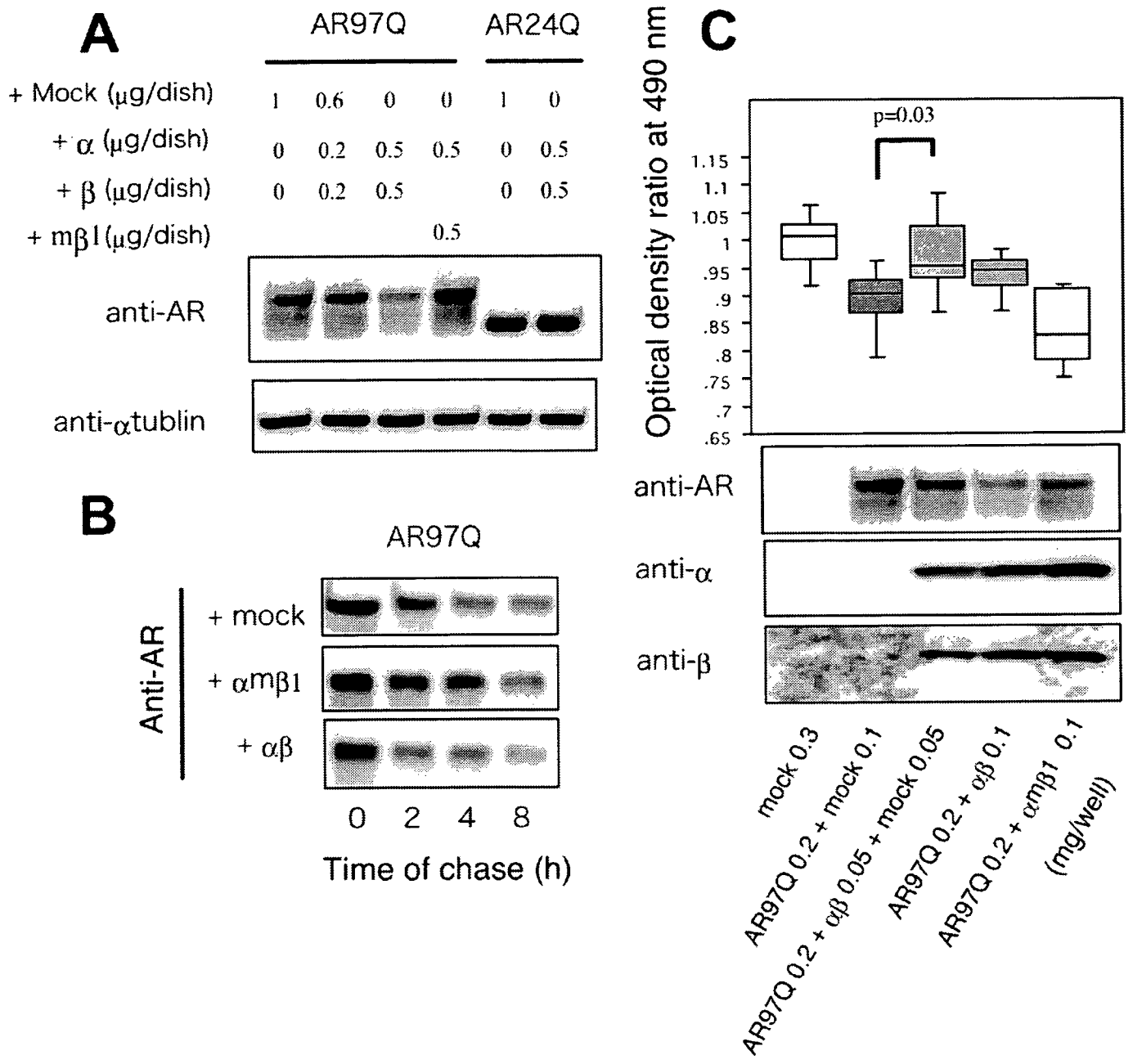

FIGURE 6. ***M. mazei* proteasome degrades mutant androgen receptor with expanded polyglutamine tract and reduces its cellular toxicity.** *A*, Neuro2a cells grown on 6-cm dishes and co-transfected with 1 μg of AR containing either normal (24Q) or expanded (97Q) polyglutamine tract vectors and increasing doses of Mm proteasome subunits were analyzed. The levels of AR^{97Q} proteins were reduced as Mm proteasome αβ increased. *B*, cycloheximide chase analysis (see "Experimental Procedures") showing that the half-lives of AR^{97Q} proteins were decreased in the presence of Mm 20 S proteasome αβ. Transfected DNA dose/6-cm dish was as follows: AR^{97Q} (1 μg), α-subunit (0.5 μg), β-subunit (0.5 μg). *C*, the rescue effect of Mm proteasome αβ expression on cell viability in AR^{97Q}-transfected HEK293 cells as shown in an MTS assay. The *box plots* show the median values (*center line* of *box*), the 25th (*lower line* of *box*), 75th (*upper line* of *box*), 10th (*lower T bar*), and 90th (*upper T bar*) percentiles in each group ($n = 3 \times 6$ wells). The *numbers* indicate transfected DNA dose in a well of a 96-well plate (αβ, 0.1 μg; α, 0.05 μg; β, 0.05 μg). The expression levels of AR, α-subunit, and β-subunit at analyzed points are shown.

GFP-positive $SOD1^{G93A}$ aggregates are also anti-His positive, whereas the cells expressing wild-type SOD1-GFP are diffusely stained with anti-His antibody. There were no GFP-negative inclusion bodies stained with anti-His antibody, indicating that Mm proteasome co-localizes with the inclusion bodies consisting of mutant SOD1 in the vicinity of the nucleus. The percentages of aggregate-positive cells among the GFP-positive cells were determined in Fig. 5*B*. $SOD1^{G93A}$ aggregates were significantly reduced when co-expressed with Mm proteasome αβ.

M. mazei Proteasome Degrades Specifically Mutant Androgen Receptor with Expanded Polyglutamine Tract and Reduces Its Cellular Toxicity—To demonstrate the ability of the Mm proteasome to degrade aggregation-prone proteins, we examined the AR with expanded polyglutamine tract (97-repeated glutamine; 97Q) protein, the causative protein of spinal and bulbar muscular atrophy. Similar to the results obtained with SOD1 proteins, Fig. 6*A* shows that in Neuro2a cells, the levels of mutant AR (97Q) were markedly reduced as the expression of

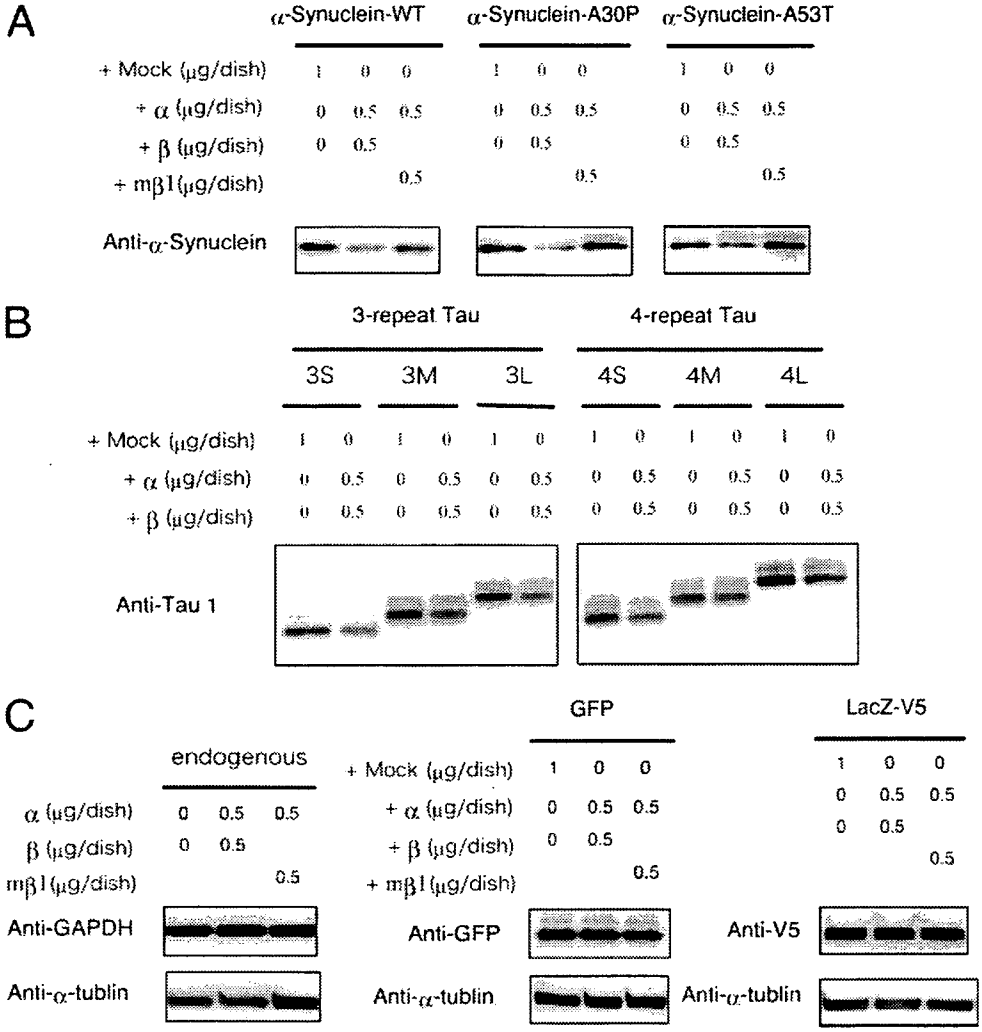

FIGURE 7. ***M. mazei* proteasome degrades aggregation-prone but not non-aggregation-prone proteins.** Neuro2a cells grown on 6-cm dishes and co-transfected with Mm proteasome subunits vectors or mock and 1 μg of α-synuclein vectors (wild type, A30P, and A53T) (*A*), Tau vectors (six isoforms: three (3L, 3M, and 3S) or four (4L, 4M, and 4S) tubulin binding domains in the C-terminal portion and two (3L and 4L), one (3M and 4M), or no (3S and 4S) inserts of 29 amino acids each in the N-terminal portion) (*B*), or empty GFP vector or LacZ-V5 vector (*C*). *A* and *B*, the expression levels of all of α-synuclein and tau proteins were reduced when co-transfected with the Mm proteasome αβ. *C*, the expression levels of endogenous glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*), GFP, and LacZ-V5 proteins were not changed in the presence of the Mm proteasome αβ.

Mm proteasome αβ increased, but they were unaffected by the expression of the Mm proteasome αmβ1. On the other hand, wild-type AR (24-repeated glutamine; 24Q) levels were not affected by the expression of Mm proteasome αβ. Cycloheximide-chasing analysis demonstrated that the half-life of mutant AR (97Q) was reduced in the presence of the Mm proteasome but not in the presence of the mutant Mm proteasome (Fig. 6*B*). The viability of cells expressing mutant AR (97Q) was reduced compared with wild-type AR (24Q), and this reduction was attenuated by the co-transfection with Mm proteasome αβ (Fig. 6*C*). These results show that Mm proteasome αβ can accelerate the degradation of the aggregation-prone mutant AR with expanded polyglutamine tract and possibly protect the cells from its toxicities.

M. mazei Proteasome Degrades Other Aggregation-prone Proteins but Not Non-aggregation-prone Proteins—To determine whether the Mm proteasome degrades other aggregation-prone proteins as well, we examined its effects on α-synuclein (wild-type, A53T, and A30P) and six isoforms of wild-type tau protein in Neuro2a cells. The six tau isoforms contained either three (3L, 3M, and 3S) or four (4L, 4M, and 4S) microtubule binding domains in the C-terminal portion and two (3L, 4L), one (3M, 4M), or no (3S, 4S) inserts of 29 amino acids each in the N-terminal portion. Similar to the results obtained with the mutant SOD1 and AR with an expanded polyglutamine tract, the expression levels of all α-synuclein and tau proteins were reduced in the presence of Mm proteasome αβ (Fig. 7, *A* and *B*). Although the degradations of wild-type SOD1 and AR proteins were not accelerated by Mm proteasome, the expression levels of α-synuclein including wild-type and all of the six forms of wild-type tau were reduced.

We also examined whether Mm proteasomes degrade non-aggregation-prone proteins such as GFP or LacZ. Fig. 7*C* shows that the Mm proteasome does not affect the degradation of the exogenously expressed proteins, GFP and LacZ.

DISCUSSION

In this study, we showed that the archaeal Mm proteasome α- and β-subunits properly assembled to have proteolytic activity and accelerate the degradation of aggregation-prone, neurodegeneration-associated proteins in mammalian cells. Archaeal proteasomes contain 14 identical active sites that, although originally classified as chymotrypsin-like, were later shown to cleave after acidic and basic residues (22), and they consist of only one type of each of the α- and β-subunits (6). A comparison between archaeal and eukaryotic proteasomes *in vitro* showed that archaeal proteasomes are far more active in degrading poly(Q) peptides than are eukaryotic proteasomes (9). We utilized this potential power and manageability of archaeal proteasomes to degrade abnormal proteins that could not be effectively degraded by eukaryotic proteasomes. This is the first report showing that archaeal proteasomes can work to accelerate degradation of aggregation-prone proteins in mammalian cells.

Mm proteasomes promoted degradation of mutant SOD1, AR with an expanded polyglutamine tract, wild-type and mutant α-synuclein, and six isoforms of wild-type tau. The first two proteins, mutant SOD1 and AR with an expanded polyglutamine tract, exhibit toxicity in cell culture models. Mice overexpressing these mutant proteins display abnormal aggrega-

tions in their motor neurons and significant loss of motor functions, and they have been used as disease models (23, 24). Mm proteasomes accelerated the degradation of only the mutant forms of these two proteins and not that of the nonaggregating wild-type forms. Furthermore, chasing studies (Fig. 3, *A* and *B*) confirmed our belief that Mm proteasomes directly accelerate the degradation of mutant proteins.

However, both the wild-type and two mutants of α-synuclein as well as six isoforms of wild-type tau were also degraded by Mm proteasomes (Fig. 7). α-Synuclein and tau are pathogenically different proteins from SOD1 and AR, since they are known to accumulate as wild-type proteins in the affected lesions of PD and AD, respectively. Aggregation of the presynaptic protein, α-synuclein, has been implicated in synucleinopathies, such as sporadic and familial PD, diffuse Lewy body disease, and multiple-system atrophy (25). In sporadic PD patients, wild-type α-synuclein is accumulated, and increased expression of wild-type α-synuclein is also observed (26). Proteasomal dysfunction has been thought to impair α-synuclein degradation and thereby to facilitate its aggregation (27). Three- and four-repeat wild-type tau are among the proteins characteristically detected in neurofibrillary tangles formed by paired helical filaments in sporadic AD (28). Decreased proteasomal activity has been also reported in the AD brain (29). α-Synuclein and tau are both relatively easily misfolded, which leads to the formation of aggregates, even in their wild-type forms (30, 31), thus possibly explaining why the Mm proteasomes degraded wild-type α-synuclein and tau. Mm proteasomes might be able to recognize a wide range of aggregation-prone proteins, whereas they do not affect the degradation of exogenously expressed nonaggregating proteins, such as GFP and LacZ, or abundant endogenous proteins, such as α-tubulin and glyceraldehyde-3-phosphate dehydrogenase (Fig. 7).

The question raised here is what is the molecular mechanism of such selective, mutant species-dependant degradation. Archaeal 20 S proteasomes contain proteasome-activating nucleotidase, PAN, enabling substrates to enter the proteasomes easily and effectively (8). PAN has a chaperone-like activity to unfold aggregated proteins (32) and is thought to be an evolutionary precursor to the 19 S base in eukaryotic cells (8). Archaeal recognition tags (like ubiquitin tags in eukaryotic cells) have not been identified yet. However, archaeal 20 S proteasomes have been reported to rapidly degrade polyglutamine aggregates *in vitro*, without the help of PAN (9). Here we confirmed that this PAN-independent degradation by Mm 20 S proteasomes could occur in mammalian cells. Since the pore diameter of the closed gate in 20 S proteasomes is estimated to be much smaller than that of aggregated proteins (33), the question is, how do the unfolded substrate proteins enter the 20 S proteasomes? One hypothesis might be that the α-ring in Mm proteasomes has chaperone-like activity to recognize and unfold the aggregation-prone proteins or misfolded proteins. The gated channel in the α-ring of the archaeal 20 S proteasomes is thought to regulate substrate entry into the proteasomes and is assumed to be in either an open (34) or a closed state (2, 33) *in vitro*. In our experiments, the gate-free Mm 20 S proteasome $\Delta\alpha\beta$ substantially reduced cell viability, but the Mm proteasome $\alpha\beta$, with the "gate," had little toxic effect on the cells and, furthermore, accelerated the degradation of mutant proteins. This would be hard to explain if the gate is always in the closed state. There is a possibility that when Mm proteasomes gather, actively or passively, near aggregation-prone proteins, the α-ring opens its gate and unfolds the aggregated proteins, enabling them to enter the proteasomes to be degraded.

Some kinds of molecular chaperones, such as Hsp90, -70, and -27, have been reported to assist in the selective degradation of mutant SOD1 and AR proteins in proteasome degradation pathways (35, 17). However, neither the protein levels of molecular chaperones (Hsp90, -70, -40, and -27) nor the ubiquitylation levels of mutant SOD1 and AR were changed in the presence of Mm proteasome $\alpha\beta$ expression (data not shown), thus supporting the idea that endogenous ubiquitin-proteasome degradation pathways possibly did not play an important role in the accelerated degradation of mutant proteins. Further study is needed to elucidate the molecular mechanisms of selective recognition of misfolded aggregation-prone proteins by Mm proteasomes.

In this paper, we demonstrated that Mm proteasomes could effectively degrade neurodegenerative disease-related aggregation-prone proteins *in vivo*. Further studies are needed to determine whether archaeal proteasomes can be available to treat diseases in which toxic gain of proteins is causative.

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Gene Expression Profile of Spinal Motor Neurons in Sporadic Amyotrophic Lateral Sclerosis

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The causative pathomechanism of sporadic amyotrophic lateral sclerosis (ALS) is not clearly understood. Using microarray technology combined with laser-captured microdissection, gene expression profiles of degenerating spinal motor neurons isolated from autopsied patients with sporadic ALS were examined. Gene expression was quantitatively assessed by real-time reverse transcription polymerase chain reaction and in situ hybridization. Spinal motor neurons showed a distinct gene expression profile from the whole spinal ventral horn. Three percent of genes examined were downregulated, and 1% were upregulated in motor neurons. Downregulated genes included those associated with cytoskeleton/axonal transport, transcription, and cell surface antigens/receptors, such as dynactin, microtubule-associated proteins, and early growth response 3 (EGR3). In contrast, cell death–associated genes were mostly upregulated. Promoters for cell death pathway, death receptor 5, cyclins A1 and C, and caspases-1, -3, and -9, were upregulated, whereas cell death inhibitors, acetyl-CoA transporter, and NF-κB were also upregulated. Moreover, neuroprotective neurotrophic factors such as ciliary neurotrophic factor (CNTF), Hepatocyte growth factor (HGF), and glial cell line–derived neurotrophic factor were upregulated. Inflammation-related genes, such as those belonging to the cytokine family, were not, however, significantly upregulated in either motor neurons or ventral horns. The motor neuron–specific gene expression profile in sporadic ALS can provide direct information on the genes leading to neurodegeneration and neuronal death and are helpful for developing new therapeutic strategies.

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Amyotrophic lateral sclerosis (ALS) is a devastating neurodegenerative disease characterized by loss of motor neurons in the spinal cord, brainstem, and motor cortex.[1] Initial symptoms include weakness of the limbs, abnormalities of speech, and difficulties in swallowing. The weakness ultimately progresses to complete paralysis, and half of the patients die within 3 years after the onset of symptoms, mostly because of respiratory failure. Approximately 10% of all ALS patients show familial traits, and 20 to 30% of familial ALS patients are associated with a mutation in the copper/zinc superoxide dismutase 1 gene (SOD1). However, more than 90% of ALS patients are sporadic, not showing any familial trait. The presence of Bunina bodies in the remaining spinal motor neurons is a hallmark of sporadic ALS cases.[2,3] So far, several hypotheses about the pathogenesis of sporadic ALS have been proposed based on extensive research on sporadic ALS: oxidative stress, glutamate excitotoxicity, impaired axonal transport, mitochondrial dysfunction, neurotrophic deprivation, proteasomal dysfunction, neuroinflammation, autoimmunity, viral infection, and others.[4–11] Nevertheless, the actual pathogenic mechanism of the selective motor neuron degeneration and ultimate cell death in sporadic ALS remains unknown. There have been extensive studies using animal models and culture systems for familial ALS, especially with SOD1 mutations, but no similar approach is available for studying sporadic ALS.

Recently advances in DNA microarray technology make it possible to analyze global gene expression profiles of thousands of genes in normal as well as pathological tissues. Global gene expression studies using DNA microarray technology have generated valuable

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information about cell behavior in tissues consisting of homogeneous cell types, cultured cells, and cancer tissues of monoclonal origin.[12,13] In the case of neuronal tissues, particularly those of patients with neurological diseases, however, the complexity of tissues containing multiple lineages of cells, such as neurons, glial cells, and vascular tissues, places limitations on the use of DNA microarray technology. In the lesions of ALS spinal cords, there are reduced numbers of motor neurons with glial cell proliferation, making it difficult to examine motor neuron–specific gene expression.

Laser-captured microdissection (LCM) has been reported to make it possible to isolate single individual neurons from neural tissues with well-preserved mRNA quality.[14,15] In addition, RNA amplification techniques preserving the relative amounts of individual mRNAs have been developed recently.[16,17] LCM and RNA amplification combined with DNA microarray analyses have been reported to enable studies of cell type–specific gene expression profiles in tissues with multiple cell lineages.[16,18] Such integrated analysis system provide an effective tool for investigating the cellular events affecting cell type–specific gene expression profiles in neurodegenerative diseases such as ALS. Indeed, we and other groups demonstrated that these integrated systems could be applied successfully to describe cell-specific gene expression profiles in neuronal tissues.[15,18]

In this study, we applied integrated LCM, RNA amplification, and DNA microarray analysis to clarify alterations of motor neuron–specific gene expression in sporadic ALS cases and successfully obtained expression gene database in situ from degenerating motor neurons in sporadic ALS spinal cord.

Patients and Methods

Tissues from Amyotrophic Lateral Sclerosis and Control Patients

Fresh specimens of lumbar spinal cord (L4 to L5 segment) from 14 sporadic ALS patients (nine men, five women) and 13 neurologically normal patients (nine men, four women) were obtained at autopsy (Table 1). Diagnosis of ALS was

Table 1. Details of Patients Examined in This Study

Patients	Sex	Age (yr)	Duration of Illness (yr)	Postmortem Delay (hr)	Diseases	Spinal Cord Neuropathology Motor Neuron Loss/Gliosis
ALS1	M	72	3.7	6	ALS (B, UL, LL)	Moderate/mild
ALS2	M	71	2.3	5	ALS (LL, UL)	Moderate/mild
ALS3	M	58	1.8	13	ALS (UL, LL, B)	Severe/severe
ALS4	M	43	2.6	5	ALS (LL, B)	Moderate/mild
ALS5	M	53	2.8	11	ALS (B, UL, LL)	Moderate/severe
ALS6	F	79	4.0	4	ALS (UL, LL, B)	Severe/severe
ALS7	F	59	2.5	3	ALS (UL)	Mild/mild
ALS8	F	67	2.0	7	ALS (UL, B)	Severe/mild
ALS9	M	74	4.3	10	ALS (LL, B)	Severe/mild
ALS10	F	47	1.8	4	ALS (B, UL, LL)	Mild/mild
ALS11	M	74	4.5	12	ALS (UL, LL)	Moderate/mild
ALS12	M	57	3.5	5	ALS (LL, UL)	Severe/mild
ALS13	F	53	3.0	8	ALS (B, UL, LL)	Severe/severe
ALS14	M	63	2.2	5	ALS (UL, B)	Mild/mild
Control1	M	57	—	7	Pneumonia	No
Control2	M	78	—	10	Cerebral infarction	No
Control3	M	72	—	9	Lung cancer	No
Control4	F	52	—	7	Pneumonia	No
Control5	F	65	—	12	Pneumonia	No
Control6	M	75	—	10	Heart failure	No
Control7	M	42	—	5	Heart failure	No
Control8	F	76	—	5	Pancreas cancer	No
Control9	F	84	—	6	Myocardial infarction	No
Control10	M	48	—	13	Heart failure	No
Control11	M	77	—	11	Heart failure	No
Control12	M	66	—	11	Cerebral infarction	No
Control13	M	75	—	4	Pneumonia	No

The age, duration of illness, and postmortem delay are indicated for the ALS and control cases. Predominant clinical features of ALS are shown: UL = upper limbs; LL = lower limbs; B = bulbar. Neuropathological involvement of spinal cords was graded as previously. Ten ALS samples were used for microarray analysis: five of them (1, 7, 10, 11, and 14) were analyzed using 4.8K array for spinal motor neurons; five (2, 4, 5, 8, and 12) using 1.0K for spinal motor neurons; five (1, 3, 10, 13, and 14) using 4.8K for spinal ventral horn gray matter; and five (1, 2, 4, 5, and 13) and five (1, 2, 7, 8, and 10) control samples using 4.8K and 1.0K. Thirteen ALS (1–13) and 11 (1–11) control samples were used for TaqMan reverse transcription polymerase chain reaction analysis. Five ALS (1, 10, 11, 13, and 14) and four control (1, 3, 5, and 12) samples were used for in situ hybridization and immunohistochemistry.
ALS = amyotrophic lateral sclerosis.

confirmed by El Escorial diagnostic criteria defined by the World Federation of Neurology and the histopathological findings, particularly the presence of the Bunina body.[2,3] All cases of ALS were sporadic and did not show any heredity. ALS patients with *SOD1* mutation were excluded. The collection of tissues and their use for this study were approved by the ethics committee of Nagoya University Graduate School of Medicine. Tissues were frozen immediately and stored at −80°C until use. The mean ages and standard deviations for ALS and control patients were 62.1 ± 11.0 and 66.7 ± 13.1 years, and the mean postmortem intervals and standard deviations were 7.0 ± 3.3 and 8.5 ± 3.0 hours, respectively. The differences between the means of either age or postmortem interval were not significant between the ALS and control groups. The cause of death in all ALS patients was respiratory failure, and the causes in the control patients were pneumonia, lung cancer, or acute heart failure (see Table 1). Parts of the lumbar spinal cord were fixed in 10% buffered formalin solution, and processed for paraffin sections. The sections were stained with hematoxylin and eosin and Klüver-Barrera and Holzer techniques, and histological assessment was performed. The degree of motor neuron loss and astrogliosis was ranked as mild, moderate or severe according to previously reported.[19,20]

Laser-Captured Microdissection of Spinal Motor Neurons

Sections (10μm) were cut with a standard cryostat, mounted on poly-L-lysin coated slides (Zeiss, Thornwood, NY), and stained with hematoxylin to identify the motor neurons located in the medial and lateral nuclei of the ventral horns of lumber spinal cords. After staining with hematoxylin, the sections were washed in RNase-free water and dried.[21,22] The PALM Robot-Microbeam system (P.A.L.M. Mikrolaser Technology AG, Bernried, Germany) was used for laser capture. The pulsed laser microbeam cut precisely around the targeted motor neurons in the spinal ventral horn (LCM; see Fig 1A–C). The identity of motor neurons was ascertained by reverse transcription polymerase chain reaction (RT-PCR) for choline acetyltransferase (ChAT) as described previously.[15] Each laser-isolated specimen subsequently was ejected from the glass slide with a single or several laser shots and collected directly into the cap of a PCR tube containing denaturing buffer by a process of laser pressure catapulting in the totally noncontact manner previously described.[23] The LCM-isolated cells (approximately 500 pooled cells) were dissolved in denaturing buffer (StrataPrep Total RNA Microprep Kit; Stratagene, San Diego, CA) and stored at −80°C until use.

RNA Extraction of Laser-Captured Microdissection Motor Neuron Samples and Spinal Ventral Horn Homogenates

LCM-isolated cells in denaturing buffer were thawed and centrifuged briefly before the RNA was extracted using a StrataPrep Total RNA Microprep Kit (Stratagene) according to the manufacturer's protocol. RNA was extracted as well from the total homogenates of ventral horn gray matter of spinal cords,[19] which was dissected under a dissecting microscope.

Reverse Transcription and T7 RNA Polymerase Amplification of RNA

Ten microliters of purified RNA obtained as described above was mixed with 1μl of 0.5μg/ml T7-oligodT primer (5′-TCTAGTCGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGT$_{21}$-3′) to initiate first-strand synthesis. The primer and RNA were incubated in 4μl of 5 × first-strand reaction buffer, 0.1M DTT (2μl), 10mM dNTPs (1μl), 1μl of RNasin, and 1μl of Superscript II reverse transcriptase (Invitrogen, Carlsbad, CA) at 42°C for 1 hour, and then 30μl of 5 × second-strand synthesis buffer, 10mM dNTPs (3μl), 4μl of DNA polymerase, 1μl of *Escherichia coli* RNase H, and 1μl of *E. coli* DNA ligase and 91μl of RNase-free H_2O were added, and the mixture was incubated at 16°C for 2 hours and then at 16°C for 10 minutes after the addition of 2μl of T4 DNA polymerase. Next, an Ampliscribe T7 Transcription Kit (Epicentre Technologies, Madison, WI) was used for RNA amplification: 8μl double-stranded cDNA, 2μl of 10 × Ampliscribe T7 buffer, 1.5μl each of 100mM ATP, CTP, GTP, and UTP, 0.1 M DTT (2μl), and 2μl of T7 RNA polymerase were incubated at 42°C for 3 hours.

For second-round amplification, 10μl of amplified RNA (aRNA) from first-round amplification was mixed together with 1μl of 1mg/ml random hexamers (Invitrogen), and then first-stranded cDNA was synthesized, followed by second-stranded cDNA synthesis as described above. The double-stranded cDNA was subjected to second-round T7 in vitro transcription as above and then subsequent third-round aRNA amplification. After third-round amplification, aRNA was treated with DNase (Wako, Kanagawa, Japan) and cleaned up using an RNeasy Kit (Qiagen, Valencia, CA) according to the manufacturer's protocol.

DNA Microarray Analysis

Fluorescent cDNA probes were synthesized from aRNA of laser-captured spinal motor neurons and RNA from ventral spinal tissue homogenates using an Atlas Glass Fluorescent Labeling Kit (Clontech, Palo Alto, CA) according to the manufacturer's protocol. Cy3-labeled cDNA probes were synthesized from ALS samples for spinal motor neurons and homogenates, and Cy5-labeled cDNA probes were synthesized from control samples. BD Atlas Glass Microarray Human 1.0 and 3.8 (Clontech) slides were hybridized with these fluorescent labeled probes overnight at 50°C and then washed four times and dried according to the manufacturer's protocol. Individual Cy3-labeled cDNA probes from ALS RNA samples of spinal motor neurons and homogenates for each patient were coupled with Cy5-labeled cDNA probes from control RNA samples of those tissues, which were prepared by mixing equal amounts of RNA samples amplified from the control patients. The microarrays were scanned in a laser scanner (GenePix 4000; Axon Instruments, Union City, CA), and the resulting signals were quantified and stored using GenePix Pro analysis software (Axon Instruments). The data for each expressed gene obtained from microarray analysis were expressed as the ratios of the values of individual ALS patients or the means of the values of ALS to the values of the control patients. The values of gene expression levels were means-calculated from motor neurons of 5 or 10 inde-

pendent individuals with ALS as well as from spinal ventral horns of 5 individuals with ALS.

Quantitative Real-Time Reverse Transcription Polymerase Chain Reaction

The probe and primers for the real-time PCR were designed using Primer3' (S. Rozen and H. J. Skaletsky, available at http://www-genome.wi.mit.edu/genome_software/other/primer3.html). TaqMan PCR was conducted using an iCycler system (Bio-Rad Laboratories, Hercules, CA) with a QuantiTect Probe PCR Kit (Qiagen) and the cDNA according to the manufacturer's protocol. The reaction conditions were 95°C for 3 minutes and then 50 cycles of 15 seconds at 95°C followed by 60 seconds at 55°C. All experiments were performed in quadruplicate, and several negative controls were included. For an internal standard control, the expression of glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was simultaneously quantified. The primers and probe sequences for the examined genes (acetyl-CoA transporter: D88152; Bak: NM_001188; CRABP1: NM_004378; cyclin C: M74091; dynactin 1: NM_004082; EGR3: NM_004430; ephrin A1: M57730; GAPDH: NM_002046; KIAA0231: D86984; and TrkC: U05012) were described in the legends for Figure 3. The threshold cycles of each gene were determined as the number of PCR cycles at which the increase in reporter fluorescence reached 10 times above the baseline signal. The weight ratio of the target gene to GAPDH gives the standardized expression level.

In Situ Hybridization

Frozen sections (10μm thick) of the spinal cord were prepared and immediately fixed in 4% paraformaldehyde. Then, they were treated with 0.1% diethylpyrocarbonate (DEPC) twice for 15 minutes and prehybridized at 45°C for 1 hour. Digoxigenin-labeled cRNA probes were generated from linearized plasmids for the genes of interest using SP6 or T7 polymerase (Roche Diagnostics, Basel, Switzerland). Gene names, Genebank accession number, probe position (nucleotide number), and probe size were as follows: acetyl-CoA transporter, D88152, nucleotides 397-741, 345bp; Bak, NM_001188, nucleotides 792–2094, 345bp; CRABP1, NM_004378, nucleotides 210–545, 336bp; dynactin 1, NM_004082, nucleotides 2392–2774, 383bp; DR5, NM_004082, nucleotides 682–1070, 389bp; EGR3, NM_004430, nucleotides 1433–1794, 362bp; KIAA0231, D86984, nucleotides 698–1053, 356bp; TrkC, U05012, nucleotides 1412–1721, 310bp. After prehybridization, the sections were hybridized with each digoxigenin-labeled cRNA probe overnight at 45°C. The washed sections were incubated with alkaline phosphatase-conjugated anti–digoxigenin antibody (Roche Diagnostics). The signal was visualized with NBT/BCIP (Roche Diagnostics).

Immunohistochemistry

Frozen sections (10μm thick) of the spinal cord were prepared and immediately fixed in 4% paraformaldehyde. Then, they were blocked with 2% bovine serum albumin (Sigma) in Tris-buffered saline at room temperature for 20 minutes and incubated with anti–cyclin C (1:200 dilution; Santa Cruz Biotechnology, Santa Cruz, CA) antibody overnight at 4°C. Subsequent procedures were performed using ENVISION++KIT/HRP (diaminobenzidine tetrahydrochloride; DAKO, Carpinteria, CA) according to the manufacturer's protocol.

Statistical Analyses

To assess the correlation of intensity values for each labeling sample, we used scatterplots and measured linear relationships. The correlation coefficient, R^2, that was calculated indicates the variability of intensity values between Cy-5– and Cy-3–labeled samples. To perform cluster analyses of hierarchical clustering, self-organizing maps (SOM) and principal component analysis after logarithmic transformation, we used Acuity 3.0 software (Axon Instruments). The data measured by quantitative real-time RT-PCR analysis were analyzed by Student's t tests.

Results

T7 Amplification Preserves Gene Expression Profiles

Because the amounts of laser-microdissected samples were extremely low and did not contain enough mRNA for further analysis, RNA amplification was required. It was critical to achieve sufficient RNA amplification and yet maintain the expression profiles of mRNAs. We performed experiments to determine how the expression profiles of mRNAs were affected by the T7 amplification procedure. RNA samples were extracted from control spinal cords and a part of RNA samples was amplified using T7 amplification. One flourescently labeled probe was synthesized from an individually amplified RNA (aRNA) or nonamplified RNA (nRNA) and was hybridized to microarrays. Independent amplification of RNA yielded quite similar expression patterns. The correlation of signal intensities between independent amplifications for the third aRNA was $R^2 = 0.9157$, $p < 0.0001$, and on the other hand, the correlation of signal intensities in nRNA was $R^2 = 0.9157$, $p < 0.0001$ (Fig 1D, E). Previous reports using similar amplification procedures as ours also have confirmed the reproducibility of T7 amplification for the preservation of RNA expression profiles.[14,15,17] In this study, the third-round amplification was performed for the LCM-isolated motor neurons, but for the spinal ventral horn homogenates a single amplification produced enough RNA for further analysis, and similar expression patterns were found between the first and third amplifications (data not shown).

Gene Expression Database of Spinal Motor Neurons and Ventral Horn Homogenates of Amyotrophic Lateral Sclerosis

aRNA samples from the motor neurons and the ventral horn homogenates from the lumbar spinal cords were subjected to microarray analysis. The differences of the gene expression levels between ALS and control sam-

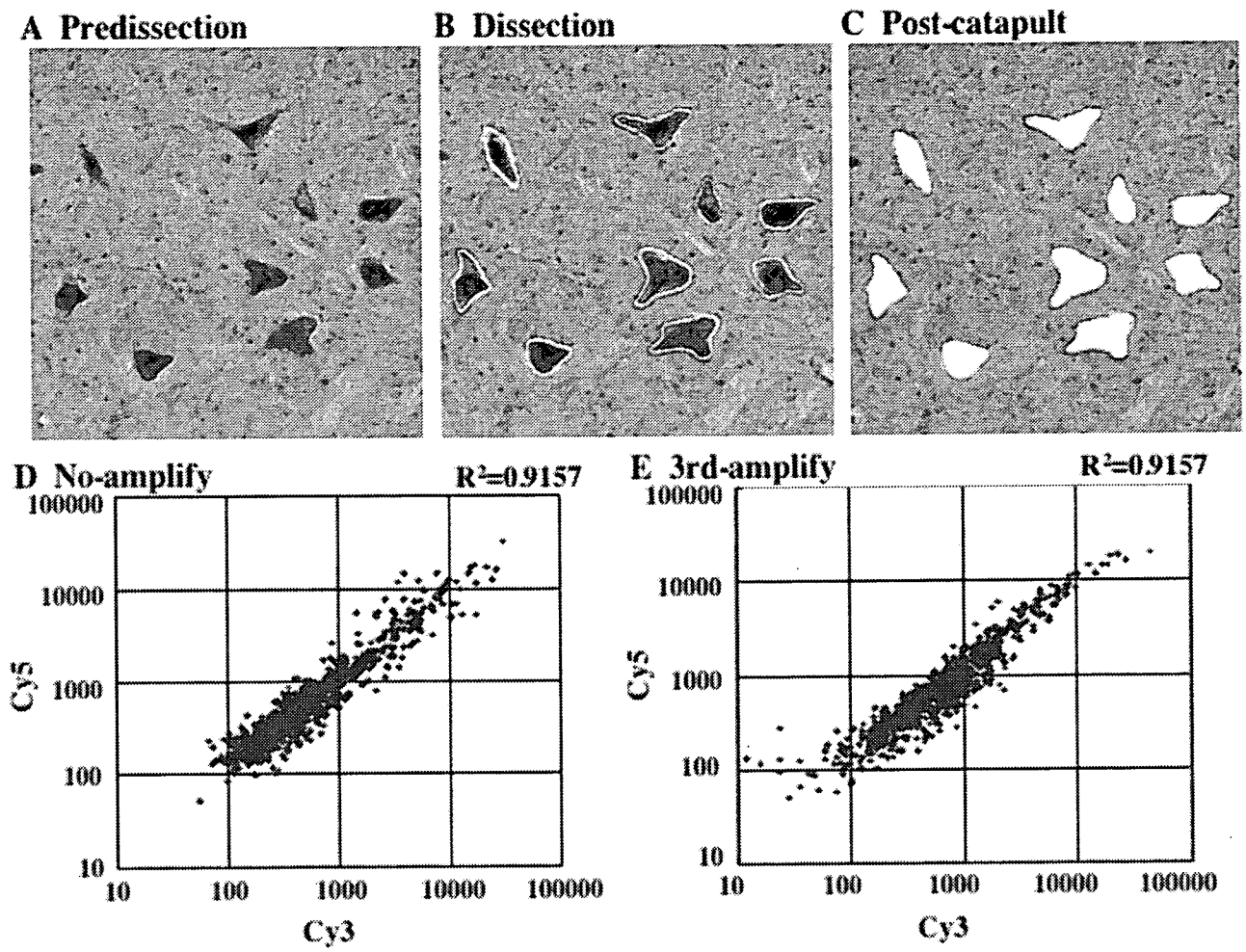

Fig 1. Verification of laser-captured microdissection (LCM) and RNA amplification. Microdissection of motor neurons in spinal ventral horn: sections were stained with hematoxylin (A); margins of motor neurons were dissected by the laser beam (B); and motor neurons were isolated from slides by laser pressure catapulting (C). Scatterplots of nonamplified and amplified RNAs: correlations between independent amplifications of control spinal cord samples are shown using nonamplified (D) and third amplified RNAs (E). These RNAs were split into two samples for labeling of Cy5 and Cy3 and hybridized separately to two microarrays. The very high squared correlations reflect the high reproducibility of the hybridization results with the same values between nonamplified and third amplified RNAs.

ples were expressed as ratios of the values of ALS individuals compared with the mean values of the controls. One percent (52/4,845) of genes examined were significantly upregulated in spinal motor neurons of ALS patients and 3% (144/4,845) were downregulated, assuming that the changes of 3.0-fold increase and 0.3-fold decrease were significant, when the mean levels of gene expression were calculated. In contrast with motor neurons, the total spinal ventral horn homogenates demonstrated 0.7% (37/4,845) and 0.2% (8/4,845) significant upregulation and downregulation of gene expression, respectively.

The genes prominently altered in ALS are listed in Tables 2 to 5 for spinal motor neurons and spinal ventral horn homogenates, respectively. Several upregulated genes listed were overlapping between spinal motor neurons (see Table 2) and ventral horns (see Table 4), suggesting that motor neuron overexpression is reflected to some extent by gene expression in ventral horn homogenates. The other genes upregulated in motor neurons were not present in the list for spinal ventral horns, because these gene expression changes were diluted and masked by changes occurring in other cell types. Because the number of spinal motor neurons was decreased in ALS spinal cords, most genes that were listed as downregulated genes in motor neurons (see Table 3) were not found in spinal ventral horns (see Table 5) except for three genes (CRABP1, EGR3, and postmeiotic segregation increased 2-like 11). When we categorized these altered genes in ALS motor neurons into several functional groups, the genes related to cell receptors and intracellular signaling, transcription,

Table 2. Upregulated Genes in ALS Motor Neurons (Top 30)

GeneBank No.	Gene Name	Fold Change (ALS/control)
NM_003419	Zinc finger protein 10 (KOX 1)	8.86
U91618	Neurotensin/neuromedin N precursor	8.33*
NM_004651	Ubiquitin-specific protease 11	8.13
D86984	KIAA0231	7.31*
A26792	Ciliary neuronotrophic factor (CNTF)	6.76
M77830	Desmoplakin I & II (DSP; DPI & DPII)	6.10
NM_005622	SA (rat hypertension-associated) homolog	5.47
NM_004733	Acetyl-coenzyme A transporter	5.33
NM_000021	Presenilin 1 (Alzheimer disease 3)	4.96
K03020	Phenylalanine-4-hydroxylase (PAH)	4.95*
AF016268	Death receptor 5 (DR5); cytotoxic TRAIL receptor, TNFR10b	4.91*
M74091	G1/S-specific cyclin C (CCNC)	4.82*
NM_000275	Oculocutaneous albinism II	4.78
AF000936	SH3-binding protein 2	4.73*
NM_000384	Apolipoprotein B	4.70
M63099	Interleukin-1 receptor antagonist	4.66*
M57730	Ephrin-A1	4.57*
L19067	NF-κ B transcription factor p65 subunit	4.52*
U66838	Cyclin A1 (CCNA1)	4.51*
NM_005021	Ectonucleotide pyrophosphatase/phosphodiesterase 3	4.48
NM_001550	Interferon-related developmental regulator 1	4.45
L25851	Integrin alpha E precursor (ITGAE)	4.43*
X16416	C-abl1 protooncogene	4.41
U08015	Transcription factor NF-ATc	4.40*
U44378	Mothers against dpp homolog 4 (SMAD4)	4.35*
NM_005067	Seven in absentia (Drosophila) homolog 2	4.22
J04536	Leukosialin precursor; sialophorin	4.19*
X06745	DNA polymerase alpha catalytic subunit	4.15*
U09564	Serine kinase	4.09*
U37139	β 3-endonexin	4.06*

Gene expression levels are expressed as means of fold-change, which is calculated by dividing the signals of each ALS sample by those of control samples, in the 5 or 10 (denoted by asterisk) patients with ALS.
ALS = amyotrophic lateral sclerosis.

metabolism, and cytoskeletal architecture were downregulated. The functional categories of secreted and extracellular communication proteins and cell cycle regulators were characteristically upregulated. A complete list of the differentially expressed genes is available online at http://www.med.nagoya-u.ac.jp/neurology/index.html.

Differential Gene Expression Profiles between Spinal Motor Neurons and Ventral Horn Homogenates of Amyotrophic Lateral Sclerosis

To compare the expression profile of motor neurons with that of spinal ventral horn homogenates, we performed cluster analyses. Because the patterns of gene expression from microarray analysis are impossible to discern by eye, data analysis software (Acuity 3.0 software; Axon Instruments) was used based on the dimensionality of the data: hierarchical clustering for high dimensional gene space and principal component analysis and SOM for low one. Hierarchical clustering clearly discriminated the expression profile of isolated motor neurons from that of ventral horn homogenates, showing two grouped branches of the dendrogram with a correlation coefficient of 0.446 (Fig 2A). Moreover, a principal component analysis confirmed the distinction of gene expression profiles between spinal motor neurons and ventral horns (see Fig 2B). The gene expression profile of motor neurons was clustered into a single cluster by the two clustering algorithms, which was well separated from that of spinal ventral horn gray matter, suggesting a relatively uniform degenerating process in spinal motor neurons in ALS.

Motor Neuron–Specific Gene Expression Profiles Identified by the Self-Organizing Map Analysis

To further analyze the expression pattern specific to spinal motor neurons, a SOM was produced as a nonhierarchical clustering.[24,25] The examined genes were subdivided into 25 clustered categories, and the selected genes are shown in a certain group of the SOM (see Fig 2C, Table 6). The genes contained in the clusters reflect the expression pattern in spinal motor neurons as well as that in spinal ventral horns, and these selected genes are somehow different from those in Tables 2 to 5 because of the different bases of classification. Clustering of the SOM showed motor neu-

Table 3. Downregulated Genes in ALS Motor Neurons (Bottom 30)

GeneBank No.	Gene Name	Fold Change (ALS/control)
NM_004378	Cellular retinoic acid–binding protein 1 (CRABP1)	0.12
NM_004430	Early growth response 3 (EGR3)	0.14
NM_005558	Ladinin 1	0.15
NM_003603	Arg/Abl-interacting protein ArgBP2	0.15
NM_000117	Emerin (Emery-Dreifuss muscular dystrophy)	0.15
NM_004357	CD151 antigen	0.15
X06820	Ras homolog gene family member B (RHOB)	0.15*
NM_003834	Regulator of G-protein signalling 11	0.16
NM_002960	S100 calcium-binding protein A3	0.16
NM_006289	Talin	0.16
NM_000964	Retinoic acid receptor, α	0.17
NM_002391	Midkine	0.17
M96944	Paired box protein PAX-5	0.17*
M74178	Hepatocyte growth factor–like protein	0.17*
NM_003822	Nuclear receptor subfamily 5, group A, member 2	0.17
NM_001188	BCL2-antagonist/killer 1; Bak	0.18
NM_000733	CD3E antigen, epsilon polypeptide (TiT3 complex)	0.18
NM_000408	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	0.18
NM_000156	Guanidinoacetate *N*-methyltransferase	0.18*
M11886	Major histocompatibility complex, class I, C	0.18*
NM_003865	Homeo box (expressed in ES cells) 1	0.18
M36340	ADP-ribosylation factor 1 (ARF1)	0.18*
NM_001725	Bactericidal/permeability-increasing protein	0.18
NM_005334	Host cell factor C1 (VP16-accessory protein)	0.19
NM_004192	Acetylserotonin *O*-methyltransferase–like	0.19
NM_002684	Postmeiotic segregation increased 2–like 11	0.19
M11233	cathepsin D precursor (CTSD)	0.19*
NM_002313	Actin binding LIM protein 1	0.19
NM_002196	Insulinoma-associated 1	0.19
NM_002277	Keratin, hair, acidic, 1	0.19

Gene expression levels are expressed as means of fold-change, which is calculated by dividing the signals of each ALS sample by those of control samples, in the 5 or 10 (denoted by asterisk) patients with ALS.
ALS = amyotrophic lateral sclerosis.

ron–specific upregulated and downregulated gene expression commonly observed in five patients.

Clusters 1 (SOM1) and 6 (SOM6) contains 110 and 169 genes, respectively, that generally are downregulated in spinal motor neurons in all five cases examined, and those are known to be involved in the functional category of cell surface antigens and cell receptors, transcription, and cytoskeleton, whereas clusters 24 (SOM24) and 25 (SOM25) have 191 and 93 genes, respectively, that are predominantly upregulated in spinal motor neurons in all cases and belong to the functional category of cell signaling with extracellular communication, and cell death–associated proteins. The pattern of subcellular localization of their gene products also confirms the characteristics of the functional categories of upregulated and downregulated genes, that is, that plasma membrane and cytoskeletal proteins are more downregulated, and extracellular secreted proteins are more upregulated, in ALS motor neurons. All the genes listed in Table 3 are included in SOM1 and SOM6, whereas SOM24 and SOM25 do not contain all of the genes listed in Table 2. The former group of genes, with downregulation in motor neurons, included BCL2-antagonist/killer 1 (Bak) and TrkC receptor. Regarding genes related to transcription, early growth response 3 (EGR3), cellular retinoic acid–binding protein 1 (CRABP1), retinoic acid receptors, and Musashi 1 were included in SOM1 and SOM6 as downregulated genes. The expression of dynactin and microtubule-associated proteins (MAPs), which belong to the functional category of cytoskeleton and axonal transport, was downregulated in ALS motor neurons. On the other hand, KIAA0231 and acetylcoenzyme A transporter were classified into the upregulated genes in motor neurons of ALS. Regarding genes related to cell death, the expression of cyclins A1 and C, death receptor 5 (DR5), and interleukin-1 receptor antagonist was upregulated together with that of NF-κB, tumor necrosis factor (TNF) receptor–associated factor 6 (TRAF6), and caspase-1, -3, and -9 in SOM24 and SOM25. For genes in the category of trophic factor cell signaling with extracellular communication, CNTF, HGF, and glial cell line–derived neurotrophic factor (GDNF) were upregulated in ALS motor neurons, whereas midkine was downregulated. The expression of vascular endothelial growth factor as

Table 4. Upregulated Genes in Spinal Ventral Horns of ALS (Top 30)

GeneBank	Gene Name	Fold Change (ALS/control)
NM_000508	Fibrinogen, A α polypeptide	8.23
D86984	KIAA0231	6.09
NM_001801	Cysteine dioxygenase, type 1	5.81
X02544	α-1-Acid glycoprotein 1 precursor	5.59
NM_001973	ELK4, ETS-domain protein (SRF accessory protein 1)	5.12
NM_000021	Presenilin 1 (Alzheimer disease 3)	5.00
NM_002097	General transcription factor IIIA	4.96
U08015	Transcription factor NF-ATc	4.96
M57730	Ephrin-A1	4.88
U91618	Neurotensin/neuromedin N precursor	4.79
AF000936	SH3-binding protein 2	4.50
NM_002949	Mitochondrial ribosomal protein L12	4.11
NM_002386	Melanocortin 1 receptor	4.03
NM_001991	Enhancer of zeste (Drosophila) homolog 1	3.93
NM_000947	Primase, polypeptide 2A (58kDa)	3.92
NM_000239	Lysozyme (renal amyloidosis)	3.88
NM_001550	Interferon-related developmental regulator 1	3.67
NM_004602	Staufen (Drosophila, RNA-binding protein)	3.66
NM_000063	Complement component 2	3.58
NM_004651	Ubiquitin-specific protease 11	3.54
NM_000397	Cytochrome b-245, β polypeptide	3.51
NM_002056	Glutamine-fructose-6-phosphate transaminase 1	3.41
L25851	Integrin α E precursor (ITGAE)	3.36
NM_004616	Transmembrane 4 superfamily member 3	3.21
NM_003720	Down syndrome critical region gene 2	3.18
J04536	leukosialin precursor; sialophorin	3.15
X06745	DNA polymerase alpha catalytic subunit	3.15
K03020	Phenylalanine-4-hydroxylase (PAH)	3.14
NM_001329	C-terminal binding protein 2	3.14
NM_000276	Oculocerebrorenal syndrome of Lowe	3.13

Gene expression levels are expressed as means of fold-change, which is calculated by dividing the signals of each ALS sample by those of control samples, in the five patients with ALS.
ALS = amyotrophic lateral sclerosis.

well as NT-3 was unchanged. Furthermore, the genes whose expression was altered significantly in spinal ventral horn homogenates as shown in Tables 4 and 5 showed similar alterations to some extent in the remaining motor neurons. However, the upregulated genes, such as integrin αE and sialophorin for cell adhesion, which were demonstrated to be spinal ventral horn–derived (see Table 4) as well as spinal motor neuron–derived (Table 2) genes, were not sorted out into SOM24 and SOM25, indicating that their upregulation occurred predominantly in glial cells.

Data Confirmation with Quantitative Real-Time Reverse Transcription Polymerase Chain Reaction, In Situ Hybridization, and Immunohistochemistry

To assure the validity of the gene expression levels detected by microarray analysis, we performed quantitative real-time RT-PCR analysis on some genes of interest using a TaqMan PCR system. Because LCM-isolated motor neurons did not contain enough RNA to perform real-time RT-PCR analysis, only selected genes were assessed in motor neurons, and for other genes the spinal ventral horn homogenates were used as the template for quantitative RT-PCR. When the extent of increase or decrease of gene expression levels was expressed as the ratio of the genes of interest to GAPDH, acetyl-CoA transporter and KIAA0231 were significantly increased 3.1-fold ($p < 0.001$) and 3.3-fold ($p < 0.01$) in spinal motor neurons of ALS, respectively (Fig 3). EGR3 expression decreased to 0.27-fold ($p < 0.01$) in ALS motor neurons. These mRNA alterations were also detected at comparable levels when using spinal ventral horn homogenates of ALS (acetyl-CoA transporter, 1.8-fold increase [$p < 0.005$]; KIAA0231, 2.3-fold increase [$p < 0.05$]; and EGR3, 0.41-fold decrease [$p < 0.01$]). In addition, the gene expression of Bak and TrkC was downregulated 0.53-fold ($p < 0.01$) and 0.40-fold ($p < 0.05$) in ALS, respectively. Moreover, increases of ephrin A1 and cyclin C expression were observed to the extents of 2.5-fold ($p < 0.05$) and 4.9-fold ($p < 0.01$), whereas dynactin 1 mRNA was downregulated 0.44-fold ($p < 0.01$), and CRABP1 mRNA was also downregulated to 0.59-fold ($p < 0.01$) in ALS.

To further verify the localization and extent of expression of genes of interest, we performed in situ hy-

Table 5. Downregulated Genes in Spinal Ventral Horns of ALS (Bottom 30)

GeneBank	Gene Name	Fold Change (ALS/control)
NM_000843	Glutamate receptor, metabotropic 6	0.22
NM_000730	cholecystokinin A receptor	0.24
NM_003134	Signal recognition particle 14kDa	0.26
NM_003163	Syntaxin 1B	0.27
NM_006476	ATP synthase, H+ transporting, mitochondrial F1F0, subunit g	0.27
NM_001610	Acid phosphatase 2, lysosomal	0.28
NM_003108	SRY (sex determining region Y)-box 11	0.29
NM_001446	Fatty acid binding protein 7, brain	0.30
NM_004583	RAB5C, member RAS oncogene family	0.31
NM_001125	ADP-ribosylarginine hydrolase	0.31
NM_003320	Tubby (mouse) homolog	0.31
NM_001731	B-cell translocation gene 1, antiproliferative	0.31
NM_000999	Ribosomal protein L38	0.32
NM_004128	General transcription factor IIF, polypeptide 2 (30kDa subunit)	0.32
NM_001765	CD1C antigen, c polypeptide	0.32
NM_004430	Early growth response 3 (EGR3)	0.33
K00558	Tubulin, α, ubiquitous	0.33
NM_006732	FBJ murine osteosarcoma viral oncogene homolog B	0.33
NM_002040	GA-binding protein transcription factor, α subunit (60kDa)	0.34
NM_006161	Neurogenin 1	0.35
NM_002684	Postmeiotic segregation increased 2–like 11	0.35
NM_000801	FK506-binding protein 1A (12kDa)	0.35
NM_001051	Somatostatin receptor 3	0.35
NM_005017	Phosphate cytidylyltransferase 1, choline, alpha isoform	0.36
NM_004927	Chromosome 11 open reading frame 4	0.36
NM_000046	Arylsulfatase B	0.37
NM_004378	Cellular retinoic acid–binding protein 1 (CRABP1)	0.37
NM_001998	Fibulin 2	0.38
NM_001839	Calponin 3, acidic	0.38
NM_001183	ATPase, H+ transporting, lysosomal, subunit 1	0.39

Gene expression levels are expressed as means of fold-change, which is calculated by dividing the signals of each ALS sample by those of control samples, in the five patients with ALS.
ALS = amyotrophic lateral sclerosis.

bridization on selected genes. The mRNAs for acetyl-CoA transporter, KIAA0231, and EGR3 were localized in the remaining motor neurons (Fig 4). Spinal motor neurons overexpressed acetyl-CoA transporter and KIAA0231 in ALS, whereas EGR3 was underexpressed. Moreover, TrkC, CRABP1, Bak, and dynactin 1 gene expression was found in motor neurons, and those signals were reduced in ALS. DR5 signals were increased in motor neurons in ALS. Cyclin C signals with punctate immunoreactivity were increased in the cytoplasm as well as in nuclei in ALS motor neurons. The nuclear staining of motor neurons for cyclin C was more prominent in ALS compared with controls.

Discussion

Although reports about differential gene expression using the postmortem spinal cords, including those of patients with ALS, have been published,[26,27] the precise gene expression profiles of the degenerating motor neurons themselves have remained to be elucidated. Laser-captured dissection of motor neurons and subsequent microarray analysis are the most appropriate approaches to understanding the motor neuron–specific gene expression profile related to the motor neuron degeneration process in sporadic ALS, because these approaches eliminate bias of motor neuron loss, reactive astroglial proliferation, and other cellular reactions. Indeed, serine kinase has been reported to be underexpressed in ALS spinal cord gray matter,[27] but this study showed it was overexpressed in isolated motor neurons, suggesting that the reported underexpression in whole gray matter was influenced by the decreased motor neuron population. In contrast, cathepsin D expression was downregulated in the ALS motor neurons in this study, whereas it was increased in spinal cord gray matter in a previous report,[27] indicating its upregulation in glial cells. In addition, clustering analyses showed that the gene expression profile in the spinal motor neurons was substantially different from that in the whole homogenates of spinal ventral horn gray matter.

The overall microarray analysis using spinal ventral horn homogenates showed gene expression changes in less than 1% of genes examined with more genes showing increased than decreased expression. On the other hand, the motor neuron–specific microarray analysis

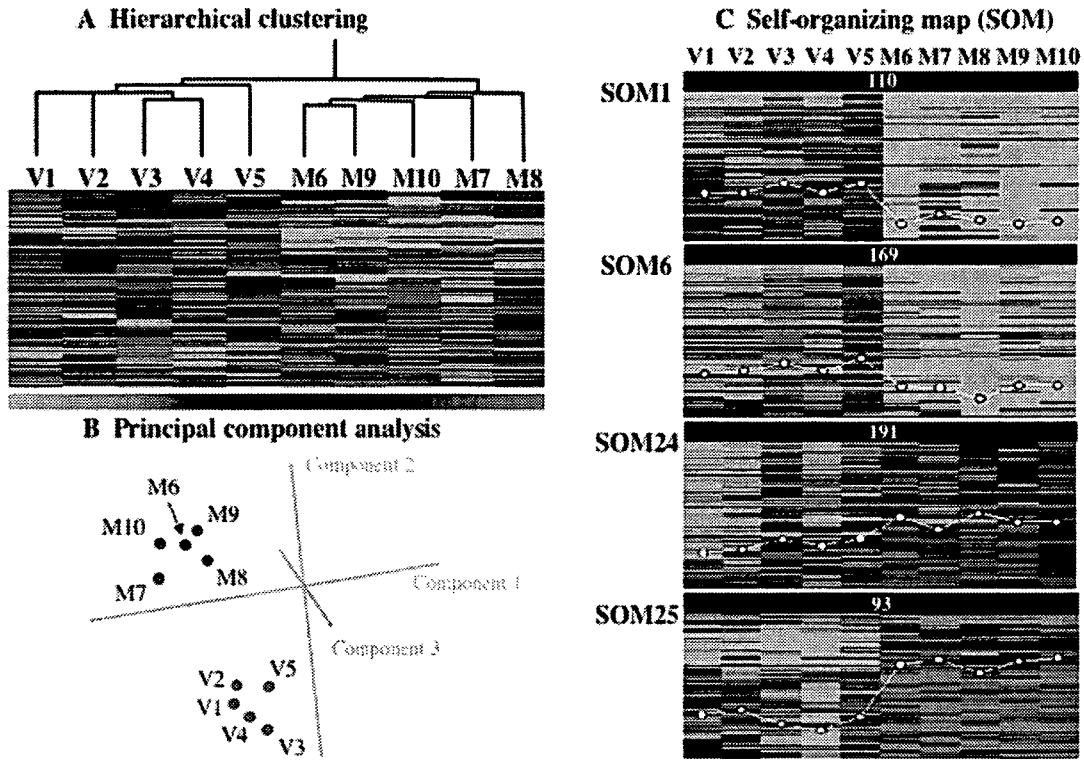

Fig 2. Clustering of gene expression in spinal motor neurons and spinal ventral horns. (A) Hierarchical clustering of gene expression in spinal motor neurons and ventral horns. The dendrogram was produced by hierarchical clustering of relative expression levels of 4,845 genes (rows) in five spinal homogenate and five motor neuron samples (columns) in making a total of 48,450 data points. Visual representation is shown with green representing downregulated (<0.44), black representing intermediate, and red representing upregulated (>2.28). The hierarchical clustering successfully detects two large clusters of amyotrophic lateral sclerosis (ALS), discriminating between spinal homogenates of ventral horns (samples V1 [ALS1], V2 [ALS10], V3 [ALS3], V4 [ALS14], and V5 [ALS13]) and motor neurons (samples M6 [ALS1], M7 [ALS10], M8 [ALS14], M9 [ALS11], and M10 [ALS7]), with a correlation coefficient of 0.446 at the branching point. (B) Principal component analysis of spinal motor neurons and ventral horns. Principal component analysis by six components for the 4,845 genes shows two main clusters consisting of spinal motor neurons (M6–10) and homogenates (V1–5). The number of patients corresponds to those in the dendrogram. (C) Self-organizing map (SOM) analysis of spinal motor neurons and ventral horns. The 4,845 genes are grouped into 25 clusters, the optimal size of which is calculated from gap statistics analysis. In SOM1 and SOM6, most genes are downregulated and in SOM24 and SOM25 the majority of genes are upregulated commonly in isolated motor neurons of five cases (M6–10). The numbers of genes are given at the top, and selected genes are listed for clusters 1, 6, 24, and 25 in Table 6.

showed that the proportion of significantly downregulated genes was 3% of the examined genes, whereas that of upregulated genes was one third of the downregulated genes. Moreover, the genes found to be downregulated specifically in motor neurons were not found to be downregulated in ventral horns, except for three genes with high expression levels. These results strongly support the notion that microarray analysis of laser-captured isolated spinal motor neurons has an advantage especially for the detection of motor neuron–specific downregulated transcripts.

In the differentially expressed genes, cell death–associated genes and genes related to cell signaling were characteristically upregulated in ALS motor neurons, whereas the genes categorized into cytoskeleton and transcription were downregulated. In the prominently altered genes of interest related to the cell death pathway, acetyl-coenzyme A transporter, which has been cloned and shown to encode a protein with multitransmembranous spanning domains,[28] was overexpressed in ALS motor neurons. Acetyl-CoA transporter functions as a cofactor for acetylation of gangliosides as well as vesicular transport of acetylcholine, which is synthesized from acetyl-CoA and choline. Acetylation has been documented to suppress proapoptotic activity of GD3 ganglioside, which increased in ALS neural tissues, as previously shown.[29,30] These results suggest that enhanced expression of acetyl-CoA transporter may be related to the antiapoptotic mechanism for cholinergic motor neuron degeneration in ALS.

Table 6. Selected Genes Characterized by SOM (select each 15)

GeneBank	Gene Name	Fold Change (ALS/control)
SOM1/6: genes downregulated in ALS motor neurons		
NM_002695	Polymerase (RNA) II (DNA directed) polypeptide E (25kD)	0.20
M24857	Retinoic acid receptor gamma 1 (RAR-γ 1)	0.20
NM_002375	Microtubule-associated protein 4	0.20
NM_001651	Aquaporin 5	0.21
NM_003178	Synapsin II	0.22
NM_004624	Vasoactive intestinal peptide receptor 1	0.23
NM_001740	Calbindin 2, (29kD, calretinin)	0.24
M73812	G1/S-specific cyclin E (CCNE)	0.25
NM_003206	Transcription factor 21	0.25
NM_004082	Dynactin 1 (p150)	0.30
U05012	TRK-C; NT-3 growth factor receptor precursor	0.31
NM_003632	Contactin associated protein 1	0.32
NM_005910	Microtubule-associated protein tau	0.49
NM_002373	Microtubule-associated protein 1A	0.51
NM_002442	Musashi (Drosophila) homolog 1	0.52
SOM24/25: genes upregulated in ALS motor neurons		
M60718	Hepatocyte growth factor (HGF)	3.42
L20814	Glutamate receptor subunit 2 (GLUR-2)	3.34
K02268	β-neoendorphin-dynorphin precursor	3.13
L19063	Glial cell line–derived neurotropic factor (GDNF)	3.08
NM_005543	Insulin-like 3	2.79
J04088	DNA topoisomerase II alpha (TOP2A)	2.58
M22489	Bone morphogenetic protein 2A (BMP2A)	2.57
U51004	Hint protein; protein kinase C inhibitor	2.26
M87507	Caspase 1, interleukin-1 β convertase precursor	2.21
NM_006196	Poly(rC)-binding protein 1	2.16
L29511	Growth factor receptor–bound protein 2	2.04
U78798	TRAF6	1.98
NM_001229	Caspase 9, apoptosis-related cysteine protease	1.89
U84388	Caspase and rip adaptor with death domain (CRADD)	1.83
U13737	Caspase-3	1.77

Gene expression levels are expressed as means of fold-change, which is calculated by dividing the signals of each ALS sample by those of control samples, in the five patients with ALS. Genes listed in Tables 2 and 3 are excluded.
SOM = self-organizing map.

KIAA0231 was one of the mostly overexpressed genes in ALS motor neurons, but the function of this gene product is not known.

In the greatly downregulated genes of interest related to transcription, EGR3, whose expression was remarkably reduced in motor neurons of ALS, is a zinc-finger immediate-early transcription factor that is important for neurotrophin-3 (NT-3) regulation. It is known that EGR3 knockout mice develop gait ataxia, scoliosis, resting tremors, and ptosis due to the degeneration of muscle spindles, through disruption of NT-3 regulation.[31] In ALS motor neurons, TrkC receptor for NT-3 was underexpressed, whereas NT-3 expression was not changed. The finding about TrkC-null mutant and NT-3–null mutant mice show that NT-3-TrkC signaling is required to maintain Ia afferent central synapses of DRG neurons.[32] The marked downregulation of EGR3 in spinal motor neurons may disrupt sensory-motor connections by decreasing NT-3-TrkC signaling, resulting in motor neuron degeneration.

For neurotrophic support for ALS motor neurons, this study showed the overexpression of CNTF, GDNF, and HGF involved in the functional category of cell signaling, suggesting that these neurotrophic factors would be secondarily and compensatorily upregulated after motor neuron degeneration. Indeed, GDNF expression has been reported to increase in the spinal cords and decrease in the muscles of sporadic ALS patients.[33] In contrast with these neurotrophic factors, midkine was one of the significantly downregulated neurotrophic factors. Because midkine plays important roles in promotion of neuronal survival as well as modulation of neuromuscular junctions,[34] its underexpression may be related to motor neuron degeneration. In addition, the gene expression of vascular endothelial growth factor, which has been identified as a critical factor for motor neuron degeneration,[35–37] did not change significantly in gene expression in this study. SOD1 gene expression was not altered in spinal motor neurons and ventral horns. Moreover, the gene expres-

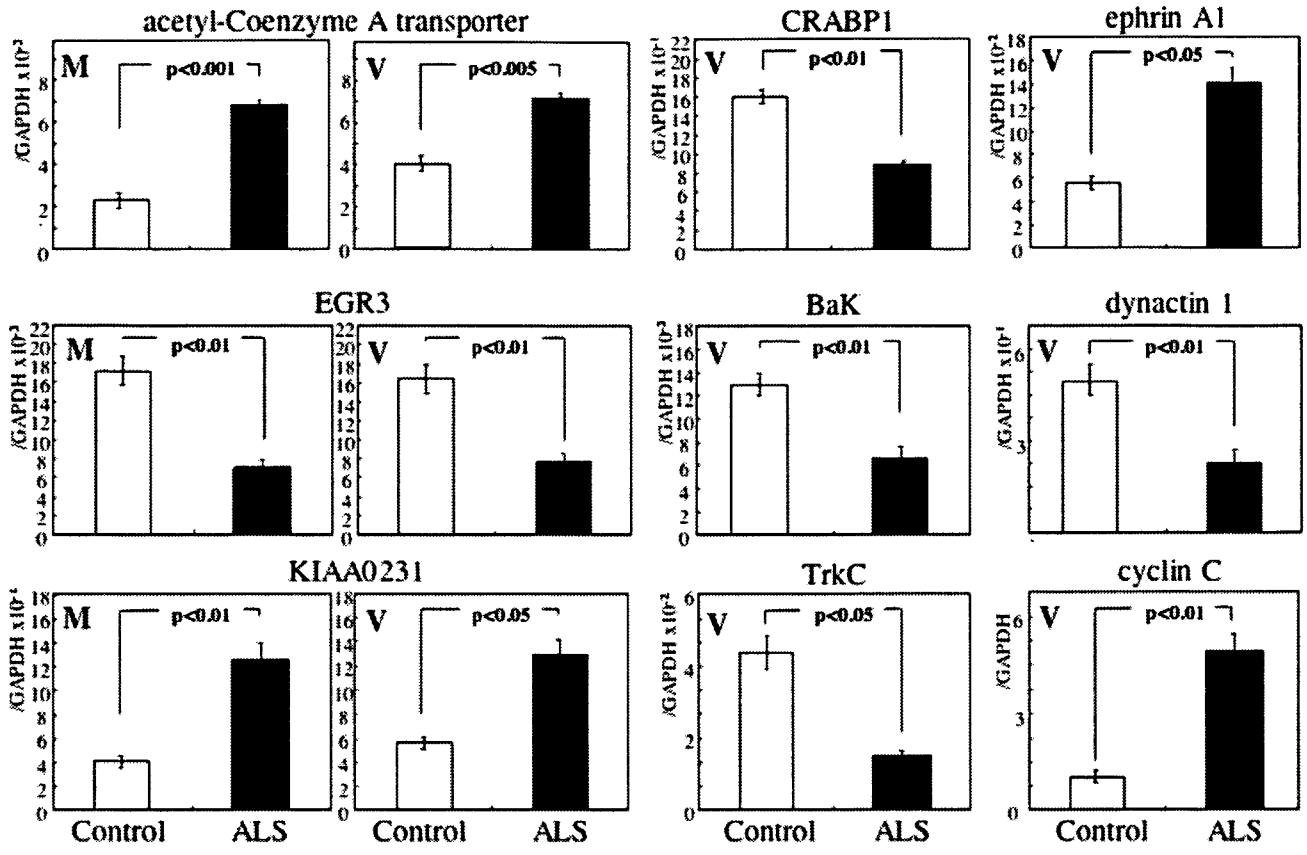

Fig 3. Quantitative real-time reverse transcription polymerase chain reaction verification of the selected genes. Expression levels of acetyl-coenzyme A transporter, EGR3, KIAA0231, CRABP1, Bak, TrkC, ephrin A1, cyclin C, dynactin 1, and GAPDH were measured using spinal motor neurons (M) and ventral horns (V), and those of the target genes were normalized against the GAPDH level. The relative expression levels are expressed as mean ± standard error for 13 amyotrophic lateral sclerosis (ALS) cases and 11 controls. Gene names (Genebank accession number), primers and probe sequences (forward primer, reverse primer, and TaqMan probe; 5' to 3' sequence) were as follows: [acetyl-CoA transporter: D88152] (GGGTTACTTTTTGGGCAATG, AACGATTCCTCTGGGTTGAG, FAM-TTGGCCCTTGAATCTGCCGA-TAMRA); [Bak: NM_001188] (CTGGAAGATCAGCACCCTAAG, CCCCTCTCCTAGTAGGTCCTG, FAM-TGCTCCCATTCCTCCCTCCG-TAMRA); [CRABP1: NM_004378] (TGCAGGAGTTTAGCCACTTG, CTCACGGGTCCAGTAGGTTT, FAM- TGAGAACAAGATCCACTGCACCCA-TAMRA); [cyclin C: M74091] (TGAGCAGTGGAAGAATTTCG, ACCCTGCTCTCCTTCACTGT, FAM- TGCCAAAACCAAAACCACCTCCA-TAMRA); [dynactin 1: NM_004082] (ATGTGAATCGGGAACTGACA, GGGCCTTAGTCTCAGCAAAC, FAM- TGGAGAGGCAACAGCAGCCAC-TAMRA); [EGR3: NM_004430] (CTTCCCCATGATTCCTGACT, TTGAATGCCTTGATGGTCTC, FAM-TTCCAGGGCATGGACCCCAT-TAMRA); [ephrin A1: M57730] (GGCAAGGAGTTCAAAGAAGG, TCACCTTCAACCTCAAGCAG, FAM- CCATCCACCAGCATGAAGACCG-TAMRA); [GAPDH: NM_002046] (TCAAGAAGGTGGTGAAGCAG, GGTGTCGCTGTTGAAGTCAG, FAM-CCTCAAGGGCATCCTGGGCT-TAMRA); [KIAA0231: D86984] (CAACGGTCTTCCAGACAATG, GAGGTTGACCAGCTGTGAGA, FAM-TCCCAGAGGTGAAGCTGCCCTCTAMRA); and [TrkC: U05012] (TGAGAACCCCCAGTACTTCC, TCAGCACGATGTCTCTCCTC, FAM-CTGCCACAAGCCGGACACGT-TAMRA).

sion level of GluR2 was upregulated, as shown by its classification in SOM25, but the expression of its editing enzyme (adenosine deaminase, RNA-specific, 2; ADAR2) was not altered in this study, although the editing efficiency of GluR2 mRNA has been demonstrated to be low in spinal motor neurons of ALS.[38]

Genes subject to transcriptional regulation constitute a crucial part of the whole human genome as demonstrated by human genome projects.[39] In addition to the gene expression of EGR3, the gene expression of retinoic acid receptor α and γ together with cellular retinoic acid–binding protein 1 (CRABP1), and Musashi 1, all of which are known to be inducers of neuronal differentiation,[40,41] was downregulated in spinal motor neurons of ALS. The dysregulation of retinoid receptor and retinol binding protein has been reported in the postmortem spinal cords of ALS and SOD1 mutant mice.[17,26] These interesting results imply the potential involvement of the differentiation signals in maintaining motor neuron integrity, which

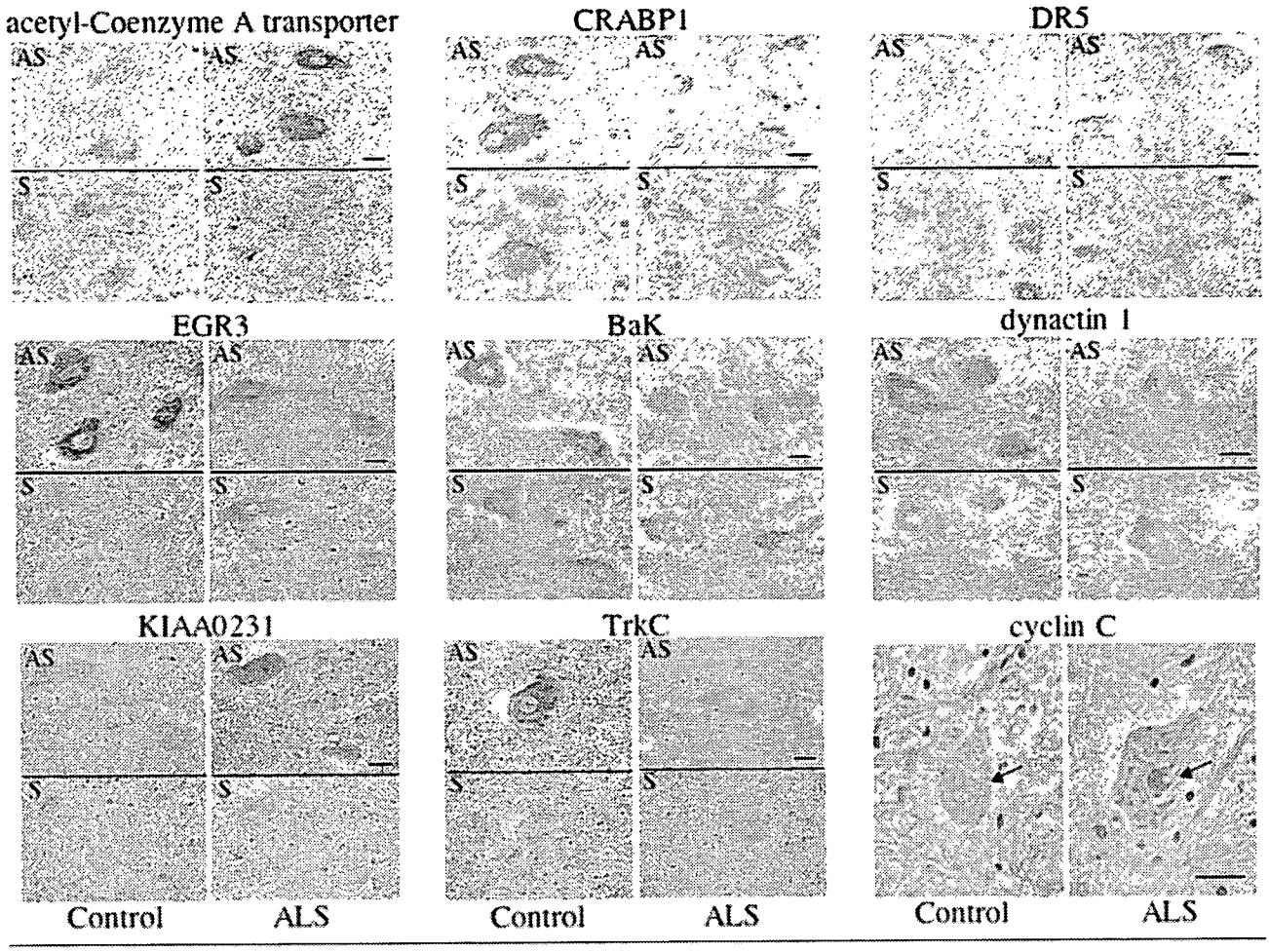

Fig 4. In situ hybridization and immunohistochemistry of the selected genes. Representative in situ hybridization is shown for acetyl-COENZYMEA transporter, EGR3, KIAA0231, CRABP1, Bak, TrkC, DR5, and dynactin 1. The antisense probe (AS) detects positive signals for the expression of each gene in spinal motor neurons for ALS and/or controls, but the sense probe (S) does not. Lipofuscin granules are seen as yellowish granules. Immunohistochemistry was preformed for cyclin C, and nuclear staining was prominent in ALS motor neurons. Arrows denote the nuclei. Bars = 25μm.

might be impaired in the neurodegenerative process of ALS. Among the genes related to transcriptional regulation, the number of significantly downregulated genes was twofold greater than that of the upregulated ones in ALS motor neurons. These downregulated transcription-related genes were not restricted to genes regulating neuronal differentiation as neuron-specific cellular properties, but also included genes such as RNA polymerase and transcription factors, which regulate general cellular functions. These observations suggest that downregulation of transcriptional activity may be the reflection of motor neuron dysfunction because of a wide range of impairments of cellular maintenance systems.

Interestingly, the expression of dynactin 1, which recently has been identified as a causative gene for human motor neuron disease,[42] was reduced in ALS motor neurons. Some other motor proteins including the kinesin family responsible for antegrade axonal transport and dyneins for retrograde axonal transport were not changed significantly, but the expression levels of MAPs 1A, 4, and tau were decreased, shown by their classification in SOM1 and SOM6. The impairment of axonal transport is thought to be an early event of motor neuron degeneration, and especially the protein levels of MAPs 1A and tau have been reported to decrease early before the onset of symptoms in mutant SOD1 transgenic mice.[43–45] The upregulation of ubiquitin-specific protease 11 (USP11), listed in Tables 2 and 3, also may be related to microtubule abnormality because the RanGTP-associated protein RanBPM, which is required for correct nucleation of microtubules, is the enzymatic substrate for USP11.[46] The present results imply that retrograde axonal transport, especially that associated with dynactin, might be affected even at the terminal stage of ALS and be crucial for motor neurons, although cytoskeletal proteins are the major functional group in the downregulated genes.

As for the death signals and inflammatory factors, we previously have reported that these genes were significantly upregulated in the spinal cord of mutant SOD1 transgenic mice,[15,17] suggesting that these inflammatory and apoptotic death signals play a crucial role in concert with motor neuron degeneration and inflammatory cellular reactions, including microglial activation.[7,47] However, in sporadic ALS spinal cords, the expression profiles of inflammation- and death signal–related genes are somewhat different from those in the Tg mouse model. Death receptor 5 (TNF receptor 10b, TNFR10b), TNF receptor–associated factor 6 (TRAF 6), interleukin-1 receptor antagonist, and ephrin A1 were overexpressed in ALS motor neurons, whereas the expression levels of the respective ligands or inducers, TNF-α, TNF superfamily member 10 (TRAIL) and IL-1β, were not markedly changed in either motor neurons or ventral horn homogenates. Because TNF-α was prominently upregulated in the Tg mouse spinal cords,[17] its almost unchanged expression level in sporadic ALS was a surprising observation. Many other inflammation-related genes were also not significantly upregulated in human ALS spinal cords, in contrast with the findings in animal models. Far less invasion and activation of microglia, a major source of TNF-α, IL-1β, and many other inflammatory factors, were seen in human ALS spinal cords at the terminal autopsy stage as compared with those of Tg mice,[48] which could explain these differences.

Genes related to apoptotic pathways, caspase-1, -3, -9, caspase, and RIP adaptor with death domain (CRADD), were upregulated in ALS motor neurons in SOM analysis (SOM24 and SOM25), and an antiapoptotic factor, NF-κB, was markedly upregulated. Although Bax, a proapoptotic Bcl-2 family member, has been reported to increase in ALS motor neurons,[49,50] and another member, Bak, was underexpressed in this study, the expression of Bcl-2 and Bcl-xL, antiapoptotic Bcl-2 family members was not significantly altered in motor neurons, possibly suggesting that Bcl-2 family members are not primarily involved in motor neuron degeneration in sporadic ALS. Cyclin A1 and C were upregulated (SOM25) and cyclin E was downregulated (SOM1) in ALS motor neurons. These cell cycle regulators are specific to G1/S phase transition, and upregulation of these cyclins enhances arrest in G1/S phase, preventing entry into S phase. Our finding on cyclin expression support the recently reported view that G1/S phase is aberrantly activated in ALS motor neurons, eventually inducing motor neuron death.[51] The subcellular localization of cyclin C in the nucleus may trigger cell death signaling mechanisms. These factors related to the cell death signaling pathway, TNFR, TRAF6, CRADD, caspases, cyclins, Bak, and NF-κB may be involved in the motor neuron degeneration process in sporadic ALS, although we cannot simply state that an apoptotic process is present in ALS motor neurons, as has been suggested by many histological analyses.[6] Becausse neuronal cell degeneration and the eventual neuronal cell death process are the results of interactions of complex pathways involving many factors and signaling molecules, we need to further elucidate the pathophysiological significance of these factors with altered expression levels in ALS motor neurons.

Microarray analysis on the laser-captured motor neurons provided us with significant information about motor neuron degeneration and dysfunction in sporadic ALS patients. Such information cannot be obtained by whole spinal cord tissue microarray assay,[52] as discussed above. Although this study was performed on postmortem patients' tissues, the remaining individual motor neurons would express ongoing or even early molecular events in the neurodegeneration process, because motor neurons in the remaining motor neuron population randomly enter into the degeneration process among up to the terminal stage in ALS.[53] We need to study larger numbers of ALS patients, and to understand the pathophysiological roles of candidate genes identified by the combined methodology of DNA microarray analysis and LCM, compared with other neurodegeneration processes. This methodology provides crucial clues about candidate genes whose related products might hamper the disease process of ALS.

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