

Table 2 Nerve conduction studies and F-wave examinations

	SBMA		Normal		P
	(Mean ± SD)	n	(Mean ± SD)	n	
Median nerve					
MCV (m/s)	54.3 ± 6.5	106	57.9 ± 3.6	79	<0.001
Distal latency (m/s)	4.3 ± 1.0	106	3.4 ± 0.4	79	<0.001
CMAP (mV)	5.1 ± 2.9	106	10.8 ± 3.3	79	<0.001
SCV (m/s)	52.3 ± 6.1	103	57.4 ± 4.4	85	<0.001
SNAP (µV)	7.0 ± 5.2	103	20.0 ± 7.9	85	<0.001
Not evoked	Three cases (2.8%)		None		
F-wave minimum latency (ms)	28.2 ± 3.0	76	22.3 ± 1.9	46	<0.001
FWCV maximum (m/s)	58.7 ± 10.5	74	66.4 ± 8.6	41	<0.001
F-wave occurrence (%)	24.5 ± 22.5	106	67.6 ± 20.3	47	<0.001
Absent	30 cases (28.3%)		None		
Ulnar nerve					
MCV (m/s)	55.9 ± 5.2	106	58.2 ± 4.7	71	0.003
Distal latency (ms)	3.2 ± 0.6	106	2.7 ± 0.3	71	<0.001
CMAP (mV)	5.1 ± 2.4	106	8.4 ± 2.4	71	<0.001
SCV (m/s)	48.1 ± 7.5	102	55.0 ± 3.8	74	<0.001
SNAP (µV)	5.6 ± 4.6	102	18.3 ± 7.4	74	<0.001
Not evoked	Four cases (3.8%)		None		
Tibial nerve					
MCV (m/s)	44.5 ± 3.8	106	47.2 ± 3.7	56	<0.001
Distal latency (ms)	5.0 ± 1.0	106	4.5 ± 0.8	56	0.003
CMAP (mV)	7.8 ± 3.7	106	10.3 ± 3.4	56	<0.001
F-wave minimum latency (ms)	48.3 ± 4.1	106	41.4 ± 3.0	31	<0.001
FWCV maximum (ms)	43.9 ± 5.6	105	47.4 ± 3.3	28	<0.001
F-wave occurrence (%)	94.3 ± 11.6	106	96.3 ± 12.5	31	NS
Absent	None		None		
Sural nerve					
SCV (m/s)	44.1 ± 5.7	94	50.8 ± 5.1	68	<0.001
SNAP (µV)	5.1 ± 3.5	94	10.8 ± 4.6	68	<0.001
Not evoked	12 cases (11.3%)		None		

MCV = motor nerve conduction velocity; CMAP = compound muscle action potential; SCV = sensory nerve conduction velocity; SNAP = sensory nerve action potential; FWCV = F-wave conduction velocity; NS = not significant.

we compared the phenotypes based on present symptoms and the electrophysiological phenotypes between patients with a CAG repeat size <47 and those with 47 or more CAGs, according to the previous report on clinical features of SBMA (Atsuta *et al.*, 2006) (Table 4). The age at onset and the age at examination were higher in patients with a shorter CAG repeat than in those with a longer repeat ($P < 0.001$). Disease duration and functional scale, including the Limb Norris score, Norris Bulbar score and ALSFRS-R,

Table 3 Frequency of patients with abnormal values in nerve conduction studies and F-wave examinations

	Number of patients with abnormal values ^a	n	Frequency (%)
Median nerve			
MCV	20	106	18.9
CMAP	43	106	40.6
SCV	23	106	21.7
SNAP	45	106	42.5
FWCV maximum	38	104	36.5
F-wave occurrence	91	106	85.8
Ulnar nerve			
MCV	5	106	4.7
CMAP	24	106	22.6
SCV	40	106	37.7
SNAP	49	106	46.2
Tibial nerve			
MCV	6	106	5.7
CMAP	8	106	7.5
FWCV maximum	17	105	16.2
F-wave occurrence	7	106	6.6
Sural nerve			
SCV	36	106	34.0
SNAP	26	106	24.5

MCV = motor nerve conduction velocity; CMAP = compound muscle action potential; SCV = sensory nerve conduction velocity; SNAP = sensory nerve action potential; FWCV = F-wave conduction velocity.

^aWe defined the abnormal values as those values that were either less than the mean – 2 SD of normal controls on the examined nerves or not evoked.

were similar between these groups. The CMAP values in the median, ulnar and tibial nerves were not significantly different, but showed a tendency to be decreased in the patients with a longer CAG repeat in all three nerves (Table 4). SNAPs in the median, ulnar and sural nerves were all significantly decreased in the patients with a shorter CAG repeat (Table 4). These observations suggest that a shorter CAG repeat is linked to a more significant SNAP decrease, while a longer CAG repeat is linked to a more profound CMAP decrease.

Furthermore, considering the possibility that action potentials are influenced by the age at examination, we compared the CMAPs and SNAPs in the patient subsets with a longer CAG repeat and those with a shorter CAG repeat between different age groups (Fig. 2). Patients <49 years old showed a significant difference in CMAPs and SNAPs ($P = 0.041–0.002$). The patients <49 years old and with a longer CAG repeat showed a more significant decrease in CMAPs, while those with a shorter CAG repeat showed a more significant decrease in SNAPs.

We selected patients with the sensory-dominant phenotype and those with the motor-dominant phenotype to further analyse the implication of CAG repeat size on the age at onset and electrophysiological phenotypes of SBMA.

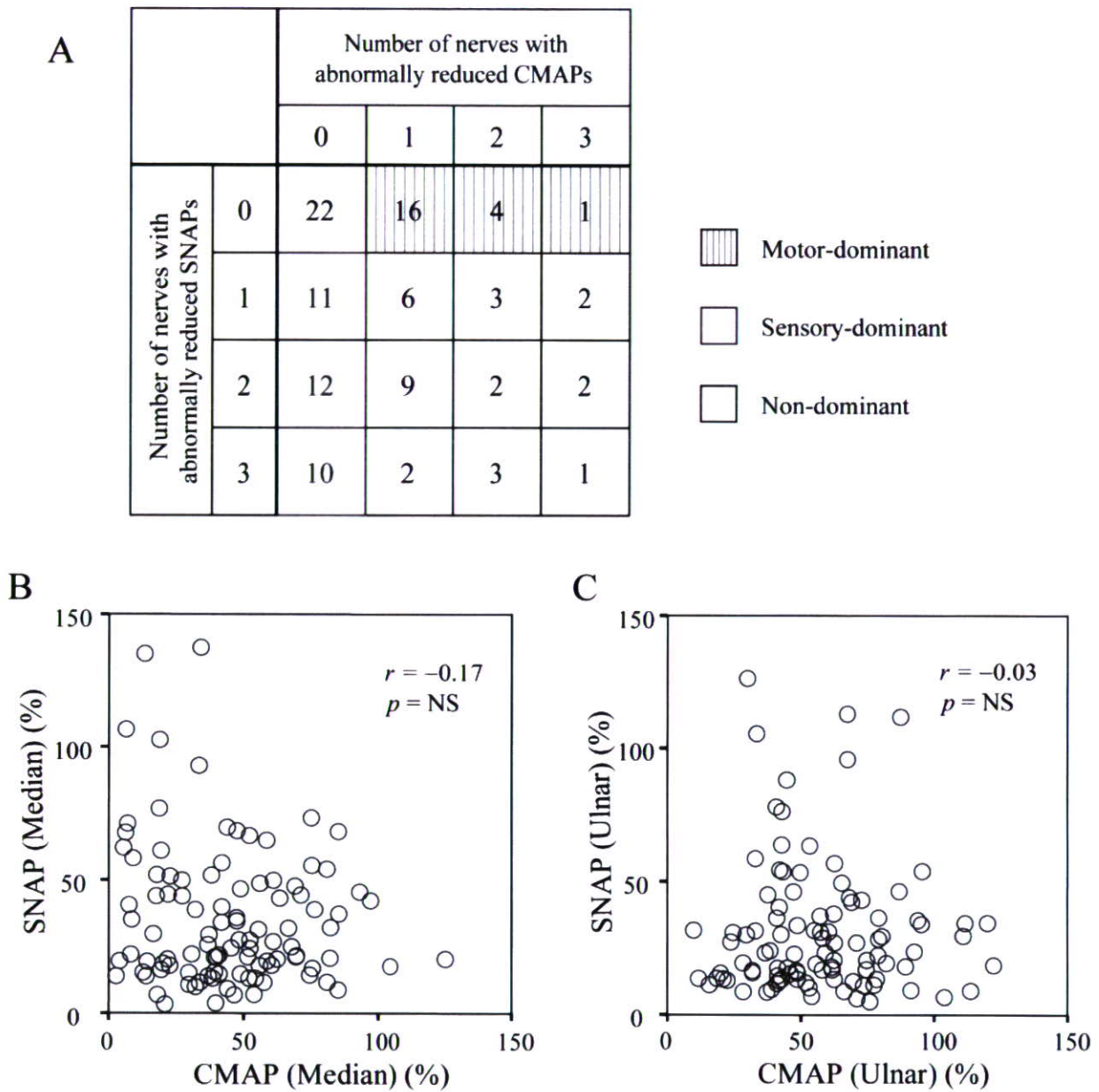


Fig. 1 Electrophysiological discrepancies in motor and sensory nerve involvement in SBMA patients. **(A)** The cross tabulation of the number of motor and sensory nerves showing an abnormally decreased action potential. The vertical stripe area corresponds to the motor-dominant phenotype and the gray area denotes the sensory-dominant phenotype. The white area represents the non-dominant phenotype. **(B and C)** Relation between CMAP and SNAP in the median and ulnar nerves on a standardized scale of percentage to normal control mean values. Some patients have only decreases of CMAP with preserved SNAP, while other patients show declines of SNAP with conserved CMAP.

As shown in Fig. 1A, the sensory-dominant phenotype was determined if patients show a reduced SNAP (less than control mean -2 SD) in at least one nerve without any decrease in CMAPs, whereas the motor-dominant phenotype denotes patients showing a reduced CMAP (less than control mean -2 SD) in at least one nerve without any decrease in SNAPs. We examined the relationship between CAG repeat number and the age at onset in these patients ($n=54$) (Fig. 3A). We found that the mean CAG repeat

number and the age at onset were significantly different between patients with motor- and sensory-dominant phenotypes ($P<0.001$, Fig. 3A), indicating that a longer CAG repeat is more closely linked to the motor-dominant phenotype, and a shorter CAG repeat is more closely linked to sensory-dominant phenotype. Similar findings were observed when we classified patients based on abnormally reduced action potentials (less than control mean -2 SD) in the median nerve or the ulnar nerve (Fig. 3B and C).

Table 4 Clinical and electrophysiological features in terms of CAG repeat size in AR gene

	CAG repeat <47		CAG repeat ≥47		P
	(Mean ± SD)	n	(Mean ± SD)	n	
Age at examination	58.9 ± 10.2	32	51.7 ± 8.9	65	0.001
Duration from onset	9.6 ± 7.4	32	10.7 ± 6.6	65	NS
Age at onset	49.3 ± 11.5	32	41.0 ± 8.9	65	0.002
Limb Norris score	54.2 ± 8.3	28	53.9 ± 7.0	63	NS
Norris Bulbar score	32.4 ± 5.1	28	33.4 ± 3.9	63	NS
ALSFRS-R	41.1 ± 4.1	28	41.2 ± 4.5	63	NS
CMAP (mV)					
Median	5.7 ± 2.4	32	4.8 ± 3.1	65	NS
Ulnar	5.6 ± 2.2	32	4.9 ± 2.4	65	NS
Tibial	8.7 ± 4.9	32	7.4 ± 3.1	65	NS
SNAP (µV)					
Median	4.8 ± 3.3	29	7.7 ± 5.6	65	0.011
Ulnar	4.1 ± 2.6	29	6.2 ± 5.0	64	0.037
Sural	3.8 ± 2.6	26	5.4 ± 3.4	59	0.022

AR = androgen receptor; ALSFRS-R = ALS functional rating scale-revised; CMAP = compound muscle action potential; SNAP = sensory nerve action potential; NS = not significant.

The CAG repeat size correlates directly with the frequency of nuclear accumulation in the motor neurons and inversely with that of cytoplasmic aggregation in the DRG

In order to investigate the relationship between CAG repeat size and the degree of motor and sensory nerve involvement, we performed immunohistochemistry using anti-polyglutamine antibody (1C2) on autopsied spinal cord and DRG specimens from SBMA patients, and quantified the primary sensory neurons in which mutant AR accumulated. In primary sensory neurons within the DRG, mutant AR was detected immunohistochemically as punctuate aggregates in the cytoplasm (Fig. 4A). On the other hand, diffuse nuclear accumulation of mutant AR was detected in motor neurons of the spinal anterior horn (Fig. 4B). The size of CAG repeat in the AR gene tended to be inversely correlated with the number of primary sensory neurons bearing cytoplasmic aggregates (Fig. 4C). This result is in contrast with the previously reported correlation between the frequency of mutant AR accumulation in spinal motor neuron and the CAG repeat size (Adachi *et al.*, 2005) (Fig. 4D).

Discussion

The present study demonstrated extensive abnormalities in both motor and sensory nerve conduction in SBMA patients, reflecting principal pathological lesions in the lower motor neurons and in the DRG. Previous studies

on nerve conduction in SBMA patients showed a characteristic decrease in SNAP compared with normal controls, whereas SCV and MCV were variably reported as either normal or decreased, and CMAP decreased to variable extents (Harding *et al.*, 1982; Olney *et al.*, 1991; Li *et al.*, 1995; Guidetti *et al.*, 1996; Polo *et al.*, 1996; Ferrante *et al.*, 1997; Antonini *et al.*, 2000; Sperfeld *et al.*, 2002). In the present study, the reductions in both CMAP and SNAP were remarkable, in agreement with previous reports. This suggests that axonal degeneration is the principal peripheral nerve damage in SBMA patients. In addition, MCVs and SCVs were significantly decreased in the SBMA patients, and distal latencies were also significantly increased.

Several reports have examined the F-wave in SBMA patients. Those studies showed that the latency is almost normal or slightly extended (Olney *et al.*, 1991; Guidetti *et al.*, 1996). In the present study, the minimum F-wave latency was significantly longer and the maximum FWCV was significantly decreased in SBMA patients compared to that in normal controls. The occurrence of F-waves in SBMA patients was significantly less in the upper limb, but not in the lower limb compared with that of controls.

As for the spatial distribution of involvement, we demonstrated that nerves of the upper limbs are more severely disturbed than those of the lower limbs in SBMA patients. These observations suggest that nerve involvement does not reflect a length-dependent process of primary neuropathy, but a neuronopathy process, which is consistent with our results from histopathological studies (Sobue *et al.*, 1989; Li *et al.*, 1995).

The most striking observations in the present study are that motor and sensory nerves are differentially affected in SBMA patients, that electrophysiologically defined motor-dominant and sensory-dominant phenotypes are present, especially in young patients, and that the CAG repeat size in the AR gene is a factor determining these electrophysiologically defined motor and sensory phenotypes. Previous studies have reported that the number of CAGs determine not only the age at onset, but also the clinical phenotype in polyglutamine diseases (Ikeutchi *et al.*, 1995; Johansson *et al.*, 1998; Mahant *et al.*, 2003). For example, DRPLA patients with a longer CAG repeat (earlier age at onset) showed a progressive myoclonus epilepsy phenotype, whereas patients with a shorter CAG repeat (later age at onset) showed a non-progressive myoclonus epilepsy phenotype, but high frequencies of choreoathetosis and psychiatric symptoms (Ikeutchi *et al.*, 1995). Moreover, in spinocerebellar ataxia type-7 (SCA7) patients with ≥59 CAGs, visual impairment was the most common initial symptom observed, while ataxia predominated in patients with <59 CAGs (Johansson *et al.*, 1998). Additionally, in HD patients, younger age at onset was associated with less chorea and more dystonia (Mahant *et al.*, 2003). In SBMA, only the relationship between CAG repeat and the age at onset or the severity of motor

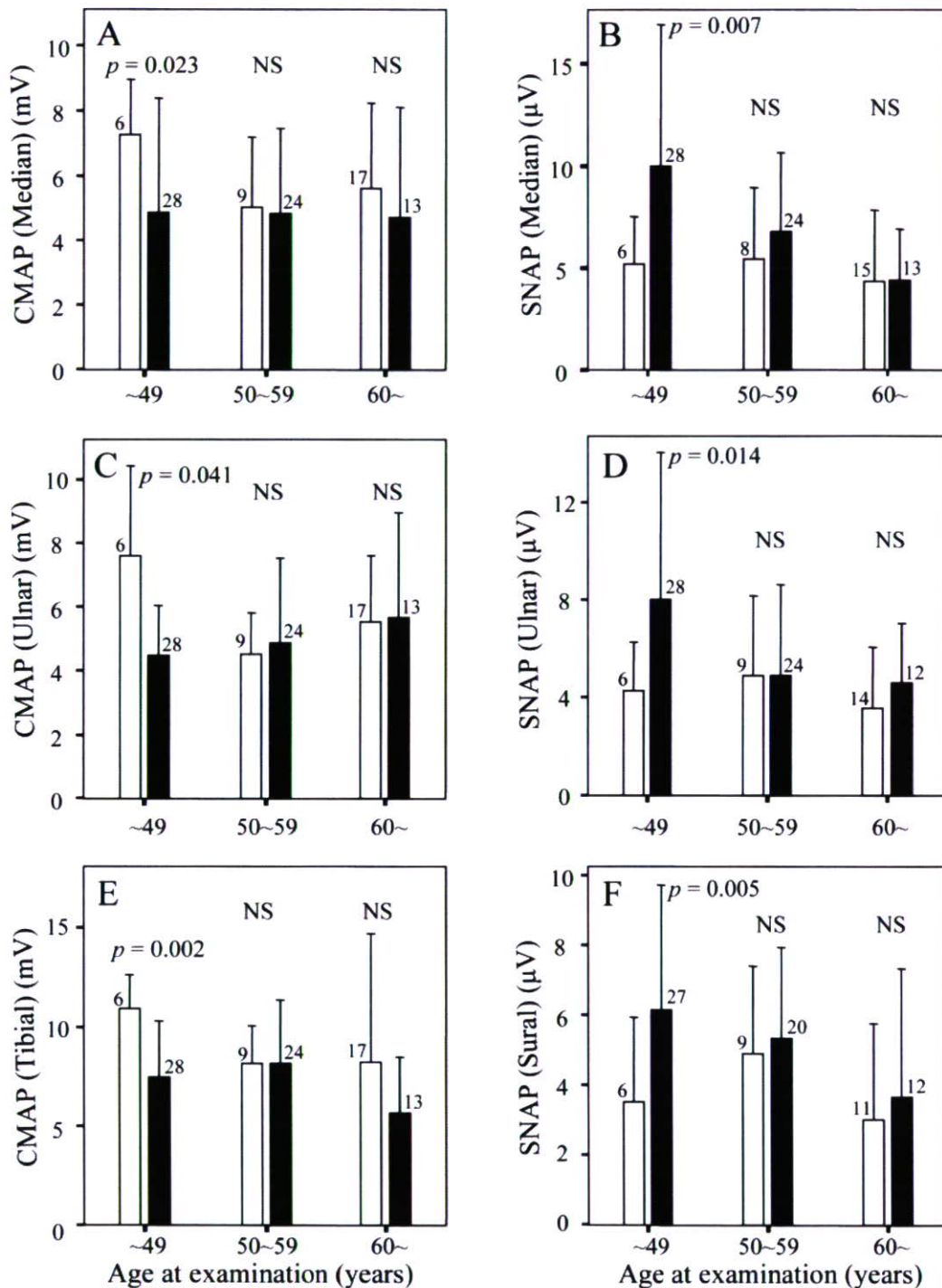


Fig. 2 (A–F) Age- and CAG-dependent changes in motor and sensory amplitudes in SBMA. CMAPs and SNAPs in the median (A and B), ulnar (C and D), tibial (E) and sural (F) nerves in different age groups are shown. The white columns are the mean values of the patients with a shorter CAG repeat (<47), while the black columns are the mean values of the patients with a longer CAG repeat (≥47). The error bars are SD. The number of patients examined is shown above each column. The young patients with a longer CAG repeat showed significantly low values of CMAPs compared to those with a shorter CAG repeat. Conversely, young patients with a shorter CAG repeat showed significantly lower values of SNAPs than those with a longer CAG repeat. Patients more than 49 years old did not show a significant difference between shorter and longer CAG repeat.

function has been reported (Doyu *et al.*, 1992; Atsuta *et al.*, 2006), but a CAG size-dependent clinical phenotype has not been described. This may be because the expansion of CAG repeat in the AR gene is shorter than that in the causative

genes for DRPLA, SCA7 or HD. Alternatively, as compared to outstanding motor dysfunction, the clinical manifestations of sensory nerve impairment are less severe in SBMA patients, which may result in overlooking the motor and

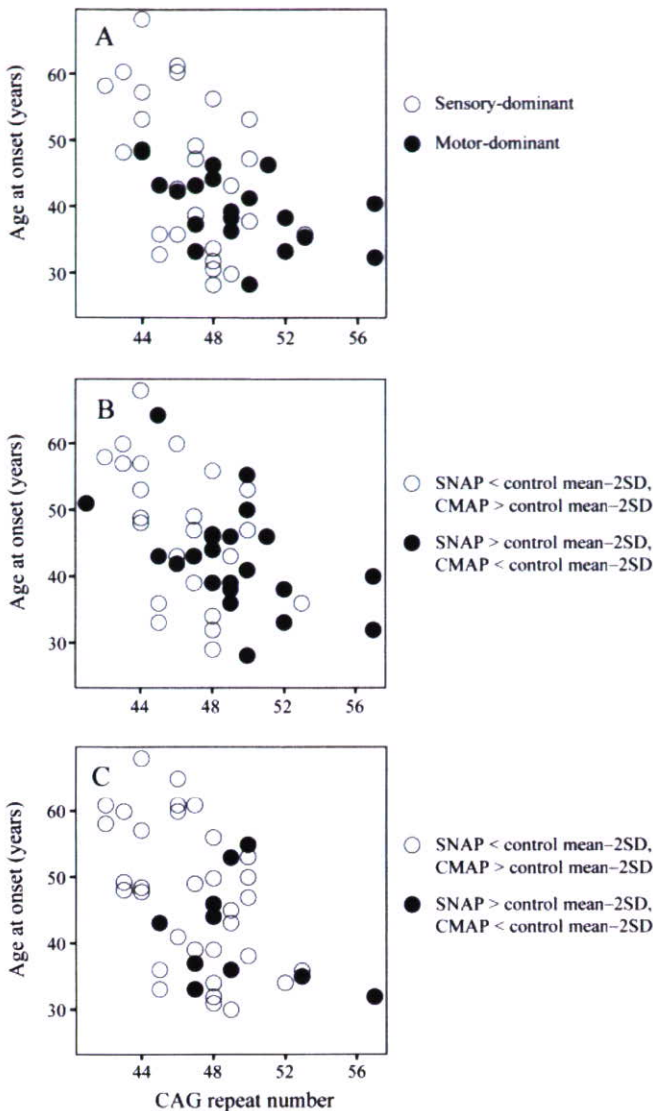


Fig. 3 CAG repeat size determines the age at onset in SBMA. **(A)** Relation between the CAG repeat size and the age at onset according to the phenotypes determined by CMAPs and SNAPs. A longer CAG repeat was closely linked to the motor-dominant phenotype, and a shorter CAG repeat was closely linked to the sensory-dominant phenotype. Motor- and sensory-phenotypes were determined as shown in Fig. 1A. **(B)** Relation between the CAG repeat size and the age at onset according to the phenotype determined by using CMAPs and SNAPs in the median nerve. **(C)** Relation between the CAG repeat size and the age at onset according to the phenotype determined by using CMAPs and SNAPs in the ulnar nerve.

sensory discrepancy. Our present findings in SBMA patients strongly suggest that the phenotypic diversity determined by CAG repeat size is a common feature shared by various polyglutamine diseases.

Although the pathological mechanism by which CAG repeat size influences clinical phenotype is unknown, a common molecular basis appears to underlie the heterogeneity of clinical presentations in polyglutamine diseases.

The polyglutamine tract encoded by an expanded CAG repeat forms a β -sheet structure, leading to conformational changes and the eventual accumulation of causative proteins (Perutz *et al.*, 2002; Sakahira *et al.*, 2002). Since the propensity of aggregation is dependent on CAG repeat size, the different length of polyglutamine tract may result in a CAG repeat size-dependent pathology.

The observations that a longer CAG repeat results in the motor-dominant phenotype, while a shorter CAG leads to the sensory-dominant presentation, are further reinforced by results of previous studies on the cell-specific histopathological changes in SBMA. A diffuse loss and atrophy of anterior horn cells accompanied by a mild gliosis is characteristic of SBMA (Kennedy *et al.*, 1968; Sobue *et al.*, 1989), suggesting that the pathology of spinal motor neurons is neuronopathy. On the other hand, no substantial neuronal loss in the DRG despite severe axonal loss in the central and peripheral rami suggests that the pathology of sensory neurons is distally accentuated axonopathy, although the primary pathological process may be present in the perikarya of sensory neurons (Sobue *et al.*, 1989; Li *et al.*, 1995). Moreover, the accumulation of mutant AR, a pivotal feature of SBMA pathology, is also different in motor and sensory neurons (Adachi *et al.*, 2005). Mutant AR accumulates diffusely in the nucleus of spinal motor neurons, but cytoplasmic aggregation is predominant in sensory neurons within the DRG (Adachi *et al.*, 2005). The extent of diffuse nuclear accumulation of mutant AR in motor neurons is closely related to CAG repeat size, providing a molecular basis for the present observations that patients with a longer CAG repeat show a greater decrease in CMAPs. On the other hand, the results of anti-polyglutamine immunohistochemistry in this study indicate that cytoplasmic aggregation of mutant AR is more frequent in the patients with a shorter CAG repeat. Taken together, the differential accumulation pattern of mutant AR between motor and sensory neurons, and their differential correlation to CAG repeat size may be the pathophysiological background for the development of motor- and sensory-dominant phenotypes.

In conclusion, the results of the present study are unequivocal electrophysiological phenotypes, motor-dominant, sensory-dominant and non-dominant, especially in young patients of SBMA. These features are dependent on the CAG repeat size within the AR gene, with a longer CAG repeat size is more closely related to the motor-dominant phenotype and a shorter CAG repeat size related to the sensory-dominant phenotype. Our observations shed light on new roles of CAG repeat size in the clinical presentation of SBMA.

Supplementary materials

Supplementary materials are available at *Brain* online.

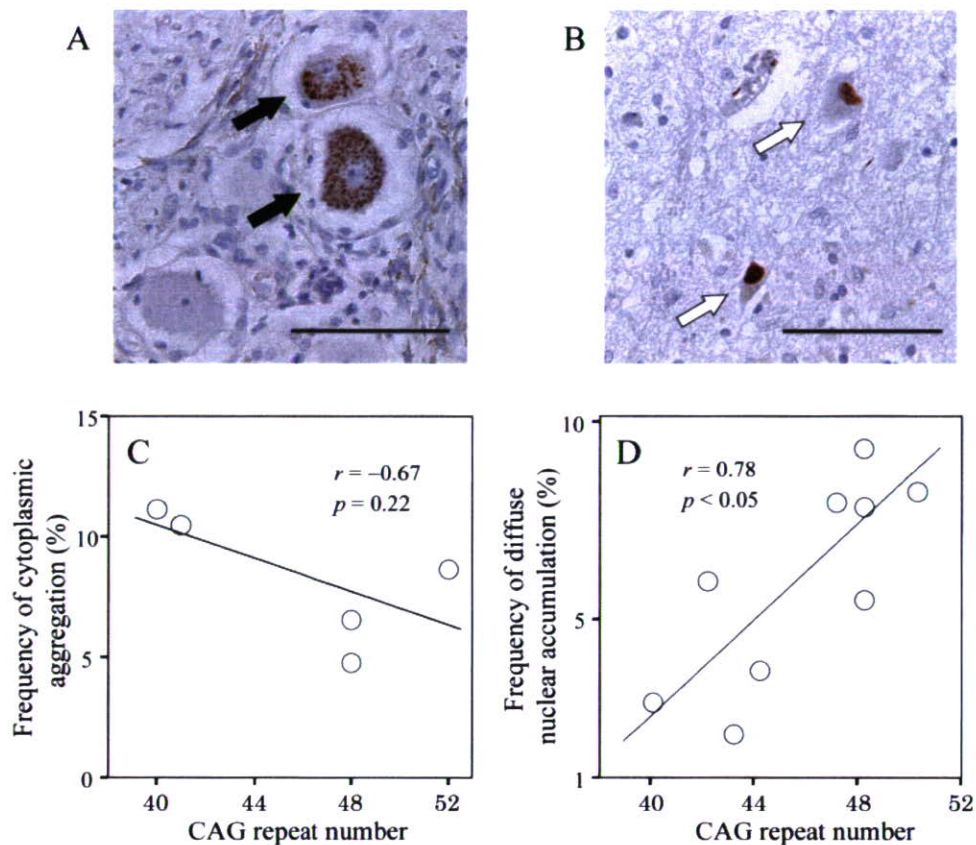


Fig. 4 Immunohistochemical analyses of mutant androgen receptor (AR) accumulation in the dorsal root ganglion (DRG) and that in the spinal anterior horn of SBMA patients. **(A)** Aggregates of mutant AR in the cytoplasm of DRG neurons (black arrows). Scale bar = 100 μ m. **(B)** Mutant AR accumulates in the motor neuron nuclei (white arrows). Scale bar = 100 μ m. **(C)** Relation between the CAG repeat size and cytoplasmic aggregations in the primary sensory neuron. Cytoplasmic aggregation tended to be more frequent in the patients with a shorter CAG repeat. **(D)** Relation between the CAG repeat size and diffuse nuclear accumulation of mutant AR in the spinal motor neuron. Panel D is reconstructed from the previous report (Adachi et al., 2005).

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Disulfide Bond Mediates Aggregation, Toxicity, and Ubiquitylation of Familial Amyotrophic Lateral Sclerosis-linked Mutant SOD1^{*[S]}

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Mutations in the Cu/Zn-superoxide dismutase (*SOD1*) gene cause familial amyotrophic lateral sclerosis (ALS) through the gain of a toxic function; however, the nature of this toxic function remains largely unknown. Ubiquitylated aggregates of mutant *SOD1* proteins in affected brain lesions are pathological hallmarks of the disease and are suggested to be involved in several proposed mechanisms of motor neuron death. Recent studies suggest that mutant *SOD1* readily forms an incorrect disulfide bond upon mild oxidative stress *in vitro*, and the insoluble *SOD1* aggregates in spinal cord of ALS model mice contain multimers cross-linked via intermolecular disulfide bonds. Here we show that a non-physiological intermolecular disulfide bond between cysteines at positions 6 and 111 of mutant *SOD1* is important for high molecular weight aggregate formation, ubiquitylation, and neurotoxicity, all of which were dramatically reduced when the pertinent cysteines were replaced in mutant *SOD1* expressed in Neuro-2a cells. Dorfin is a ubiquityl ligase that specifically binds familial ALS-linked mutant *SOD1* and ubiquitylates it, thereby promoting its degradation. We found that Dorfin ubiquitylated mutant *SOD1* by recognizing the Cys⁶- and Cys¹¹¹-disulfide cross-linked form and targeted it for proteasomal degradation.

Cu/Zn superoxide dismutase (*SOD1*),² a major intracellular antioxidant enzyme, metabolizes superoxide radicals to molecular oxygen and hydrogen peroxide (1, 2). Because mutations in *SOD1* linked to familial amyotrophic lateral sclerosis (ALS) were first identified (3), more than 100 mutations at over 70 residues in the 153-amino acid *SOD1* protein have been reported (4). Most mutations are missense mutations, with a few causing early termination or frame shifts near the carboxyl

terminus of the protein. *SOD1* mutations account for ~20% of familial ALS, which is characterized by selective degeneration of motor neurons. *SOD1* is primarily a cytosolic protein (5), and the active enzyme is a homodimer of two subunits (6). Each subunit contains four cysteine (Cys) residues at positions 6, 57, 111, and 146. An intramolecular disulfide bond between Cys⁵⁷ and Cys¹⁴⁶ of each subunit facilitates its correct folding and stabilizes the active homodimeric structure (7, 8), but it is not known how the disulfide is formed in the reducing environment of the cytosol. Although the endoplasmic reticulum is the specialized site for oxidative folding (9), there is no *SOD1* localization to the endoplasmic reticulum (10). Most familial ALS-linked mutations render *SOD1* more susceptible to intramolecular disulfide bond reduction (11) and accelerate the rate of protein turnover (12, 13). Recent lines of evidence implicate the disulfide-reduced monomer as the common aggregation-prone, neurotoxic intermediate of mutant *SOD1* proteins (8, 11, 14–16), and a significant fraction of the insoluble *SOD1* aggregates in the spinal cord of mutant *SOD1* transgenic mice contains high molecular weight species cross-linked via intermolecular disulfide bonds (17). Hence, modulation of disulfide bond formation may be important in mutant *SOD1*-linked motor neuron-selective neurotoxicity.

ALS-linked mutant *SOD1* proteins are turned over more rapidly than wild-type *SOD1*, and proteasome inhibitors increase the amount of mutant *SOD1* (18, 19). To date, two distinct ubiquityl ligases, Dorfin and NEDL1, have been reported to ubiquitylate mutant *SOD1* (20, 21). Dorfin is a RING-finger/IBR (in-between ring-finger) domain-containing ubiquityl ligase, which we previously identified from human spinal cord (22), and belongs to the RBR (RING-Between rings-RING) family of proteins (23). Dorfin physically binds and ubiquitylates various familial ALS-linked *SOD1* mutants and subsequently targets them for proteasomal degradation, but it has no effect on the stability of wild-type *SOD1* (20). Overexpression of Dorfin protects neuronal cells against the toxic effects of mutant *SOD1* and reduces the number of aggregates composed of mutant *SOD1* (20). However, the mechanism by which Dorfin discriminates between the normal and pathogenic status of *SOD1* proteins remains unknown. There are numerous variants causing familial ALS, thus it seems reasonable that Dorfin recognizes a common protein modification among mutant *SOD1*s that is not present in wild-type *SOD1*.

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[S] The on-line version of this article (available at <http://www.jbc.org>) contains supplemental Fig. S1.

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² The abbreviations used are: *SOD1*, superoxide dismutase 1; ALS, amyotrophic lateral sclerosis; 2-ME, 2-mercaptoethanol; WST-1, 4-[3-(4-iodophenyl)-2-(4-nitrophenyl)-2H-5-tetrazolio]-1,3-benzene disulfonate; GFP, green fluorescent protein.

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In this study, we generated SOD1 proteins with various combinations of the four Cys residues replaced by serines and assessed their disulfide bond status, the changes in the formations of their high molecular weight species, and their neurotoxicity. Moreover, by studying the interaction between Dorfin and these engineered SOD1s, we investigated whether disulfide bonds are critical for Dorfin recognition and ubiquitylation of mutant SOD1s.

EXPERIMENTAL PROCEDURES

Construction of Expression Vectors—Construction of pcDNA3.1/MycHis-SOD1, pEGFP-N1-SOD1, and pcDNA4/HisMax-Dorfin vectors were described previously (20, 22). Cys to Ser missense mutations were introduced into pcDNA3.1/MycHis-SOD1 and pEGFP-N1-SOD1 with a QuikChange site-directed mutagenesis kit (Stratagene, La Jolla, CA). Primer pairs for each Cys to Ser mutant were as follows: 5'-CGAAGGCCGTGTCCGTGCTGAAGGGC-3' and 5'-GCCCTTCAGCACGGACACGGCCTTCG-3' for C6S; 5'-GATAATACAGCAGGCTCTACCAGTGCAGGTCC-3' and 5'-GGACCTGCACTGGTAGAGCCTGCTGTATTATC-3' for C57S; 5'-CTCAGGAGACCATCCATCATTGGCCGCAC-3' and 5'-GTGCGGCCAATGATGGAATGGTCTCCTGAG-3' for C111S; and 5'-GGAAGTCGTTTGGCTTCTGGTGTAATTGGGATCG-3' and 5'-CGATCCCAATTACACCAGAAGCCAAACGACTTCC-3' for C146S. Multiple Cys to Ser replaced vectors were obtained by repeatedly applying a mutagenesis.

Cell Culture, Transfection, and Antibodies—Neuro-2a cells (American Type Culture Collection, Manassas, VA), a line derived from mouse neuroblastoma, were maintained in Dulbecco's modified Eagle's medium containing 10% fetal calf serum, 5 units/ml penicillin, and 50 μ g/ml streptomycin. Transfections were performed using Lipofectamine 2000 (Invitrogen) in the WST-1 assay or Effectene Transfection Reagent (Qiagen, Valencia, CA) in other experiments according to the manufacturers' instructions. To inhibit cellular proteasome activity, cells were treated with 1 μ M (except as otherwise indicated) MG132 (Z-Leu-Leu-Leu-al, Sigma) or epoxomicin (Sigma) as indicated concentration for 24 h after overnight transfection. To differentiate Neuro-2a cells, they were changed to Dulbecco's modified Eagle's medium culture medium containing 2% fetal calf serum and 20 μ M retinoic acid and cultured for 48 h. Primary antibodies used were as follows: anti-Myc mouse monoclonal antibody (9E10, Sigma), anti-Myc rabbit polyclonal antibody (A-14, Santa Cruz Biotechnology, Santa Cruz, CA), anti-SOD1 rabbit polyclonal antibody (SOD100, Stressgen Bioreagents, Victoria, Canada), anti- α -tubulin mouse monoclonal antibody (B-5-1-1, Sigma), anti-ubiquitin mouse monoclonal antibody (4PD1, Santa Cruz Biotechnology), and anti-Xpress mouse monoclonal antibody (Invitrogen).

Transgenic Mice—17-week-old symptomatic B6SJL-TgN(SOD1-G93A)1Gur ALS mice overexpressing the human mutant SOD1^{G93A} (The Jackson Laboratory, Bar Harbor, ME) were used. The experimental design of this study was fully approved by the Experimental Animal Ethical Committee of the Nagoya University Graduate School of Medicine. Tissues were homogenized in 10 volumes of lysis buffer (TNE) consist-

ing of 50 mM Tris-HCl, 150 mM NaCl, 1% Nonidet P-40, and 1 mM EDTA with a protease inhibitor mixture (Complete Mini, Roche Diagnostics, Indianapolis, IN) and centrifuged at 20,000 \times g for 30 min at 4 $^{\circ}$ C. Supernatants were used for Western blotting analysis.

Immunoprecipitation and Western Blotting Analysis—5 \times 10⁵ cells from a 6-cm dish were lysed on ice with 1 ml of TNE lysis buffer. The lysate was centrifuged at 1,000 \times g for 15 min at 4 $^{\circ}$ C to remove nuclei and cell debris. Denucleated cell lysates (crude fraction) were separated into supernatant (soluble fraction) and pellet fractions by centrifuging at 20,000 \times g for 20 min at 4 $^{\circ}$ C. The pellets were lysed (insoluble fraction) with 1 ml of TNES lysis buffer consisting of 50 mM Tris-HCl, 150 mM NaCl, 1% Nonidet P-40, 2% SDS, and 1 mM EDTA with a protease inhibitor mixture (Complete Mini, Roche Diagnostics). Protein concentrations were determined with a DC protein assay kit (Bio-Rad). Immunoprecipitation from the soluble fraction was performed with 2 μ g of anti-Myc or anti-Xpress antibodies and Protein A/G Plus-agarose (Santa Cruz Biotechnology), and the precipitates were washed four times in TNE buffer. Cell lysates or immunoprecipitates were separated by SDS-PAGE (5–20% gradient gel) and analyzed by Western blotting with ECL plus detection reagents (GE Healthcare Bio-Sciences, Piscataway, NJ). Non-reducing SDS-PAGE was conducted without 2-mercaptoethanol (2-ME) in the sample buffer. Because omitting reducing agents from the protein samples can lead to adventitious air oxidation or disulfide scrambling, 100 mM iodoacetamide was added to the lysates to prevent these changes during sample preparation.

Filter Trap Assay—Each of the various fractions from the cell lysates (crude, soluble, and insoluble fractions) was filtered under vacuum through 0.2- μ m cellulose acetate membranes (Sartorius, Göttingen, Germany) followed by two washes in Tris-buffered saline. The membranes were then incubated with 5% milk powder in Tris-buffered saline at room temperature for 1 h, followed by an overnight incubation at 4 $^{\circ}$ C with anti-Myc antibody in Tris-buffered saline with 0.1% Tween 20. Primary antibodies were detected with horseradish peroxidase-conjugated secondary antibodies (GE Healthcare Bio-Sciences), which were then detected with ECL plus chemiluminescence reagent (GE Healthcare Bio-Sciences). To confirm equal loading of proteins, the same samples were blotted onto 0.45- μ m nitrocellulose membranes (Bio-Rad) and probed with anti-Myc or anti- α -tubulin antibodies.

Neurotoxicity Analysis and Quantification of SOD1 Aggregates—2 \times 10⁴ Neuro-2a cells were grown overnight on four-chamber, collagen-coated slides (Nalge Nunc, Rochester, NY) and then transfected with 0.2 μ g of pEGFP-N1-SOD1. After overnight incubation, the cells were differentiated in Dulbecco's modified Eagle's medium containing 2% fetal calf serum and 20 μ M retinoic acid for 48 h. Inclusion bodies were counted in more than 100 randomly selected cells, and the percentages of cells with such inclusions were calculated. Data from three independent experiments were averaged. For the cell viability assay, 5 \times 10³ Neuro-2a cells were grown in 96-well collagen-coated plates overnight, and then transfected with 0.1 μ g of pEGFP-N1-SOD1 or pcDNA3.1/MycHis-SOD1, with or without 0.1 μ g of pcDNA4/HisMax-Dorfin. pcDNA4/HisMax

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mock vector was used as a control. A 4-[3-(4-iodophenyl)-2-(4-nitrophenyl)-2H-5-tetrazolio]-1,3-benzene disulfonate (WST-1)-based cell proliferation assay (Roche Diagnostics) was performed 48 h after differentiation. Absorbance was measured in a multiple plate reader (PowerscanHT, Dainippon Pharmaceutical, Japan). The assay was carried out in triplicate and statistically analyzed by one-way analysis of variance or unpaired *t* test.

Quantitative Analysis of Gene Expression Levels—Total RNA was extracted from Neuro-2a cells expressing SOD1-GFP and their Cys to Ser derivatives by using an RNA Easy Kit (Qiagen), followed by cDNA synthesis primed with oligo(dT) using Superscript II (Invitrogen). The gene expression level was examined by quantitative reverse transcription-PCR using primer sets specific to target genes and QuantiTect SYBR Green PCR kit (Qiagen). PCR was performed on an iCycler system (Bio-Rad) under the manufacturer's recommended conditions.

Isolation of SOD1 Aggregates—Isolation of SOD1 inclusion bodies was carried out according to Lee *et al.* (24) with a slight modification. 5×10^5 Neuro-2a cells in a 60-mm dish expressing SOD1-GFP were washed with cold phosphate-buffered saline before addition of TNE buffer. After a 5-min incubation at room temperature, the supernatant containing Nonidet P-40-soluble proteins was carefully removed from dishes. After gentle washing of dishes with phosphate-buffered saline, the Nonidet P-40-insoluble materials were scraped and incubated on ice for 5 min. The extract was then centrifuged at $80 \times g$ for 15 min. The pellet containing big inclusions was put onto a slide glass, sealed with a coverslip, and observed under a BX51 epifluorescence microscope (Olympus, Tokyo, Japan).

Cycloheximide Chase Analysis—Neuro-2a cells grown on 6-cm dishes were transfected with 1 μ g of pcDNA3.1/MyHis-SOD1 with or without 1 μ g of pcDNA4/HisMax-Dorfin. 24 h after transfection, cycloheximide (50 μ g/ml) was added to the culture medium, and the cells were harvested at the indicated time points. The samples were subjected to SDS-PAGE and analyzed by Western blotting with anti-Myc antibody. The intensities of the bands were quantified by Image-Gauge software (Fuji Film, Tokyo, Japan). The assay was carried out in triplicate and statistically analyzed by one-way analysis of variance or unpaired *t* test.

RESULTS

Proteasome Inhibition Increases SDS-resistant Disulfide-linked Species as Well as Insoluble Ones of ALS-linked Mutant SOD1—Mutant SOD1 is a fairly unstable protein, and the increased turnover of mutant SOD1 is mediated by the ubiquitin-proteasome pathway (18, 19). Thus, we first examined the effect of proteasome inhibition on mutant SOD1 proteins. When cellular proteasome activity was blocked by the proteasome inhibitor MG132, the level of soluble mutant SOD1^{G85R} and SOD1^{G93A} increased in a dose-dependent manner (Fig. 1B, *arrowhead*), and an SDS-resistant mutant SOD1 dimer appeared (Fig. 1B, *arrow*). The increase in the amount of wild-type SOD1 was much smaller than that of mutant SOD1 (Fig. 1B, *arrowhead*). Detergent-insoluble, sedimentable mutant SOD1 also increased as proteasome activity was inhibited (Fig.

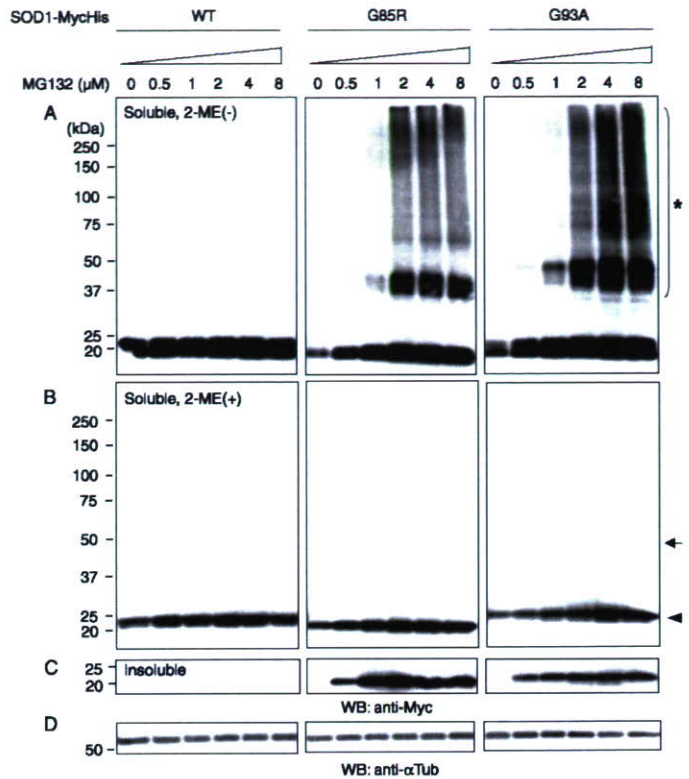


FIGURE 1. Proteasome inhibition leads to the accumulation of intermolecular disulfide bond-linked mutant SOD1. Neuro-2a cells expressing wild-type (WT), G85R, and G93A mutant SOD1-MycHis were treated with MG132 for 24 h at the indicated concentrations. Soluble fractions were analyzed by SDS-PAGE in the absence (A) or presence (B) of 2-ME. Insoluble fractions were analyzed by SDS-PAGE in the presence of 2-ME (C). *Arrow*, a soluble SDS-resistant dimer; *arrowhead*, a soluble monomeric SOD1; *asterisk*, disulfide-linked high molecular weight-species of SOD1. *D*, anti- α -tubulin as loading control.

1C). Interestingly, as the proteasome activity was inhibited, aberrant high molecular weight SDS-resistant disulfide-linked mutant SOD1^{G85R} and SOD1^{G93A} became more abundant (Fig. 1A, *asterisk*). There were almost no SDS-resistant disulfide-linked species of the wild-type SOD1. The same findings were obtained when blots were probed with anti-SOD1 antibody (supplemental Fig. S1A). These results were also confirmed with epoxomicin, a selective and irreversible proteasome inhibitor (supplemental Fig. S1B). Thus, intermolecular disulfide bond-linked mutant SOD1 is unstable and prone to degradation by the proteasome.

Free Cys⁶ and Cys¹¹¹ Are Important for Generating Disulfide Bond-linked Species and Insoluble, Sedimentable Forms of Mutant Human SOD1—We examined the role of Cys residues in the formation of aberrant disulfide-bond linked high molecular weight species. Various combinations of the four Cys residues at positions 6, 57, 111, and 146 replaced with serines were introduced into SOD1 protein-expression vectors using site-directed mutagenesis. The effects of amino acid replacement at one of the four Cys residues, at two of the four Cys residues, and at all four Cys residues on wild-type and two familial ALS-linked SOD1 mutants, SOD1^{G85R} and SOD1^{G93A}, were investigated. We used Myc-His-tagged SOD1 expression vectors and an antibody against the tag peptide to detect SOD1 protein so as to avoid possible reduced detection of SOD1 with multiple

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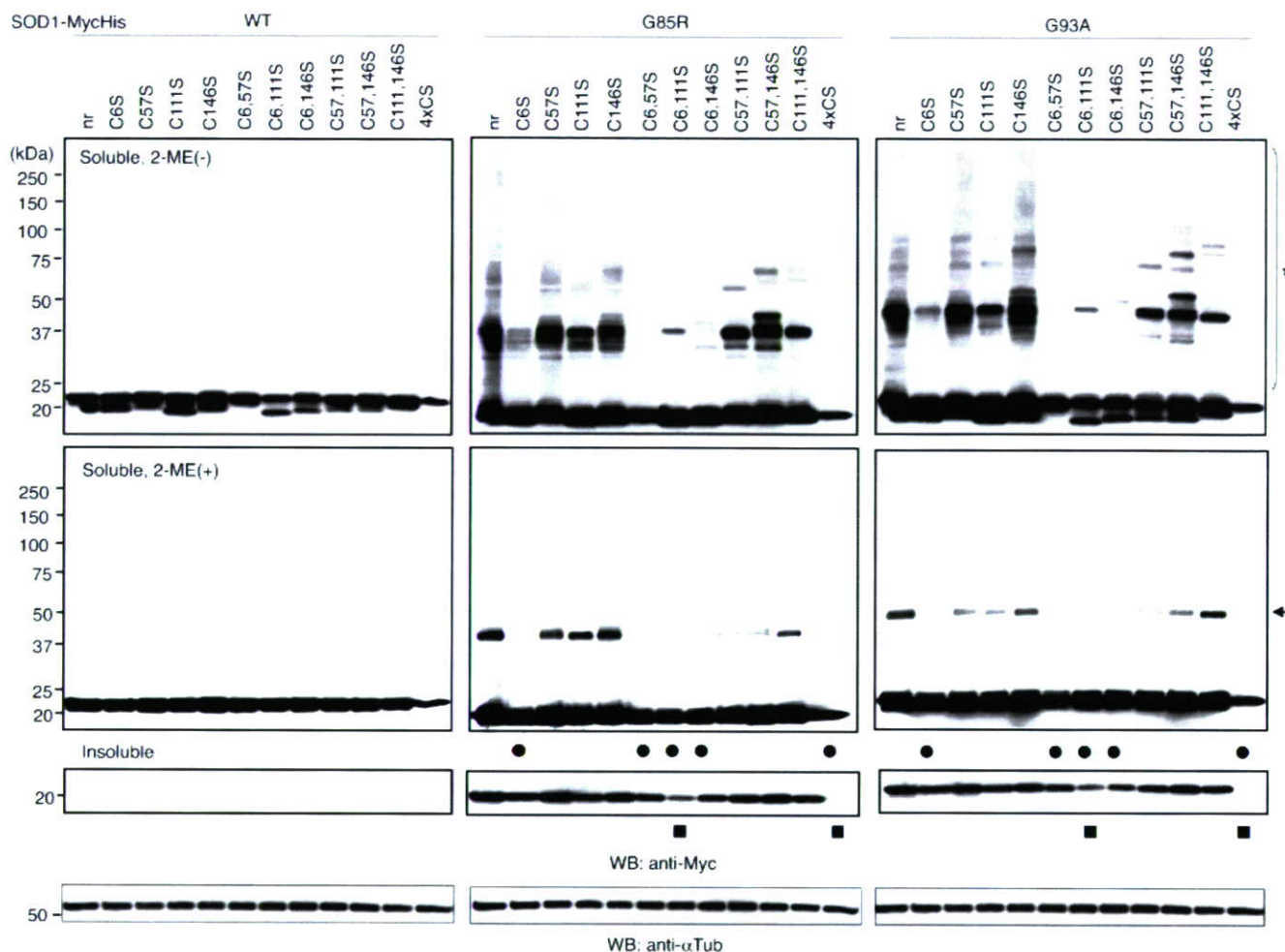


FIGURE 2. Free Cys⁶ and Cys¹¹¹ are important for generating intermolecular disulfide-linked species and insoluble, sedimentable forms of mutant human SOD1. Various combinations of replacing Cys with Ser were introduced into wild-type (WT) and mutant (G85R and G93A) SOD1-MycHis. Neuro-2a cells expressing SOD1-MycHis were treated with 2 μ M MG132 for 24 h. Soluble fractions were analyzed by SDS-PAGE in the absence (*upper panels*) or presence (*middle panels*) of 2-ME. Insoluble fractions were analyzed by SDS-PAGE in the presence of 2-ME (*lower panels*). Asterisk, a disulfide-linked high molecular weight species; arrow, an SDS-resistant dimer of mutant SOD1. Filled circles, marked reduction of an SDS-resistant dimer with a Cys⁶ replacement of mutant SOD1; filled squares, further reduction of the detergent-insoluble, sedimentable form of mutant SOD1 with simultaneous Cys⁶ and Cys¹¹¹ replacements. nr, SOD1 without replacement in cysteine residue; 4xCS, all four cysteines replaced by serines.

amino acids changes by the anti-SOD1 antibody. Interestingly, none of the Cys residue replacements generated disulfide-linked species in wild-type SOD1 proteins (Fig. 2, *left panel*). Under reducing conditions, replacement of Cys⁶ had a stronger effect on the formation of disulfide-linked species of mutant SOD1 than did the other three Cys residue replacements (Fig. 2, *middle and right panels, asterisk*). Combinations of replacing Cys⁶ and one of the other Cys residues further attenuated the aberrant disulfide-linking of mutant SOD1 seen with the single substitution of Cys⁶ (Fig. 2, *filled circle*). Under usual reducing conditions, the same reduced oligomerization of mutant SOD1 was observed when combinations of Cys⁶ and other Cys residues were replaced (Fig. 2, *arrow*). The detergent-insoluble, sedimentable form of mutant SOD1 was also reduced especially if both Cys⁶ and Cys¹¹¹ were replaced (Fig. 2, *filled square*). Replacement of all four Cys residues completely abolished the disulfide-linked species in the non-reducing condition and the oligomeric, detergent-insoluble form of mutant SOD1 in the reducing condition (Fig. 2, *lane 4xCS*). Because simultaneous substitutions of Cys⁶ and

Cys¹¹¹ had the strongest effects on the formation of aberrant species of mutant SOD1 in both non-reducing and reducing conditions, we compared C6S and C111S mutants with C57S and C146S mutants in the following experiments.

Substituting Both Cys⁶ and Cys¹¹¹ Greatly Reduces High Molecular Weight Aggregate Formation and Ubiquitylation of Mutant SOD1—In studies of polyglutamine disorders, it has been demonstrated that high molecular weight aggregates of mutant proteins are retained by filtration through cellulose acetate (25, 26). Cellulose acetate membranes usually bind protein very poorly and are used to trap high molecular weight structures from complex mixtures through filtration. This assay was also successfully applied to detect mutant SOD1 aggregation (27). Thus we used a cellulose acetate filter trap assay to investigate whether SOD1 proteins with Cys substitutions are retained in high molecular weight aggregates from lysates of SOD1-MycHis expressing Neuro-2a cells. Cells were lysed in TNE buffer, fractionated into crude denucleated, soluble, and insoluble fractions, and each fraction was then filtered through a 0.22- μ m cellulose acetate membrane. Subsequent staining

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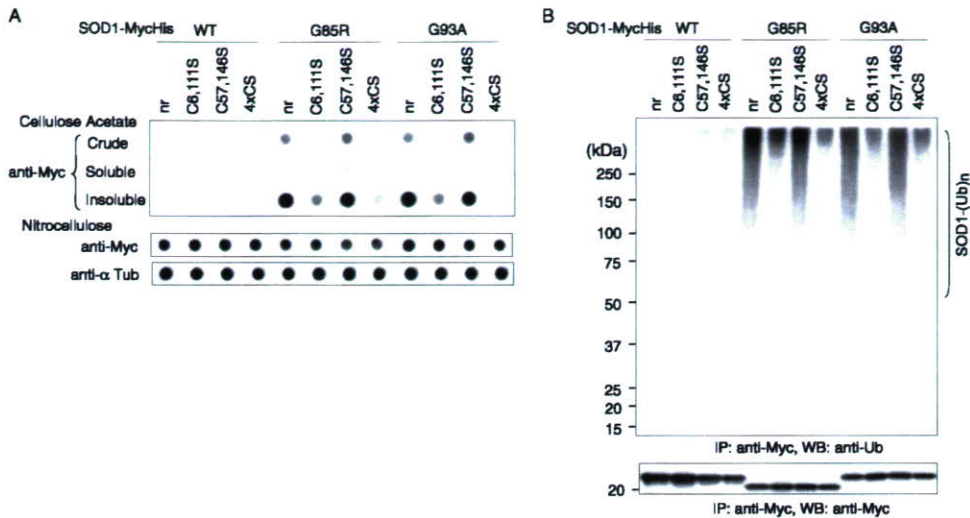


FIGURE 3. Replacing both Cys⁶ and Cys¹¹¹ greatly reduces high molecular weight aggregate formation and ubiquitylation of mutant SOD1-MycHis. *A*, crude, soluble, and insoluble fractions of cell lysates were analyzed by filter trap assay (*upper panel*). Nitrocellulose dot blots probed with anti-Myc (*middle panel*) and anti- α -tubulin (*lower panel*) antibodies were used as loading controls. *B*, *in vivo* ubiquitylation assay. Western blotting of SOD1-Myc-His immunoprecipitates with anti-ubiquitin antibody demonstrated polyubiquitylation of mutant SOD1s and their C57, 146S derivatives. Replacement of Cys⁶ and Cys¹¹¹ abolished polyubiquitylation of mutant SOD1. *nr*, SOD1 without replacement in cysteine residue; 4XCS, all four cysteines replaced by serines.

with anti-Myc antibody revealed trapped SOD1 proteins (Fig. 3*A*, *upper panel*). Interestingly, high molecular weight aggregates were abundantly detected in mutant SOD1^{G85R}, SOD1^{G93A}, and their C57S and C146S derivatives. Replacements of Cys⁶ and Cys¹¹¹ greatly reduced high molecular weight structures of mutant SOD1. No high molecular weight aggregates were present in either wild-type SOD1 or their Cys-substituted mutants.

Mutant, but not wild-type, SOD1 is conjugated to a multi-ubiquitin chain and degraded at the proteasome (20, 28). To assess whether SOD1 proteins are ubiquitylated, we carried out an *in vivo* ubiquitylation analysis by expressing SOD1^{WT}, SOD1^{G85R}, SOD1^{G93A}, and their Cys to Ser mutants in Neuro-2a cells in the presence of the proteasome inhibitor MG132. When SOD1 was then immunoprecipitated, mutant SOD1s, but not wild-type SOD1, were polyubiquitylated (Fig. 3*B*, *lane 1*). Replacement of both Cys⁶ and Cys¹¹¹ abolished ubiquitylation of mutant SOD1, whereas replacement of Cys⁵⁷ and Cys¹⁴⁶ did not affect the ubiquitylation status of mutant SOD1 (Fig. 3*B*, *lane 2 versus lane 3*). Wild-type SOD1 and its Cys-replacement mutants were not ubiquitylated at all. Replacing only one of the four Cys residues attenuated neither the formation of high molecular weight species nor the ubiquitylation of mutant SOD1 (data not shown). Thus, the presence of both Cys⁶ and Cys¹¹¹ is important for high molecular weight aggregate formation and ubiquitylation of mutant SOD1. Disulfide bond formation at Cys⁶ or Cys¹¹¹ is critical step for ubiquitylation of mutant SOD1.

Formation of Disulfide-linked Species of Mutant SOD1 Strongly Correlates with Visible Aggregate Formation and Neurotoxicity—Expression of mutant, but not wild-type, SOD1 induces large perinuclear intracytoplasmic aggregates in differentiated Neuro-2a cells and reduces cellular viability (20). We analyzed the role of mutant SOD1 Cys residues in aggregate

formation and neurotoxicity in Neuro-2a cells. Replacements of Cys⁶ and Cys¹¹¹ significantly reduced the percentage of mutant SOD1^{G85R} and SOD1^{G93A} cells with visible aggregates (Fig. 4*A*). To further demonstrate the extent of aggregate formation, we isolated SOD1 aggregates with a procedure according to Lee *et al.* (24). Differentiated Neuro-2a cells bearing SOD1-GFP aggregates were extracted with 1% Nonidet P-40 in the culture dish, and the Nonidet P-40-soluble proteins were gently removed. Under this condition, the soluble monomeric SOD1 was completely removed, and the aggregates remained in the culture dish due to their association with unknown structures (24). The remaining Nonidet P-40-insoluble portion was then scraped and centrifuged at 80 \times *g*.

After the centrifugation at 80 \times *g* for 15 min, the pellet fraction was found to contain exclusively the large inclusion bodies. Replacements of Cys⁶ and Cys¹¹¹ markedly reduced the number of inclusion bodies in G93A mutant SOD1-GFP (Fig. 4*B*). Mutant SOD1^{G85R} and SOD1^{G93A}, but not wild-type SOD1, are toxic in differentiated Neuro-2a cells as previously described (20). However, replacement of the Cys⁶ and Cys¹¹¹ residues markedly reduced this neurotoxicity (Fig. 4*C*), which was not affected by replacing the Cys⁵⁷ and Cys¹⁴⁶ residues. There were no significant differences among the expression levels of all the constructs (Fig. 4*D*). Thus, changes in inclusion formation and toxicity are not due to differences in altered expression. These results provide evidence of direct links among intermolecular disulfide bonding, ubiquitylated complex formation, visible aggregate formation, and neurotoxicity.

Preferential Occurrence of Disulfide-cross-linked Mutant SOD1 in the Affected Lesions of ALS Model Mice—Although mutant SOD1 is expressed at similar levels in both neuronal and non-neuronal tissues, the aggregated and ubiquitylated forms are selectively found in the pathological lesions of patients and mutant SOD1-transgenic mice (29, 30). Thus, we next examined whether mutant SOD1 is aberrantly disulfide-linked in various tissues from symptomatic mutant SOD1 transgenic mice. Western blotting analysis, using anti-SOD1 antibody under reducing and non-reducing (omitting reducing agent 2-ME) conditions, demonstrated that the expression levels of mutant SOD1 were nearly the same in all tissues examined. Each of the tissues showed some of the disulfide-linked mutant SOD1 species; however, in the brain stem and spinal cord, the areas predominantly affected in mutant SOD1-linked ALS, there was increased formation of intermolecular disulfide-linked species of mutant SOD1 (Fig. 5). Thus, intermolecular disulfide-linked

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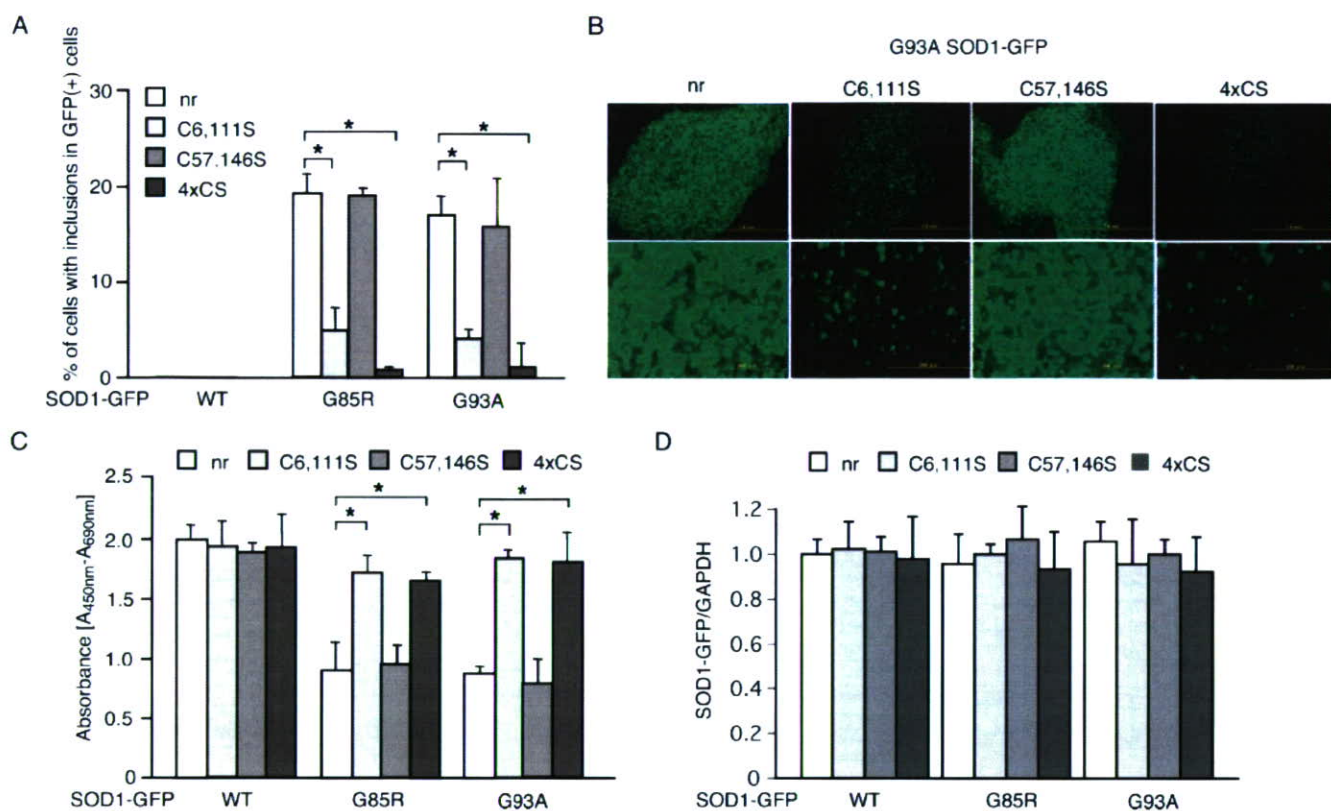


FIGURE 4. Formation of disulfide-linked species of mutant SOD1 strongly correlates with visible aggregate formation and neurotoxicity. *A*, the frequency of inclusion-bearing cells transfected with wild-type (WT), G85R, and G93A mutant SOD1-GFP and their Cys to Ser derivatives. *B*, G93A mutant SOD1-GFP inclusion bodies in $80 \times g$ pellet. Lower panels are a high magnification image of the portion on the upper panels showing the whole pellet. The scale bar is equivalent to 10 mm in the upper panels, and 200 μ m in the lower panels. *C*, change in the neurotoxic effect of mutant SOD1-GFP by Cys replacements to Ser. Cell viability was measured by the WST-1-based assay. *D*, all the constructs have equal expression. Transcription levels of SOD1-GFP in Neuro-2a cells expressing WT, G85R, and G93A mutant SOD1 and their Cys to Ser derivatives were examined by quantitative reverse transcription-PCR. Data were normalized with glyceraldehyde-3-phosphate dehydrogenase expression and then represent relative expression levels compared with levels in cells expressing WT SOD1-GFP. Data are mean \pm S.D. values of triplicate assays. Statistical analyses were carried out by analysis of variance. *, $p < 0.01$. nr, SOD1 without replacing cysteine residues; 4xCS, all four cysteines replaced by serines.

species are implicated as the aggregation-prone and neurotoxic intermediate of mutant SOD1 *in vivo*.

Effects of Cys⁶- and Cys¹¹¹-mediated Disulfide Linking on the Rate of Mutant SOD1 Degradation—To determine whether replacement of Cys residues affects the degradation of SOD1 proteins, we examined the stability of mutant SOD1 proteins expressed in Neuro-2a cells (Fig. 6, *A* and *B*). Chase experiments with cycloheximide, which halts all cellular protein synthesis, demonstrated that replacement of Cys residues did not influence the stability of wild-type SOD1 protein (Fig. 6*A*). By contrast, although mutant SOD1 showed the enhanced degradation compared with wild-type proteins previously described (18–20), when both Cys⁶ and Cys¹¹¹ were replaced with Ser, the degradation of mutant SOD1 was markedly increased (Fig. 6*B*). Replacement of Cys⁵⁷ and Cys¹⁴⁶ did not significantly change the rate of degradation compared with Cys-native mutant SOD1 protein.

Ubiquityl Ligase Dorfin Ubiquitylates and Promotes Degradation of Disulfide-linked Mutant SOD1—We have previously shown that Dorfin physically binds and ubiquitylates various familial ALS-linked SOD1 mutants and enhances their degradation (20). Thus, we examined whether Cys residues on SOD1 affect the binding and ubiquitylating activities of Dorfin. To this end, Dorfin was co-expressed with wild-type or mutant SOD1 in Neuro-2a cells. Dorfin co-im-

munoprecipitated with G85R and G93A mutant SOD1s and their Cys⁵⁷- and Cys¹⁴⁶-replaced derivatives (Fig. 7*A*). However, Dorfin interacted with Cys⁶- and Cys¹¹¹-replaced mutant SOD1 only very weakly and failed to bind to mutant SOD1 when all four Cys residues were replaced (Fig. 7*A*). Dorfin did not bind at all to wild-type SOD1. Using an *in vivo* ubiquitylation assay, we further examined whether co-expressed Dorfin enhances the ubiquitylation of Cys-substituted mutant SOD1 (Fig. 7*B*). When Cys-native or Cys⁵⁷- and Cys¹⁴⁶-replaced mutant SOD1s were co-expressed with Dorfin, ubiquitylation of mutant SOD1s were increased; however, co-expression of Dorfin with mutant SOD1 in which Cys⁶ and Cys¹¹¹ or all four Cys residues were replaced did not promote ubiquitylation of these mutant SOD1s (Fig. 7*B*). Chase experiments with cycloheximide in the presence or absence of Dorfin demonstrated that degradation of Cys-native and Cys⁵⁷- and Cys¹⁴⁶-replaced mutant SOD1^{G93A} was greatly accelerated when Dorfin was overexpressed, whereas the stability of Cys⁶ and Cys¹¹¹ or all four Cys-replaced mutant SOD1^{G93A} were unaffected (Fig. 7*C*). We have previously shown that Dorfin exerts neuroprotective effects by promoting degradation of mutant SOD1 through its ubiquityl ligase activities (20). Co-expression of Dorfin improved the viability of Neuro-2a cells expressing Cys-

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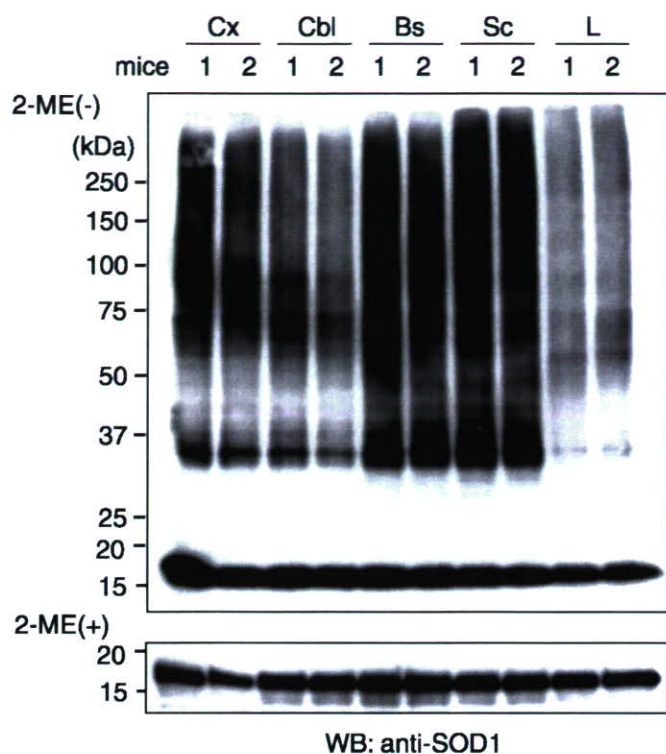


FIGURE 5. Preferential occurrence of disulfide-cross-linked mutant SOD1 in the affected lesion of ALS model mice. Western blotting of tissue samples from two 17-week-old symptomatic G93A mutant SOD1-transgenic mice under non-reducing (upper panel) and reducing (lower panel) conditions. Cx, cerebral cortex; Cbl, cerebellum; Bs, brain stem; Sc, spinal cord; L, liver.

native and Cys⁵⁷- and Cys¹⁴⁶-replaced mutant SOD1^{G93A} (Fig. 7D).

DISCUSSION

Mutations in the *SOD1* gene cause familial ALS through the gain of a toxic function, however, the nature of this toxic function remains largely unknown (31). Ubiquitylated aggregates of mutant SOD1 proteins in affected lesions are a pathological hallmark of the disease (32) and suggest their relation to neurotoxicity. Recent biochemical studies suggest that the immature disulfide-reduced forms of the familial ALS mutant SOD1 proteins play a critical role in this neurotoxicity; *in vitro*, these forms tend to misfold, oligomerize, and readily undergo incorrect disulfide bond formation upon mild oxidative stress (16, 33). Among the more than 100 ALS-associated human SOD1 mutants, some cannot intrinsically form the essential intramolecular disulfide bonds. One of the conserved Cys residues, Cys¹⁴⁶, is missing in some of the mutants, such as the Leu¹²⁶ del TT (stop at 131) and Gly¹²⁷ ins TGGG (stop at 133); however, it has been reported that minute quantities of SOD1 aggregates can cause the disease in mice expressing the truncated mutant, Gly¹²⁷ ins TGGG (stop at 133) (34). Furthermore, a significant fraction of the insoluble SOD1 aggregates in the spinal cord of ALS model mice contain multimers cross-linked via intermolecular disulfide bonds (17, 35). In the present study, we showed that non-physiological intermolecular disulfide bonds involving Cys⁶ and Cys¹¹¹ of the mutant SOD1 were important for high molecular weight aggregate formation, ubiquitylation, and neurotoxicity *in vivo*, all of which were dramatically reduced in

Neuro-2a cells when these residues were replaced with serines.

Human SOD1 has two free cysteine residues, Cys⁶ and Cys¹¹¹ (36). Cys⁶ is located adjacent to the dimer interface pointed toward the interior of the β -barrel and is solute-inaccessible in the native, folded conformation. Cys¹¹¹ is located near the surface and is solute-accessible and -reactive, often becoming blocked during purification (37). Replacement of the free Cys residues increased the resistance to thermal inactivation (38). Increased resistance of mutant SOD1s is due to increased resistance to irreversible unfolding and relatively unaffected by changes in conformational stability (39). Our data, showing that aggregate formation of mutant SOD1 is reduced when Cys⁶ and Cys¹¹¹ are replaced with serines, are compatible with these observations. Mutations of the Cys⁶ residue (C6F and C6G) still result in familial ALS (4), and in a transgenic mouse expressing mouse SOD1 retaining cysteines 6, 57, and 146 but lacking

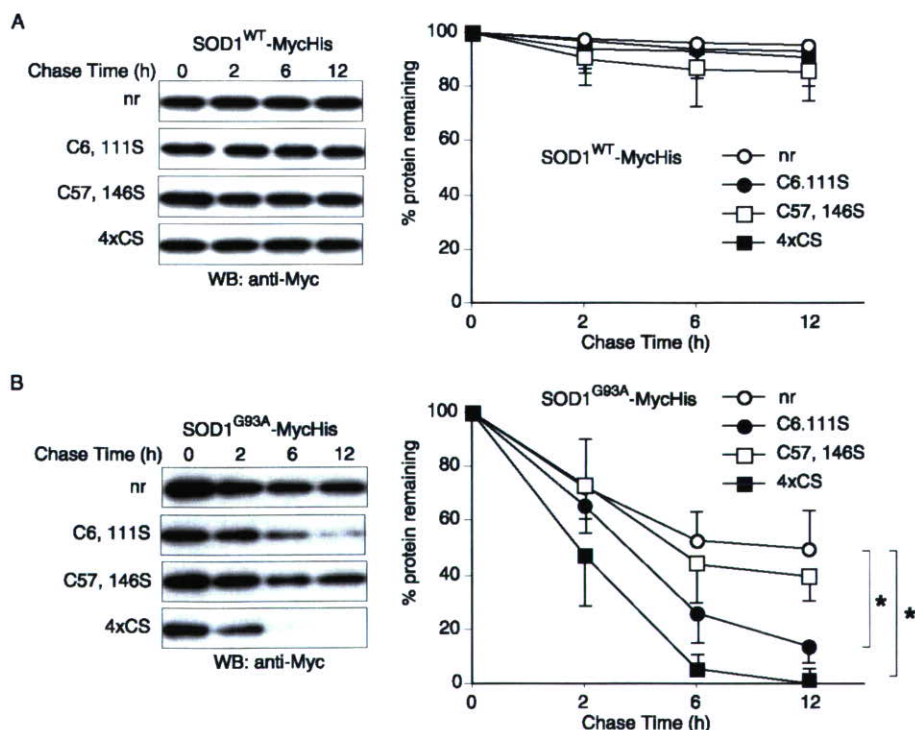


FIGURE 6. Effects of disulfide-linking at Cys⁶ and Cys¹¹¹ on the rate of mutant SOD1 degradation. Cycloheximide chase analysis on Neuro-2a cells expressing (A) wild-type (WT) and (B) G93A mutant SOD1 and their Cys to Ser derivatives. Western blots showing levels of SOD1 protein at various times after the cycloheximide chase are in the left panels. Quantitative data on the right are mean \pm S.D. values of three independent experiments. Statistical analyses were carried out by analysis of variance. *, $p < 0.01$. nr, SOD1 without cysteine residue replacement; 4xCS, all four cysteines replaced by serines.

Disulfide Linking and Ubiquitylation of Mutant SOD1

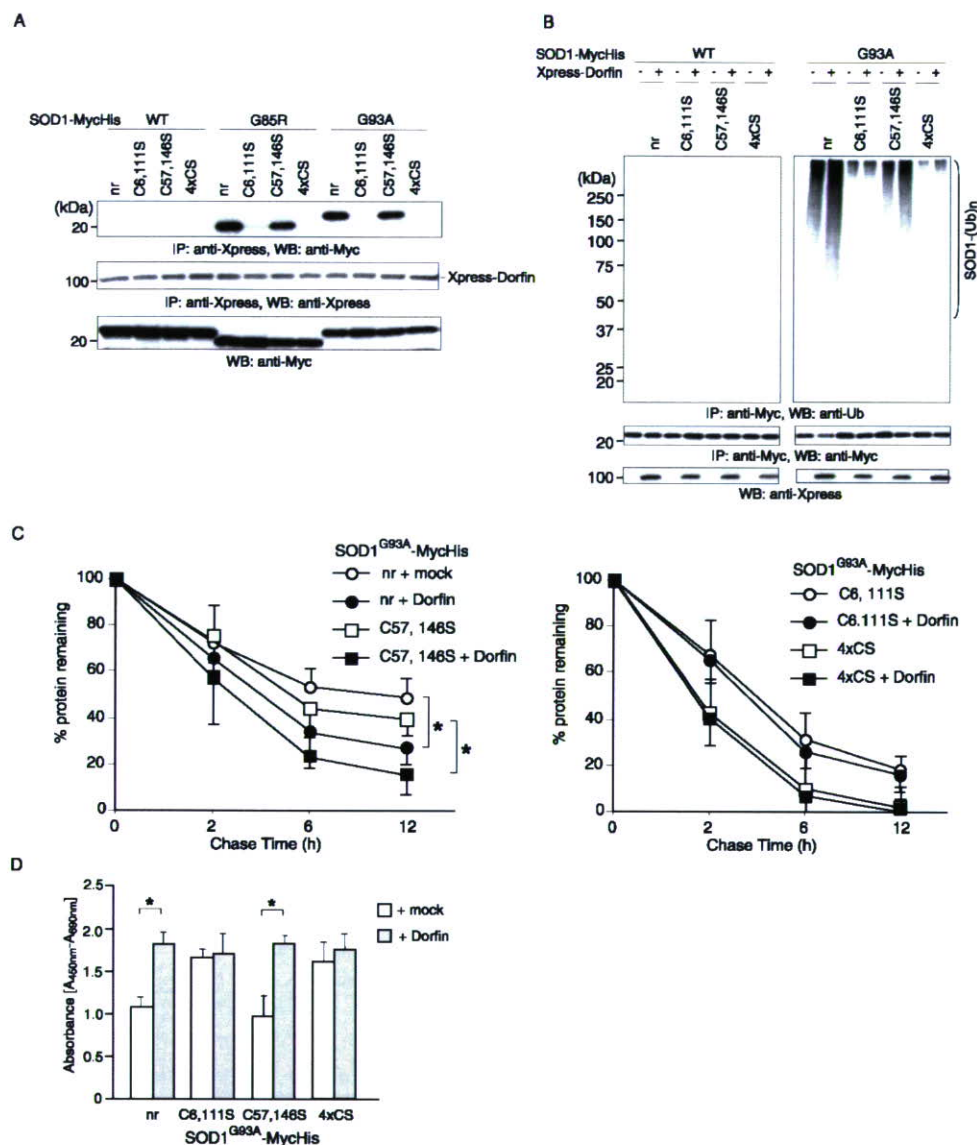


FIGURE 7. Ubiquitylation of mutant SOD1 by Dorfin. A, replacement of Cys⁶ and Cys¹¹¹ nearly eliminated the interaction of Dorfin with mutant SOD1. Various SOD1-MycHis were co-transfected with Xpress-Dorfin. After immunoprecipitation with anti-Xpress antibody, the resulting precipitates and cell lysates were analyzed by Western blotting with anti-Myc antibody. B, *in vivo*, Dorfin failed to promote ubiquitylation of mutant SOD1 with the Cys⁶ and Cys¹¹¹ replacement. Western blotting of SOD1-Myc-His immunoprecipitates with anti-ubiquitin antibody. C, Dorfin failed to promote degradation of mutant SOD1 with both Cys⁶ and Cys¹¹¹ replaced. Cycloheximide chase analysis of G93A mutant SOD1 with Cys⁶ and Cys¹¹¹-replacements (left panel) or with Cys⁵⁷ and Cys¹⁴⁶-replacements (right panel) in the presence or absence of overexpressed Xpress-Dorfin. D, Dorfin prevented neurotoxicity by mutant SOD1 with intact Cys⁶ and Cys¹¹¹ residues. Cell viability was measured by the WST-1-based assay. Data are mean \pm S.D. values of three independent experiments. Statistical analyses were carried out by unpaired *t* test. *, *p* < 0.01. nr, SOD1 without replacement in cysteine residue; 4xCS, all four cysteines replaced by serines.

111 and with a G86R mutation corresponding to G85R mutation in human SOD1, degeneration of motor neurons in the spinal cord has been observed (40). These results imply that, if one of either the Cys⁶ or Cys¹¹¹ residues is present, it can still be a disease-causing SOD1. Our data here also revealed that replacement of only one of the Cys residues at positions 6 or 111 had modest effects on the formation of aggregates (Fig. 2).

Cytoplasmic proteins are degraded mainly via two pathways, the ubiquitin-proteasome pathway (6) and via autophagy (7). Previous studies have shown that mutant SOD1 proteins are turned over more rapidly than wild-type SOD1 (12, 18, 19). Two distinct ubiquitin ligases, Dorfin and NEDL1, were

reported to specifically ubiquitylate mutant but not wild-type SOD1 (20, 21). These studies suggest that mutant SOD1 is degraded by the ubiquitin-proteasome pathway and that the accelerated turnover of mutant SOD1 is mediated in part by this pathway. Impairment of the proteasome activities may contribute to ALS pathogenesis (28, 41, 42). We showed here that proteasome inhibition led to a dose-dependent accumulation of aberrant disulfide-linked high molecular weight mutant SOD1 (Fig. 1), suggesting that disulfide-linking mediates ubiquitylation of mutant SOD1. In fact, we found that Dorfin ubiquitylated mutant SOD1 by recognizing the Cys⁶ and Cys¹¹¹ disulfide cross-linked form and targeted it for proteasomal degradation (Fig. 7). Mutant SOD1, in which the Cys⁶ and Cys¹¹¹ were replaced, was not ubiquitylated (Fig. 3), and its rate of degradation was not affected in the presence of Dorfin (Fig. 7). It is possible that mutant SOD1 lacking Cys⁶ and Cys¹¹¹ may be degraded directly by the proteasome without ubiquitylation (43) or by autophagy (44), but further studies are needed to address this issue.

The appearance of mutant SOD1 aggregates in motor neurons of familial ALS patients and mouse models has suggested that aggregation plays an important role in neurotoxicity (31). However, conflicting results have been reported on the correlation between aggregate formation and cell death. One report showed that aggregate formation of mutant SOD1^{A4V} and SOD1^{V148G} does not correlate with cell death (45), whereas another

study using live cell-imaging techniques reported that the ability of mutant SOD1^{G85R} and SOD1^{G93A} proteins to form aggregates directly correlates with neuronal cell death (46). These controversies also exist in other neurodegenerative diseases (47, 48). In this study, we clearly showed a direct link among intermolecular disulfide bond-mediated high molecular weight complex formation, visible aggregate formation, and neurotoxicity (Figs. 2–4).

Furukawa *et al.* (16) reported that formation of disulfide-linked multimers need not involve the non-conserved Cys residues, Cys⁶ and Cys¹¹¹, and that the conserved Cys residues, Cys⁵⁷ and Cys¹⁴⁶, play an important role in the apo-form of

SOD1 multimerization upon oxidative stress. Our results underscore the importance of Cys⁶ and Cys¹¹¹ for high molecular weight aggregate formation, ubiquitylation, and neurotoxicity in Neuro-2a cells. This discrepancy may result from differences in experimental conditions; we studied human SOD1 proteins expressed in Neuro-2a cells, and Furukawa *et al.* used the purified apo-form of human SOD1 from *Escherichia coli*. Further studies will clarify the roles of each of the Cys residues of the mutant SOD1 protein in the ALS pathogenesis *in vivo* by generating transgenic mice bearing mutant SOD1 lacking Cys⁶ and Cys¹¹¹ or Cys⁵⁷ and Cys¹⁴⁶.

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ORIGINAL ARTICLE

Gene Expressions Specifically Detected in Motor Neurons (Dynactin 1, Early Growth Response 3, Acetyl-CoA Transporter, Death Receptor 5, and Cyclin C) Differentially Correlate to Pathologic Markers in Sporadic Amyotrophic Lateral Sclerosis

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Abstract

In a differential gene expression profile, we showed previously that dynactin 1 (*DCTN1*), early growth response 3 (*EGR3*), acetyl-CoA transporter (*ACATN*), death receptor 5 (*DR5*), and cyclin C (*CCNC*) were prominently up- or downregulated in motor neurons of sporadic amyotrophic lateral sclerosis (ALS). In the present study, we examined the correlation between the expression levels of these genes and the levels of pathologic markers for motor neuron degeneration (i.e. cytoplasmic accumulation of phosphorylated neurofilament H [pNF-H] and ubiquitinated protein) and the numbers of residual motor neurons in 20 autopsies of patients with sporadic ALS. *DCTN1* and *EGR3* were widely downregulated, and the changes in gene expression were correlated to the number of residual motor neurons. In particular, *DCTN1* was markedly downregulated in most residual motor neurons before the accumulation of pNF-H, even in cases with well-preserved motor neuron populations. *ACATN*, *DR5*, and *CCNC* were upregulated in subpopulations of residual motor neurons, and their expression levels were well correlated with the levels of pNF-H accumulation and the number of residual motor neurons. The expressions of *DCTN1*, *EGR3*, *ACATN*, and *DR5* were all markedly altered before ubiquitinated protein accumulation. *DCTN1* downregulation appears to be an early event before the appearance of neurodegeneration markers, whereas upregulations of *DR5* and *CCNC* are relatively later phenomena associated with pathologic markers

and leading to neuronal death. The sequence of motor neuron-specific gene expression changes in sporadic ALS can be beneficial information in developing appropriate therapeutic strategies for neurodegeneration.

Key Words: Amyotrophic lateral sclerosis (ALS), Axonal transport, Cell death, Dynactin 1, Motor neuron.

INTRODUCTION

Amyotrophic lateral sclerosis (ALS) is a devastating neurodegenerative disease characterized by loss of motor neurons in the spinal cord, brainstem, and motor cortex (1), causing weakness of the limbs, abnormalities of speech, and difficulties in swallowing. The weakness ultimately progresses to respiratory impairment and half of the patients die within 3 years of the onset of symptoms, largely due to respiratory failure. About 5% to 10% of all patients with ALS show familial traits, and 20% to 30% of patients with familial ALS have a mutation in the copper/zinc superoxide dismutase 1 gene (*SOD1*). However, in more than 90% of patients with ALS, the disease is sporadic and does not show any familial traits. The presence of Bunina bodies in the remaining spinal motor neurons is a hallmark of cases of sporadic ALS (2, 3). There is at present no obvious consensus understanding of the pathogenic mechanism or an effective therapeutic approach for sporadic ALS, although several hypotheses, including oxidative stress, glutamate excitotoxicity, impaired axonal transport, neurofilament disintegration, mitochondrial dysfunction, neurotrophic deprivation, and proteasomal dysfunction have been proposed as causal mechanisms of motor neuron degeneration (4–11). In contrast, wide-ranging research activities have been initiated for a subgroup of patients with familial ALS, those with mutant *SOD1*, including a search for the pathogenic mechanisms of mutant *SOD1*-induced motor neuron death and the examination of therapeutic perspectives using a transgenic rodent model for mutant *SOD1* familial ALS (12–14).

One effective approach to begin the uncovering of the pathogenic mechanism of sporadic ALS is a description of

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the gene expression profile of motor neurons. Motor neuron-specific gene expression profiling would eventually lead us to a profound understanding of the pathophysiology of motor neuron degeneration in sporadic ALS. We have successfully created such a motor neuron-specific gene expression profile in patients with sporadic ALS by using microarray technology combined with laser-captured microdissection, the results of which were further verified by *in situ* hybridization and quantitative wide-ranging research activities (15). The genes with differential expressions in these profiles were particularly related to axonal transport, transcription, energy production, cell death, and protection from cell death. Gene expressions of dynactin 1 (*DCTN1*) and early growth response 3 (*EGR3*), related to cytoskeleton/axonal transport and transcription, respectively, were markedly decreased in motor neurons, whereas cell death-associated genes such as death receptor 5 (*DR5*), cyclin C (*CCNC*), and acetyl-CoA transporter (*ACATN*) were greatly upregulated. It is, however, uncertain how these gene expression alterations correlate with motor neuron degeneration and death and whether they play a role in the pathogenesis of sporadic ALS. A description of the molecular events underlying motor neuron degeneration in sporadic ALS, even particular short aspects of a long sequence of the degeneration process, would provide a beneficial therapeutic avenue for sporadic ALS by enabling development of a disease model simulating these molecular events.

In this study we further characterized the gene expression profiles of *DCTN1*, *EGR3*, *ACATN*, *DR5*, and *CCNC* in individual motor neurons and compared their expression levels with those of known motor neuron neurodegeneration markers, cytoplasmic accumulations of phosphorylated neurofilament H (pNF-H), ubiquitylated proteins, and with neuronal loss (5, 16–18). We found that changes in expression levels of these genes differentially reflect the motor neuron degeneration process, and, in particular, *DCTN1* is extensively downregulated before the appearance of these degeneration markers.

MATERIALS AND METHODS

Tissues From Patients with Amyotrophic Lateral Sclerosis and Control Patients

Specimens of lumbar spinal cord (L4–L5 segments) from 20 patients with sporadic ALS (11 male and 9 female) and 8 neurologically normal patients (4 male and 4 female) as controls were obtained at autopsy. The diagnosis of ALS was confirmed by El Escorial diagnostic criteria defined by the World Federation of Neurology and by histopathologic findings, particularly the presence of Bunina bodies (2, 3). All patients with ALS had sporadic ALS and showed no hereditary traits. Patients with a *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. The ages for patients with ALS and control patients were 63.3 ± 11.5 (mean \pm SD) (range 43–80) and 65.4 ± 12.7 (42–79) years, respectively, and the ALS illness duration was 2.9 ± 0.87 (1.2–4.3) years. The postmortem intervals to autopsy for patients with ALS

and control patients were 7.3 ± 3.9 (3–15) and 8.6 ± 3.2 (4–13) hours, respectively. There were no significant differences in either age or postmortem interval between the ALS and control groups. Among 20 patients, severe bulbar symptoms were seen in 14 cases, severe upper limb wasting in 17 cases, and severe lower limb wasting in 13 cases in the advanced stage. The upper motor neuron signs were seen in 13 patients, whereas others showed predominantly lower motor neuron signs. Most of the patients with ALS developed respiratory dysfunction in various degrees, with eventually resulted in respiratory failure in all patients, which was the cause of death. The cause of death in the control patients was pneumonia, cancer, stroke, or acute heart attack. Tissues were immediately frozen in liquid nitrogen and stored at -80°C until use. 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 techniques and further histologic assessments were performed.

Selection of Genes Examined Based on Our Previous Microarray Analysis in Laser-Captured Motor Neurons of Patients with Sporadic Amyotrophic Lateral Sclerosis

By using microarray technology combined with laser-captured microdissection, gene expression profiles of degenerating spinal motor neurons isolated from autopsied patients with sporadic ALS were previously reported (15). Three percent of genes examined were downregulated, and 1% were upregulated. We selected 5 genes (*DCTN1* associated with cytoskeleton/axonal transport *EGR3* as a transcription factor, and *ACATN*, *DR5* and *CCNC* as cell death-associated genes), which were most prominently down- or upregulated (15). These changes in gene expression were confirmed by cluster analyses of hierarchical clustering, self-organizing maps, and principal component analyses after logarithmic transformation, as motor neuron-specific gene expression changes distinctive from the spinal ventral horn as a whole, and their alterations were further quantitatively verified by real-time wide-ranging research activities and *in situ* hybridization. In addition, these 5 genes were chosen for the present study because they cover a wide range and represent different aspects of the functional hierarchy.

In Situ Hybridization

Frozen, 10- μm -thick spinal cord sections were prepared and immediately fixed in 4% paraformaldehyde. The sections were then treated with 0.1% diethylpyrocarbonate 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, GenBank accession numbers, probe positions (nucleotide [nt] number), and probe sizes (base pairs [bp]) were as follows: acetyl-CoA transporter (*ACATN*), D88152, nt 397–741, 345 bp; dynactin 1 (*DCTN1*), NM_004082, nt 2392–2774, 383 bp; death receptor 5 (*DR5*), NM_004082, nt 682–1070, 389 bp; and early growth response 3 (*EGR3*), NM_004430, nt 1433–1794, 362 bp. After prehybridization

the sections were hybridized with digoxigenin-labeled cRNA probes overnight at 45°C. The washed sections were incubated with alkaline phosphatase-conjugated, anti-digoxigenin antibody (Roche Diagnostics). The signal was visualized with nitro blue tetrazolium/5-bromo-4-chloro-3-indolyl phosphate (Roche Diagnostics). No hybridization signal was observed with the sense probe for the expression of each gene in spinal motor neurons.

Immunohistochemistry

Frozen, 10- μ m-thick spinal cord sections were prepared and immediately fixed in 4% paraformaldehyde. The sections were then blocked with 2% bovine serum albumin (Sigma) in Tris-buffered saline at room temperature for 20 minutes and incubated with either a monoclonal antibody against the phosphorylated epitope in the tail domain of neurofilament H (anti-SMI 31, 1:1000; Sternberger Monoclonals Inc., Lutherville, MD), anti-cyclin C antibody (1:200; Santa Cruz Biotechnology, Santa Cruz, CA), or anti-ubiquitin (1:1000; Santa Cruz Biotechnology) overnight at 4°C. Subsequent procedures were carried out using the EnVision+Kit/HRP (DAB) (DAKO, Glostrup, Denmark) according to the manufacturer's protocol.

Quantitative Assessment of Gene Expression Levels, Population of Residual Motor Neurons, and Cytoplasmic Accumulation of Phosphorylated Neurofilament H and Ubiquitylated Proteins

To assess gene and protein expression levels in spinal motor neurons, signal intensities of in situ hybridization and immunohistochemistry, respectively, were quantified using a CCD image analyzer (Zeiss Axiovert S100TV) as described previously (19, 20). Images of individual motor neurons on transverse sections of spinal cord with signals for *DCTN1*, *EGR3*, *ACATN*, *DR5*, or *CCNC* and pNF-H were captured at the desired magnification and stored with image software (Adobe Photoshop). Grey-scale levels in 65,536 gradations of the images were quantitatively analyzed with image analysis software (Image Gauge version 4.0, Fujifilm, Tokyo, Japan). Signal intensities were expressed as individual intracellular cytoplasmic signal levels (arbitrary absorbance units/ mm^2) of motor neuron for each gene of interest by subtracting the mean background levels of 3 regions of interest in each section. We also assessed motor neurons harboring ubiquitylated proteins on the anti-ubiquitin-stained sections. Motor neurons with dot-like accumulations, skein-like accumulations, or large inclusions of cytoplasmic ubiquitylated proteins were designated as positive for ubiquitylated protein accumulation.

To count the number of remaining spinal motor neurons, 10- μ m-thick serial sections were prepared from the lumbar segment of spinal cords and every 10th section was stained with the Klüver-Barrera technique. The ventral spinal horn was designated as the grey matter ventral to the line through the central spinal canal perpendicular to the ventral spinal sulcus, and the residual motor neuron population was defined as the number of relatively large-sized

ventral horn cells of 24.8 μ m or more in diameter with distinct nucleoli on 10 sections, as described previously (21). Our previous study demonstrated the neuron loss predominantly in the relatively large neurons in ALS (21).

The frequency of motor neurons showing changes in gene expression levels was assessed in at least 10 transverse sections from each of 20 patients with ALS and 8 control patients. The number of motor neurons with gene expression levels more than ± 2 SDs from the control levels was expressed as a percentage of motor neurons. Ten to > 100 motor neurons were examined for each individual case.

To investigate the correlation between gene expression levels and pathologic markers in an individual motor neuron we used consecutive transverse spinal cord sections. Ten sets of consecutive sections for each gene of interest were prepared from each patient and the correlations of gene expression levels with pNF-H accumulation levels and positive or negative ubiquitylated protein accumulations were assessed on individual motor neurons. This assessment was performed for 8 representative patients with ALS and 8 control patients whose sections were available for examination.

Statistical Analyses

Simple correlation tests were performed to assess the correlation of gene expression levels of *DCTN1*, *EGR3*, *ACATN*, and *DR5* and protein expression of *CCNC*, with the degree of pNF-H accumulation in individual motor neurons. This test was also applied to assess the correlation of the gene expression changes with the numbers of residual motor neurons. Mann-Whitney U tests were used to compare gene expression levels among the motor neurons that were either positive or negative for ubiquitylated proteins in patients with ALS and in control patients. Significance levels were set to $p < 0.05$.

RESULTS

Differential Frequencies of Gene Expression Changes in Residual Motor Neurons: *DCTN1* Is Highly Downregulated

Among the genes examined, *DCTN1* and *EGR3* were downregulated in the vast majority of spinal motor neuron populations in most patients (Fig. 1A, B). In 15 of 20 patients, all of the residual motor neurons had reduced *DCTN1* expression compared with controls (Fig. 1B). Ten of the 20 patients showed downregulation of *EGR3* in all residual neurons (Fig. 1B). *ACATN*, by contrast, was upregulated in all residual motor neurons in only 8 of 20 patients (Fig. 1A, B). *DR5* was upregulated in subpopulations of motor neurons, whereas only 4 patients had upregulated gene expression in all of the residual neurons (Fig. 1A, B). Nuclear accumulation of *CCNC* protein assessed by immunohistochemistry was observed in only a small percentage of motor neurons in most patients (Fig. 1A, B). There were no patients with *CCNC* nuclear accumulation in all of the residual neurons (Fig. 1B). Cytoplasmic accumulation of pNF-H was seen in more than half of the residual motor neurons in most of the patients (Fig. 1A). Quantitative assessment showed

that in 9 of the 20 patients, all of the residual motor neurons were positive for pNF-H (Fig. 1B). Thus, the frequency of residual motor neurons with gene up- or downregulation was markedly different depending on the individual gene. This

gene-dependent differential gene expression among the residual motor neurons is clearly demonstrated in Figure 1C. Two consecutive transverse sections were subjected to in situ hybridization with different gene probes. *DCTN1*

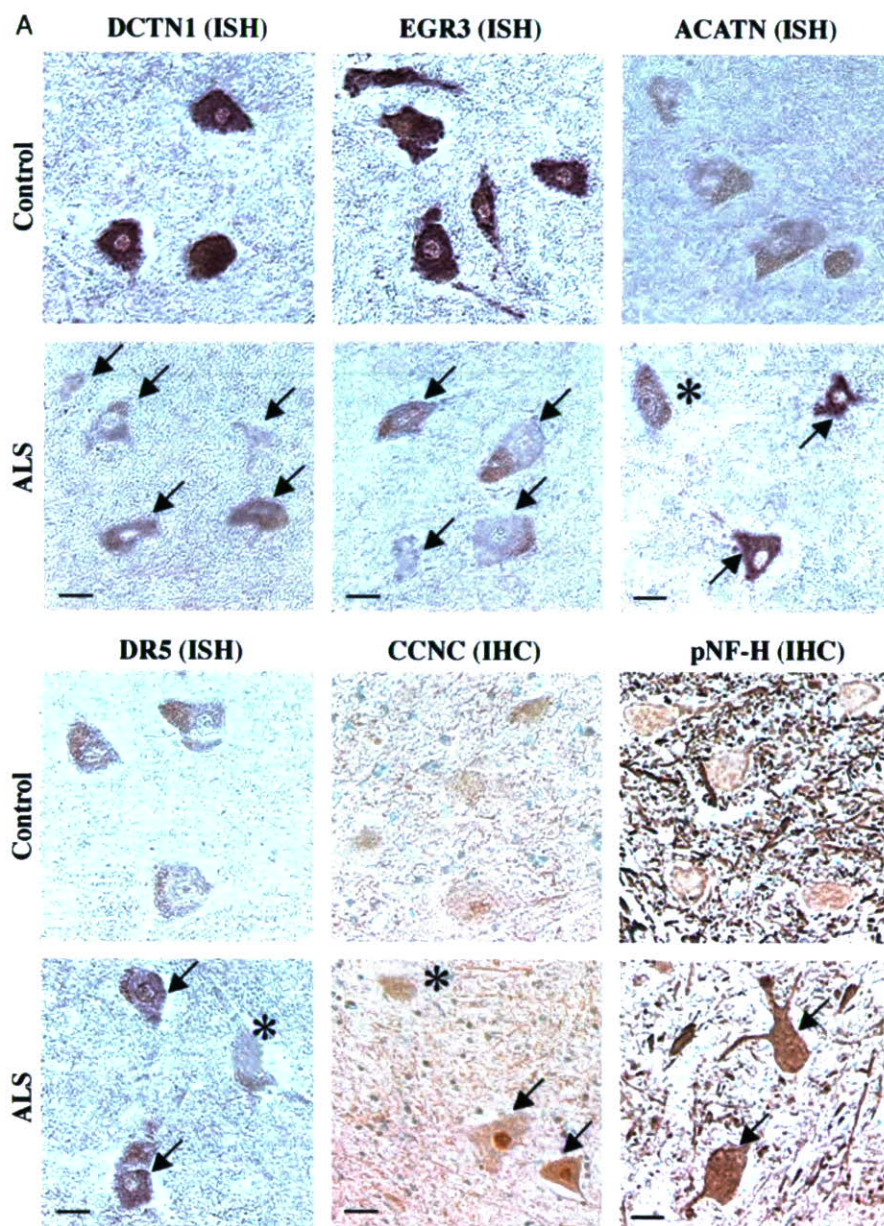


FIGURE 1. In situ hybridization (ISH) and immunohistochemistry (IHC) in spinal motor neurons. **(A)** Representative ISHs are shown for dynactin 1 (*DCTN1*), early growth response 3 (*EGR3*), acetyl-CoA transporter (*ACATN*), and death receptor 5 (*DR5*). The antisense probe detects positive signals for the expression of each gene in spinal motor neurons for patients with amyotrophic lateral sclerosis (ALS) and/or control patients, but the sense probe does not (15). RNase treatment before the hybridization abolished the hybridization signals. IHC was performed for cyclin C (*CCNC*) and phosphorylated neurofilament H (pNF-H). The nuclear staining of *CCNC* was prominent in ALS motor neurons. Lipofuscin granules are seen as yellowish granules. **(B)** Percentage of motor neurons with gene expression or protein accumulation changes, relative to control levels, among the residual motor neurons in 20 patients with ALS. The quantitative analyses of gene expression and frequency assessments are described in the Materials and Methods section. **(C)** ISH of 2 genes in consecutive sections demonstrates the relationship between up- and downregulated genes in individual motor neurons. *DCTN1* was downregulated to a great extent in all the remaining motor neurons in ALS, whereas *ACATN* and *DR5* were upregulated in only a subpopulation of motor neurons. Arrows denote motor neurons with gene expression changes, and asterisks denote those without changes compared with controls. Scale bars = 25 μ m.