

11:40~12:25

セッションⅢ【遺伝子治療】

座長：野本 明男（東京大学微生物学）

7. AAV ベクター脳内投与における安全性

○村松 慎一¹⁾、中野 今治¹⁾、水上 浩明²⁾、小澤 敬也²⁾、
島崎久仁子³⁾

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- 2) 自治医科大学遺伝子治療
- 3) 自治医科大学神経脳生理

8. ALS 病態進行遅延を目指したポリオウイルスベクターの開発

千葉 妃織、五十嵐博子、大岡 静衣、○野本 明男^{のもと あきお}
東京大学大学院医学系研究科微生物学講座

9. HGF による ALS 依存的なグリオシスの制御機構の解析

— ALS に対する最適な HGF 治療法の確立に向けて —

○大谷 若菜¹⁾、船越 洋¹⁾、角山 圭一^{1), 2)}、中村 敏一¹⁾

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- 2) 姫路独協大学薬学部

12:25~13:20

***** 昼食・班会議 *****

13:20~14:00

特別講演

座長：祖父江 元(名古屋大学神経内科)

【オートファジー (Self-eating) と神経変性】

田中 啓二(東京都臨床医学総合研究所・先端研究センター)

14:00~14:45

セッションⅣ 【再生治療】

座長：糸山 泰人(東北大学神経内科)

10. 胚性幹細胞、神経幹細胞を用いた神経系の再生医学

○岡田 洋平¹⁾、松本 有史^{1), 3)}、熊谷玄太郎^{1), 4)}、
中村 雅也^{1), 5)}、戸山 芳昭⁵⁾、岡野 栄之¹⁾

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- 3) 東北大学大学院医学系研究科神経内科
- 4) 弘前大学医学部整形外科
- 5) 慶應義塾大学医学部整形外科

11. EGF+FGF2 髄腔内投与による ALS モデルマウス脊髄での内在性未分化神経幹細胞および神経前駆細胞増殖の試み

阿部 康二、○太田 康之、永井真貴子、武久 康、
永田 哲也、倉田 智子、森本 展年、宮崎 一徳、
池田 佳生、神谷 達司
岡山大学医学部神経内科

12. ALS ラットモデル脊髄におけるコンドロイチン硫酸の役割

糸山 泰人¹⁾、○割田 仁¹⁾、水野 秀紀¹⁾、青木 正志¹⁾、
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- 2) 慶應義塾大学医学部生理学

14:45~15:30

セッションV 【病態モデル】

座長：郭

伸（東京大学神経内科）

13. ADAR2 コンディショナルノックアウトマウスにおける運動ニューロン死と孤発性 ALS

○^{ひ で やまたく と}日出山拓人¹⁾、山下 雄也¹⁾、辻 省次¹⁾、高橋 良輔²⁾、
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3) 共立薬科大学薬理学

4) 共立薬科大学基礎生物学

14. Angiogenin を標的とした筋萎縮性側索硬化症モデルマウス作製の試み

○^{ささぐり ひろき}笹栗 弘貴¹⁾、横田 隆徳¹⁾、山本 由紀¹⁾、安齋 政幸²⁾、
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15. 孤発性 ALS 線虫モデルの開発

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VI. 研究者一覽

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「筋萎縮性側索硬化症の画期的診断・治療法に関する研究」班（課題番号 H17-難治-一般-044）

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VII. 研究成果の刊行物・別刷

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

Yue-Mei Jiang, PhD, Masahiko Yamamoto, MD, Fumiaki Tanaka, MD, Shinsuke Ishigaki, MD, Masahisa Katsuno, MD, Hiroaki Adachi, MD, Jun-ichi Niwa, MD, Manabu Doyu, MD, Mari Yoshida, MD, Yoshio Hashizume, MD, and Gen Sobue, MD

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 ubiquitylated 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 ubiquitylated 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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Drs. Jiang and Yamamoto contributed equally to this work.

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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), ubiquitinated 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/mm²) 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*

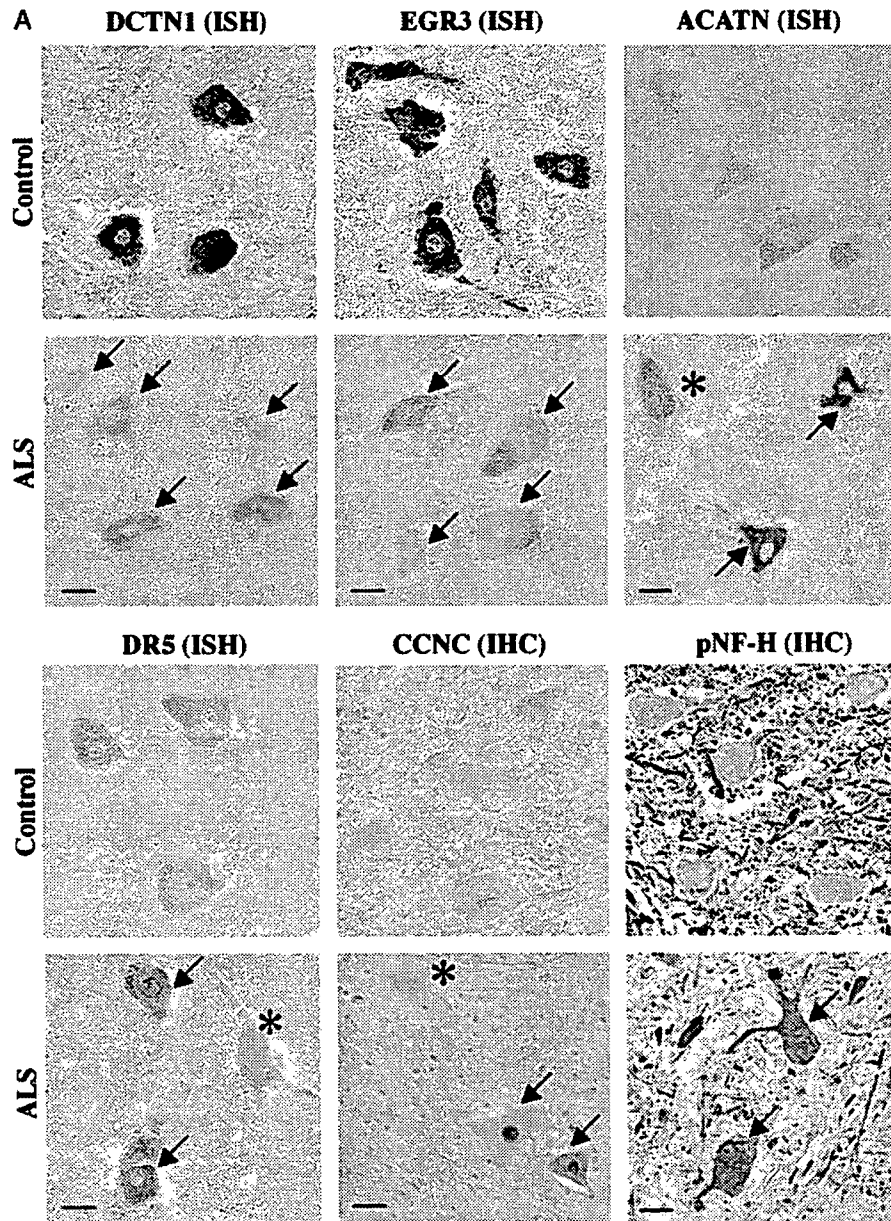


FIGURE 1. In situ hybridization (ISH) and immunohistochemistry (IHC) in spinal motor neurons. **(A)** Representative ISHs are shown for dynactin 1 (*DCTN1*), early growth response 3 (*EGR3*), acetyl-CoA transporter (*ACATN*), and death receptor 5 (*DR5*). The antisense probe detects positive signals 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.

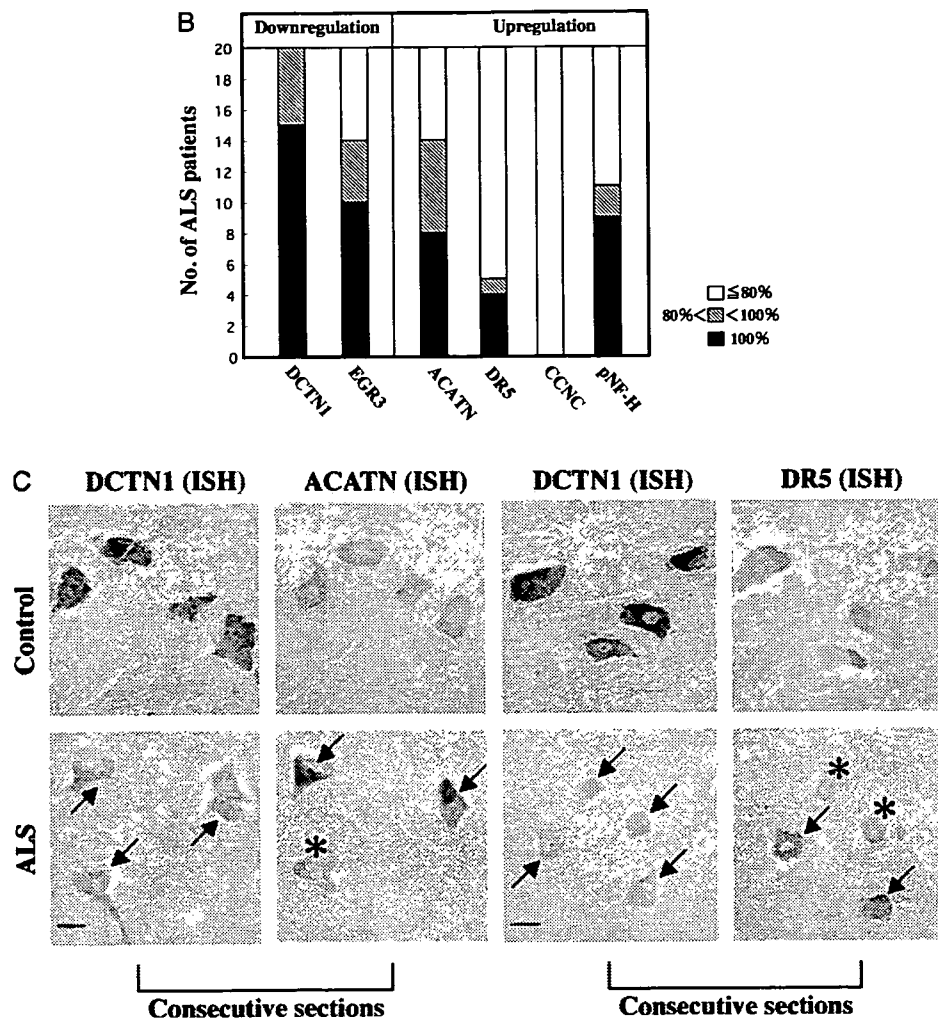


FIGURE 1. (continued)

expression was reduced in all the neurons in each panel, whereas some of the residual motor neurons showed unchanged *ACATN* and *DR5* gene expression (Fig. 1C). Moreover, *DCTN1* expression was preserved in neurons other than motor neurons such as those in the dorsal nucleus of Clarke and the intermediolateral nucleus in spinal cords, Purkinje cells of the cerebellum and cortical neurons in the occipital cortex in patients with ALS as well as control patients (data not shown). These findings indicate that, among the genes examined, downregulation of *DCTN1* was specific and extensive in the spinal motor neurons, whereas cell death-related genes such as *ACATN* and *DR5*, and the protein *CCNC* were upregulated in only subpopulations of motor neurons.

Gene Expression Changes Are Differentially Correlated With the Population of Residual Motor Neuron: *DCTN1* is Markedly Downregulated Even in Patients With Relatively Well-Preserved Motor Neuron Populations

When the numbers of motor neurons with given gene expression or protein accumulation changes were compared with the numbers of residual motor neurons in the

20 patients, changes in *DR5*, pNF-H, *EGR3*, *ACATN* and *DCTN1* were correlated with the residual motor neuron population ($r = 0.49-0.83$, $p < 0.05$ to 0.0001 , Fig. 2). Among them, *DCTN1* expression was most prominently downregulated, even in patients with relatively well-preserved motor neurons, suggesting that *DCTN1* downregulation may be occurring even in early stages of the disease. The changes in expression of *EGR3*, *ACATN*, and *DR5* in patients with well-preserved motor neuron populations were relatively mild compared with that of *DCTN1* (Fig. 2). The change in *DR5* expression was less correlated with the residual motor neuron population than that of other genes.

Gene Expression Changes are Differentially Correlated With the Extent of Motoneuronal Cytoplasmic Phosphorylated Neurofilament H Accumulation: *DCTN1* and *EGR3* Are Markedly Downregulated Before Phosphorylated Neurofilament H Accumulation

The correlation of gene expression and pNF-H accumulation, a marker of neuronal degeneration, in individual motor

neurons was assessed on consecutive sections (Fig. 3A, B). *DCTN1* and *EGR3* downregulations were both marked and independent of the degree of cytoplasmic pNF-H accumulation (Fig. 3B), implying that these genes were widely downregulated even in motor neurons with little or no pNF-H accumulation. By contrast, levels of *ACATN*, *DR5*, and *CCNC* ranged from just above the control levels to much higher levels and were well correlated with the degree of cytoplasmic pNF-H accumulation ($r = 0.48-0.60$, $p < 0.001$ to 0.0001 , Fig. 3B).

These observations indicate that downregulation of *DCTN1* and *EGR3* occurs before the appearance of the neurodegeneration marker pNF-H and thus is a relatively early event in the neurodegeneration process. In contrast, the changes in *ACATN* and *DR5* expression were milder than those in *DCTN1* and *EGR3*, but proportional to pNF-H accumulation, suggesting that their upregulation is a relatively late event, occurring after the appearance of the neurodegeneration marker pNF-H.

Gene Expression Changes Occur Before Appearance of Motoneuronal Cytoplasmic Accumulation of Ubiquitylated Proteins: *DCTN1*, *EGR3*, *ACATN* and *DR5* Are Changed Even in the Motor Neurons Without Ubiquitylated Protein Accumulation

The correlation of gene expression with cytoplasmic accumulation of ubiquitylated protein in individual motor neurons was assessed on consecutive sections (Fig. 4A, B). In patients with ALS, *DCTN1* and *EGR3* were markedly downregulated, and *ACATN* and *DR5* were upregulated in motor neurons both with and without cytoplasmic accumu-

lation of ubiquitylated proteins (Fig. 4B). However, the degree of downregulation or upregulation was significantly greater in the motor neurons with ubiquitylated protein accumulation compared with those without (Fig. 4B), suggesting that cytoplasmic accumulation of ubiquitylated proteins may be partially correlated to expression changes of *DCTN1*, *EGR3*, and *ACATN*. However, because the expression of these genes changed markedly even in the motor neurons without ubiquitylated proteins, it would imply that cytoplasmic ubiquitylated protein accumulation is a rather late event in the process of motor neuron degeneration.

We further examined the correlation between these 4 gene expression levels and subgroups of motor neurons with 3 different types of ubiquitylated protein accumulation (i.e. dot-like accumulations, skein-like accumulations, and large round inclusions of ubiquitylated proteins), and found that the expression levels of all 4 genes were changed before all types of ubiquitylated protein accumulation (data not shown).

DISCUSSION

We demonstrated that *DCTN1*, *EGR3*, *ACATN*, *CCNC*, and *DR5* are differentially expressed in the residual motor neurons in sporadic ALS. Furthermore, the expression levels of these genes are differentially correlated with the levels of pathologic markers, the numbers of residual motor neurons, and the degrees of cytoplasmic accumulation of pNF-H and ubiquitylated protein, which are considered to reflect degeneration processes of motor neurons in sporadic ALS (5, 16–18, 22). These 5 genes were selected from those showing the most marked and specific altered expression levels among 4,845 genes that we had previously assessed in

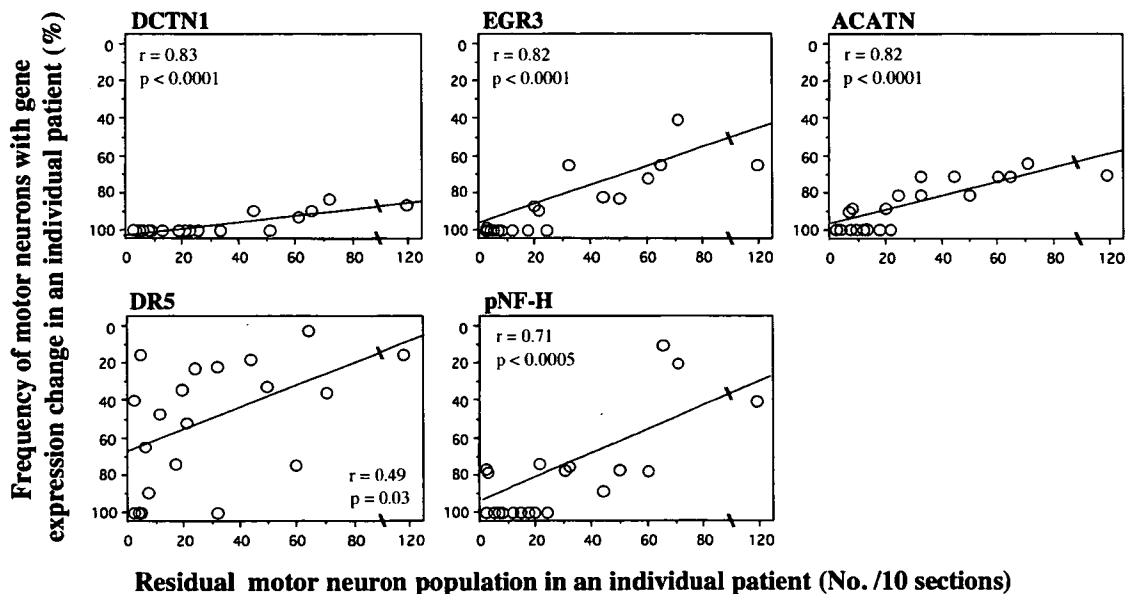


FIGURE 2. Frequency of motor neurons with gene expression change correlates with the extent of motor neuron loss. The correlation analyses between frequencies of motor neurons with gene expression changes (relative to controls) for *DCTN1*, *EGR3*, *ACATN*, *DR5*, and pNF-H and numbers of residual motor neurons were performed in the 20 patients with amyotrophic lateral sclerosis. The mean number of motor neuron patients in controls was 195 ± 17 (\pm SD) (range 176–225)/10 sections ($n = 8$). The values are inversely ordered on the y axis.

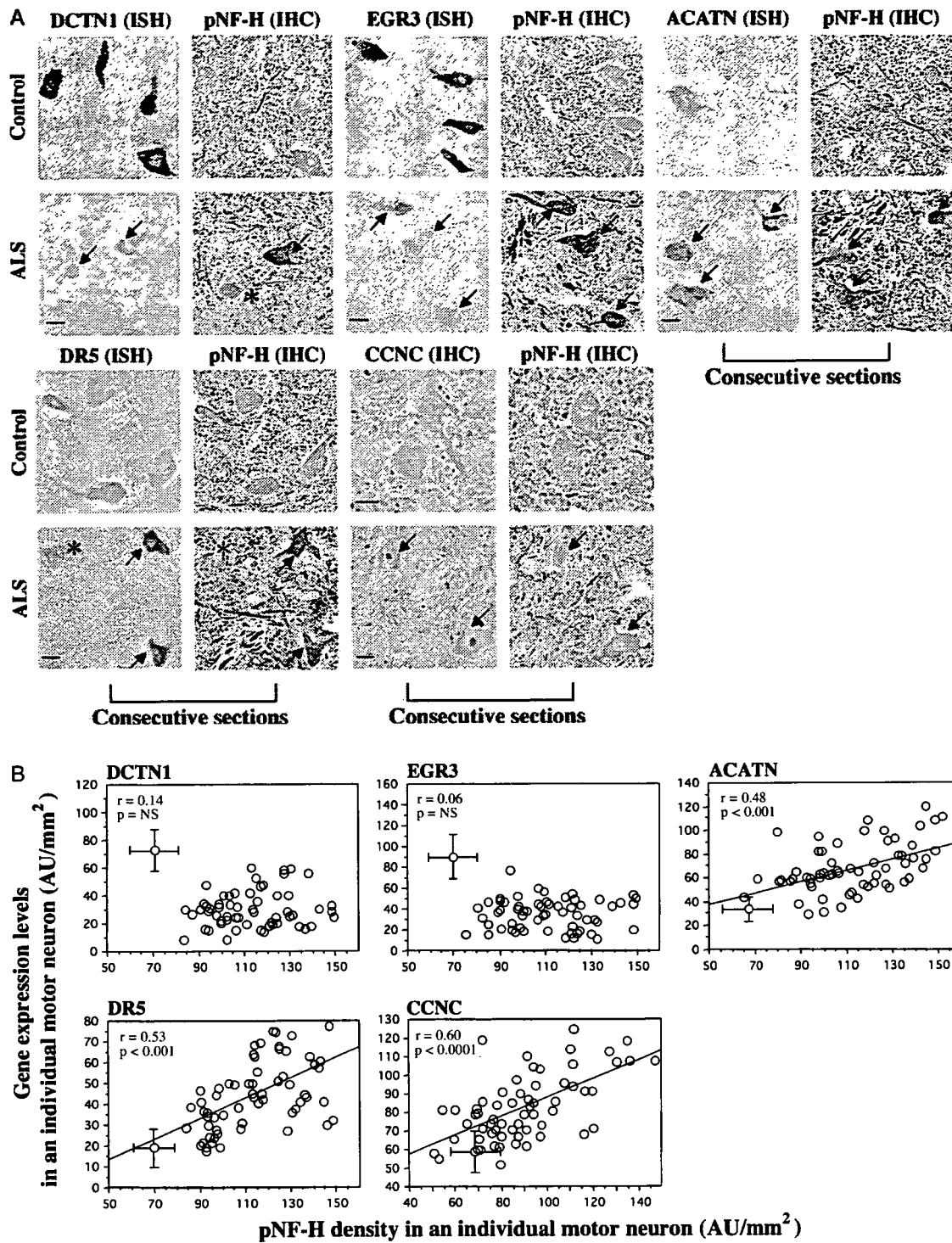


FIGURE 3. Gene expression and cytoplasmic phosphorylated neurofilament H (pNF-H) accumulation. **(A)** Gene expressions and pNF-H accumulation in identical motor neurons. Representative in situ hybridization (ISH) for *DCTN1*, *EGR3*, *ACATN*, and *DR5*, and immunohistochemistry (IHC) for *CCNC* are shown compared with pNF-H staining (IHC) on consecutive spinal cord sections from patients with amyotrophic lateral sclerosis (ALS) and control patients. The accumulation of cytoplasmic pNF-H was prominent in ALS motor neurons. Arrows denote motor neurons with gene expression or protein accumulation changes compared with control patients, and asterisks denote those with unchanged levels. Scale bars = 25 μ m. **(B)** Expression levels of genes were compared with the level of pNF-H accumulation in individual motor neurons. Expression levels of *ACATN*, *DR5*, and *CCNC* were correlated with the accumulation of pNF-H, whereas those of *DCTN1* and *EGR3* were not. Consecutive transverse spinal cord sections were assessed from 8 representative patients with ALS. The control values for gene and protein expression levels and the accumulation of pNF-H are shown as means \pm SD for 8 control cases. AU, arbitrary absorbance units; NS, not significant.

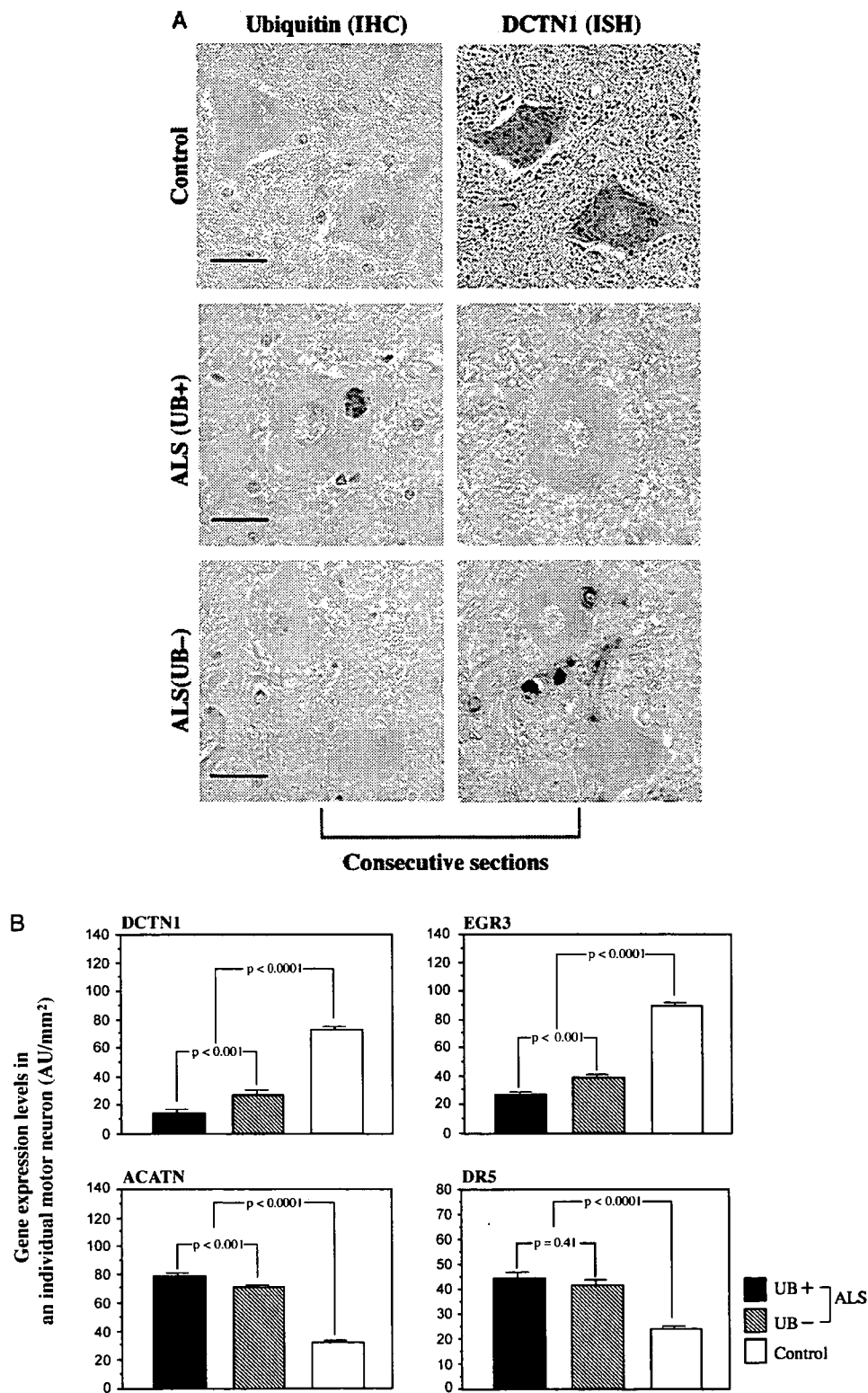


FIGURE 4. Gene expression and cytoplasmic accumulation of ubiquitylated proteins. **(A)** Representative *DCTN1* in situ hybridization (ISH) and ubiquitin (UB) immunohistochemistry (IHC) in identical motor neurons of consecutive sections are shown in patients with amyotrophic lateral sclerosis (ALS) and control patients. Scale bars = 25 μ m. **(B)** Expression levels of genes were compared among the motor neurons that were either positive (n = 56) or negative (n = 175) for ubiquitylated proteins in 8 representative patients with ALS and those (n = 209) in 8 control patients. Expression levels of *DCTN1*, *EGR3*, and *ACATN* were significantly different in ubiquitin-positive neurons compared to ubiquitin-negative neurons in ALS, whereas that of *DR5* was not. The values are shown as means \pm SE. AU, arbitrary absorbance units.

a differential gene expression profile in isolated, laser-captured motor neurons from patients with sporadic ALS (15). Thus, we consider these gene expression levels to reflect most significantly the molecular events of neurodegeneration processes in motor neurons.

We selected 3 pathologic features as markers for neurodegeneration: the residual population of spinal motor neurons, cytoplasmic accumulation of pNF-H, and cytoplasmic accumulation of ubiquitylated proteins. Cytoplasmic accumulation of pNF-H has been demonstrated to occur in ALS motor neurons, even when they have normal morphologic appearances, and is thought to be a consequence of impaired axonal transport (5, 23–25). Hence, it is considered to be a histologic marker indicating neuronal degeneration and dysfunction before neuronal death (5, 16, 17). Hence, the accumulation of pNF-H is a rather early event in the motor neuron degeneration process. The presence of ubiquitylated proteins in the motor neuron cytoplasm has also been identified as a histopathologic marker of motor neuron degeneration (18). Ubiquitylated inclusions are thought to be aggregated, modified, and misfolded proteins that are ubiquitylated by motor neuron ubiquitin ligase (9). Although ubiquitylated, round inclusions are considered to occur in rather advanced stages of degeneration, it is not known whether dot-like and skein-like small faint ubiquitylated accumulations occur in the early stages of neurodegeneration.

The striking observation was that *DCTN1* expression was the most widely and most strongly downregulated among the genes examined in the residual motor neuron population, and was also severely downregulated even in the patients with large populations of motor neurons and in the motor neurons without pNF-H accumulations. The dramatic change in *DCTN1* in ALS seems to be specific for motor neurons because *DCTN1* expression was preserved in neurons in the dorsal nucleus of Clarke and the intermediolateral nucleus in the spinal cord, Purkinje cells of the cerebellum, and cortical neurons in the occipital cortex in patients with ALS. These observations suggest that *DCTN1* downregulation is the specific molecular event that occurs before the appearance of these pathologic markers, and is, therefore, a rather early event in the molecular sequences of neurodegeneration, at least among the events related to the genes examined. *DCTN1* codes for a protein that is a component of the retrograde transport protein complex with dynein (26, 27) and has been identified as a causative gene for human lower motor neuron disease (28, 29). Furthermore, it has been suggested that polymorphic amino acid substitution is a modifying factor accelerating pathogenesis and progression of sporadic ALS (30). A mouse model overexpressing dynamin, which eventually results in late-onset progressive motor neuron degenerative disease, demonstrates the involvement of the dynactin-dynein complex (23). Two dominant point mutations in dynein cause progressive motor neuron degeneration in mice (31). These findings suggest that retrograde axonal transport involving the dynactin-dynein complex is strongly associated with motor neuron dysfunction and eventual motor neuron degeneration (32). By taking into account these findings, our present results

strongly suggest that the downregulation of *DCTN1* in motor neurons may play a significant role in this process and may lead to the subsequent sequences of motor neuron degeneration in sporadic ALS. This hypothesis should be tested by further study on another cohort of patients with ALS and by in vitro and in vivo experiments.

Another interesting observation was that *ACATN*, *DR5*, and the *CCNC* protein were upregulated in subpopulations of residual motor neurons and that their upregulation was well correlated to the accumulation of pNF-H and the degree of motor neuron loss. *ACATN* functions as a cofactor for acetylation of gangliosides and has been demonstrated to suppress proapoptotic activity of GD3 ganglioside (33–36). In the *Drosophila* model, knockout of *ACATN* leads to a lethal phenotype owing to brain damage (Y. Hirabayashi, personal communication, 2007). *DR5* is another cell death-related receptor as a member of the tumor necrosis factor (TNF) receptor family (TNFR10b) (37). *CCNC* is a cell cycle regulator protein and increases in *CCNC* expression are associated with its nuclear translocation, as was also demonstrated in this study (38). The aberrant activation of cell cycle regulators has been proposed as a pathway inducing motor neuron death in ALS (39, 40). Moreover, upregulated *DR5* was colocalized in motor neurons with *CCNC* nuclear translocation and also in those with downregulated TNFR-associated factor 6 (TRAF6) in our study (data not shown). The downregulated TRAF6, which is associated with nuclear factor- κ B activation for cell survival, may not be able to sequester the overexpressed *DR5* signaling, leading to a pathway of cell death (41). Taken together, expressions of these genes are involved in the cell death-related pathway. Upregulation of these genes occurs in subpopulations of motor neurons in parallel to or after the emergence of histopathologic markers such as pNF-H accumulation and motor neuron loss, suggesting that they occur in a relatively late phase of neurodegeneration, especially compared with *DCTN1* downregulation. The observation that active motor neuron degeneration processes for cell death that are probably mediated via cell death-related gene expression, such as *ACATN*, *DR5* and *CCNC* upregulation, occur in subpopulations of the remaining motor neurons with sustained *DCTN1* downregulation is consistent with our previous results that motor neurons in the remaining motor neuron pool randomly enter into the active degeneration process even up to the terminal stage in sporadic ALS (42).

The appearance of ubiquitylated protein accumulations or ubiquitylated inclusions is one of the hallmarks of motor neuron degeneration in sporadic ALS (18). In this study, however, the expression levels of *DCTN1*, *EGR3*, *ACATN*, and *DR5* were significantly altered before the appearance of ubiquitylated protein accumulations. Because the morphologic features of cytoplasmic ubiquitylated protein accumulations vary considerably, ranging from fine dot-like or skein-like accumulations to large inclusions, the simple assessment of ubiquitin-positive or negative materials may not be sufficient to identify neurodegeneration. However, even when we assessed ubiquitylated accumulation in a more precise manner, the expressions of these 4 genes were markedly altered independent of the appearance

of ubiquitylated protein accumulations. These findings suggest that appearance of ubiquitylated protein accumulation is a later pathologic event, occurring after the expressions of a number of genes are already altered. Alternatively, we may speculate that ubiquitylated protein accumulation is a secondary consequence of the series of molecular events accompanied by the alterations of a wide-range of gene expressions.

The present study also demonstrates that microarray analyses on laser-captured motor neurons followed by histopathologic analyses on tissues from large numbers of patients can provide significant information about molecular events in motor neuron degeneration and dysfunction in patients with sporadic ALS. The most serious problem in developing effective therapy for sporadic ALS is the lack of animal or cell models that properly reflect the motor neuron degeneration processes of sporadic ALS or even certain aspects of them. This is not a longitudinal and chronologic analysis of degeneration process in identical motor neurons, and it is not clear whether the changes seen in the present study represent the primary causes or secondary effects in the disease process because of the inherent problem of studying human disease using autopsy materials. However, we may be able to speculate that these results of human studies reflect the molecular sequence of motor neuron degeneration of ALS. Our present approach would provide an avenue for developing new molecular-targeted therapies for sporadic ALS by creating animal or cell models mimicking the molecular events seen in human patients.

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

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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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[§] 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.

Disulfide Linking and Ubiquitylation of Mutant SOD1

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'-CGAAGCCGTGTCCGTGCTGAAGGGC-3' and 5'-GCCCTTCAGCACGGACACGGCCTTCG-3' for C6S; 5'-GATAATACAGCAGGCTCTACCAGTGCAGGTCC-3' and 5'-GGACCTGCACTGGTAGAGCCTGCTGTATTATC-3' for C57S; 5'-CTCAGGAGACCA-TTCCATCATTGGCCGCAC-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 $\mu\text{g}/\text{ml}$ 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 μM (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 μM 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 $^{\circ}\text{C}$. Supernatants were used for Western blotting analysis.

Immunoprecipitation and Western Blotting Analysis—5 $\times 10^5$ 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 $^{\circ}\text{C}$ 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 $^{\circ}\text{C}$. 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 μg 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- μm cellulose acetate membranes (Sartorius, Gottingen, 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 $^{\circ}\text{C}$ 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- μm nitrocellulose membranes (Bio-Rad) and probed with anti-Myc or anti- α -tubulin antibodies.

Neurotoxicity Analysis and Quantification of SOD1 Aggregates—2 $\times 10^4$ Neuro-2a cells were grown overnight on four-chamber, collagen-coated slides (Nalge Nunc, Rochester, NY) and then transfected with 0.2 μg 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 μM 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 $\times 10^3$ Neuro-2a cells were grown in 96-well collagen-coated plates overnight, and then transfected with 0.1 μg of pEGFP-N1-SOD1 or pcDNA3.1/MycHis-SOD1, with or without 0.1 μg of pcDNA4/HisMax-Dorfin. pcDNA4/HisMax

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.

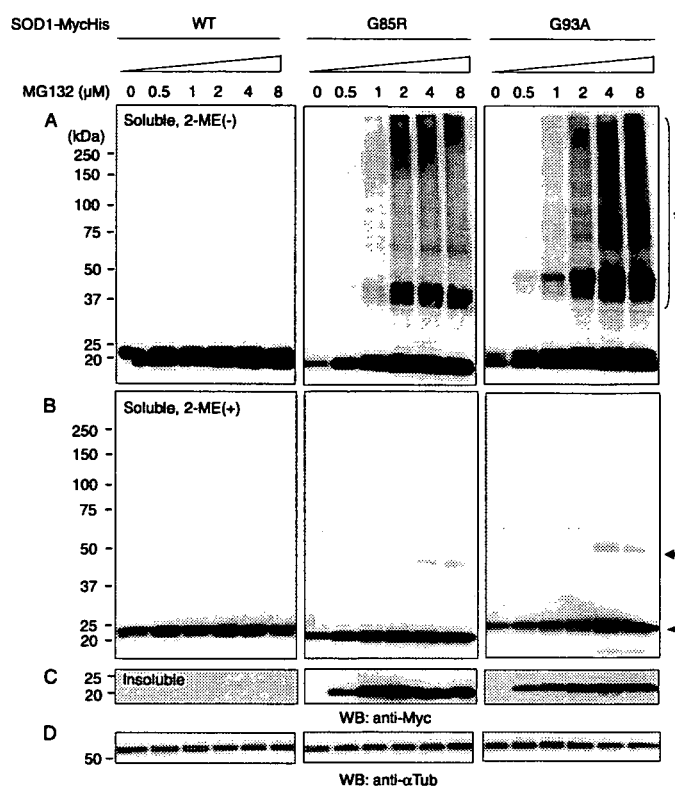


FIGURE 1. Proteasome inhibition leads to the accumulation of intermolecular disulfide bond-linked mutant SOD1. Neuro-2a cells expressing wild-type (WT), G85R, and G93A mutant SOD1-MycHis were treated with MG132 for 24 h at the indicated concentrations. Soluble fractions were analyzed by SDS-PAGE in the 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