cells, respectively (data not shown). After 4 days of proliferating culture, the SM/C-2.6-positive fraction expressed MyoD, a typical myogenic transcription factor (Fig. 2a), while the negative fraction did not (Fig. 2d). The culture medium was then changed to differentiation medium, and the cells were cultured for an additional 7 days and examined for the expression of muscle-related molecules. Many myotubes were formed in the SM/C-2.6-positive fraction and were

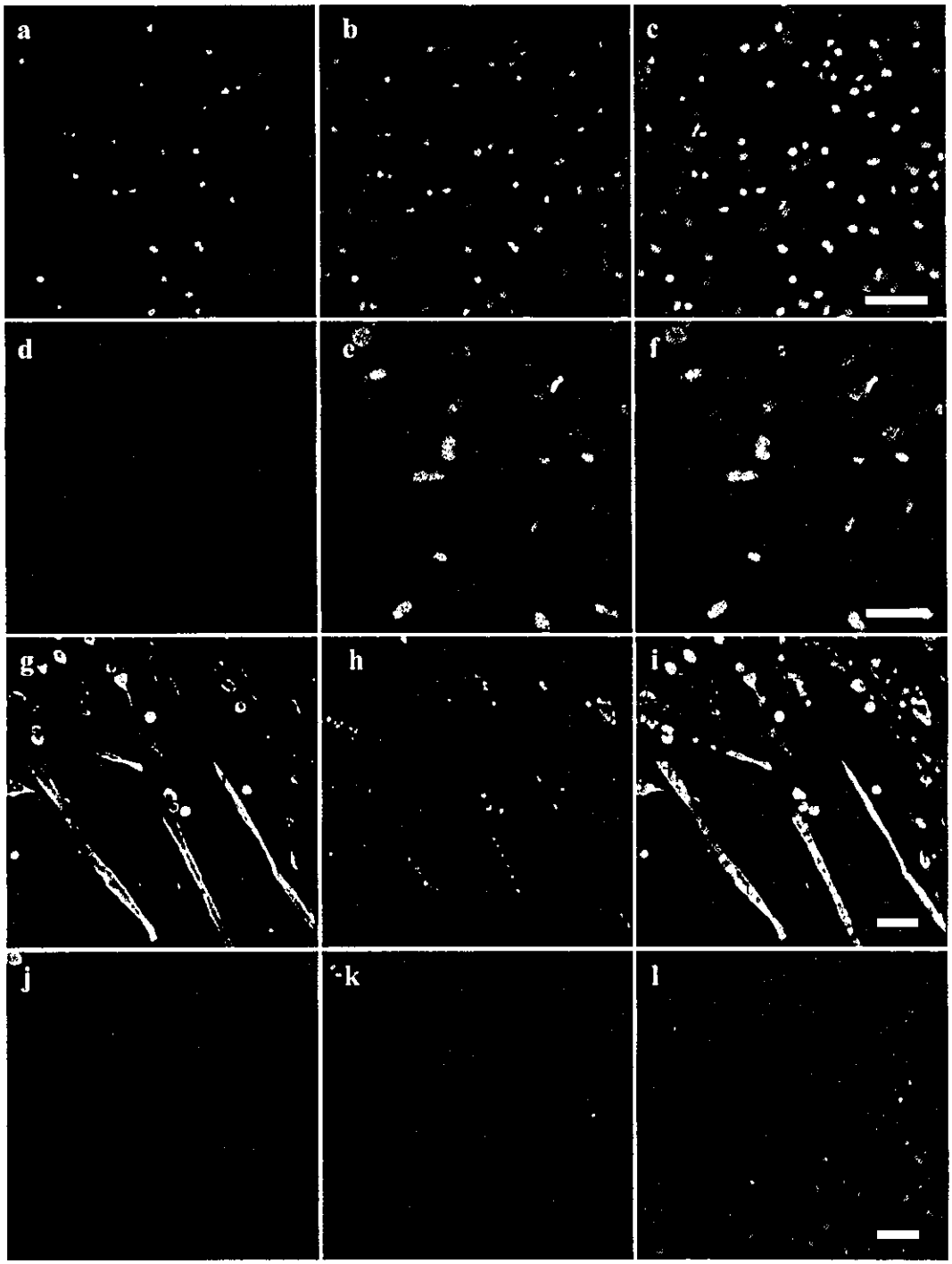

Fig. 2. SM/C-2.6-positive cells differentiate to myotubes in vitro. Freshly isolated single cells from neonatal (day 2) muscles were separated by their reactivity with SM/C-2.6. SM/C-2.6-positive cells compose approximately 25% of the cells in neonatal muscle. The positively and negatively sorted fractions contain 90% and 1% SM/C-2.6-positive cells, respectively. Positively (a–c) and negatively (d–f) sorted cells were cultured for 4 days under proliferating conditions, and the expression of MyoD was determined. Positively sorted cells became MyoD$^+$ (a). b and e; DAPI, c and f; merged. Positively (g–i) and negatively (j–l) sorted cells were then cultured for an additional 7 days under differentiating conditions. Positively sorted cells formed myotubes and became desmin$^+$ (g). Note that lines of MyoD$^+$ myonuclei formed in the newly generated myotubes (h). i and l, merged. Scale bars: 50 μm (a–i).

stained with desmin (Fig. 2g), a muscle-specific intermediate filament protein. MyoD-positive signals formed lines in the satellite cell-derived myonuclei of the myotubes (Fig. 2h), while no such structures were observed in the negative fraction (Figs. 2j–l). These results suggest that SM/C-2.6 specifically detects skeletal muscle satellite cells.

SM/C-2.6-positive cells differentiate into myofibers in vivo

We then examined the satellite cell activity of SM/C-2.6-positive cells in vivo. SM/C-2.6-positive cells were sorted from adult GFP-Tg mice, injected into the TA muscles of *mdx* mice, and the cryosections were examined 2 weeks after transplantation. The SM/C-2.6-positive fraction gave rise to several GFP-positive fibers (Figs. 3a and e), but the negative fraction did not (Figs. 3c and g). Then, we further confirmed that GFP-positive myofibers (Fig. 3i) were positive for dystrophin expression (Figs. 3j and k). Therefore, the SM/C-2.6-positive fraction includes satellite cells.

Age-related changes in SM/C-2.6-positive muscle satellite cells

SM/C-2.6-positive satellite cells were examined in C57BL/6 mice of different ages. Neonatal mice (postnatal day 2) contain approximately 25% satellite cells among the muscular mononuclear cells (Fig. 4a), and this amount declines with age: 13.1% at 4 weeks and 8.9% at 8 weeks of age (Figs. 4b and c). The results agree with earlier studies in which the number of satellite cells was seen to decline with age [13,36–38].

SM/C-2.6 detects neither M-cadherin nor c-met

The antigen recognized by SM/C-2.6 remains to be determined. As shown earlier (Figs. 1Bd and e), SM/C-2.6-positive cells co-express M-cadherin. C2/4 (C2C12) cells express both SM/C-2.6 and M-cadherin (Figs. 5a and b). To investigate whether SM/C-2.6 detects M-cad-

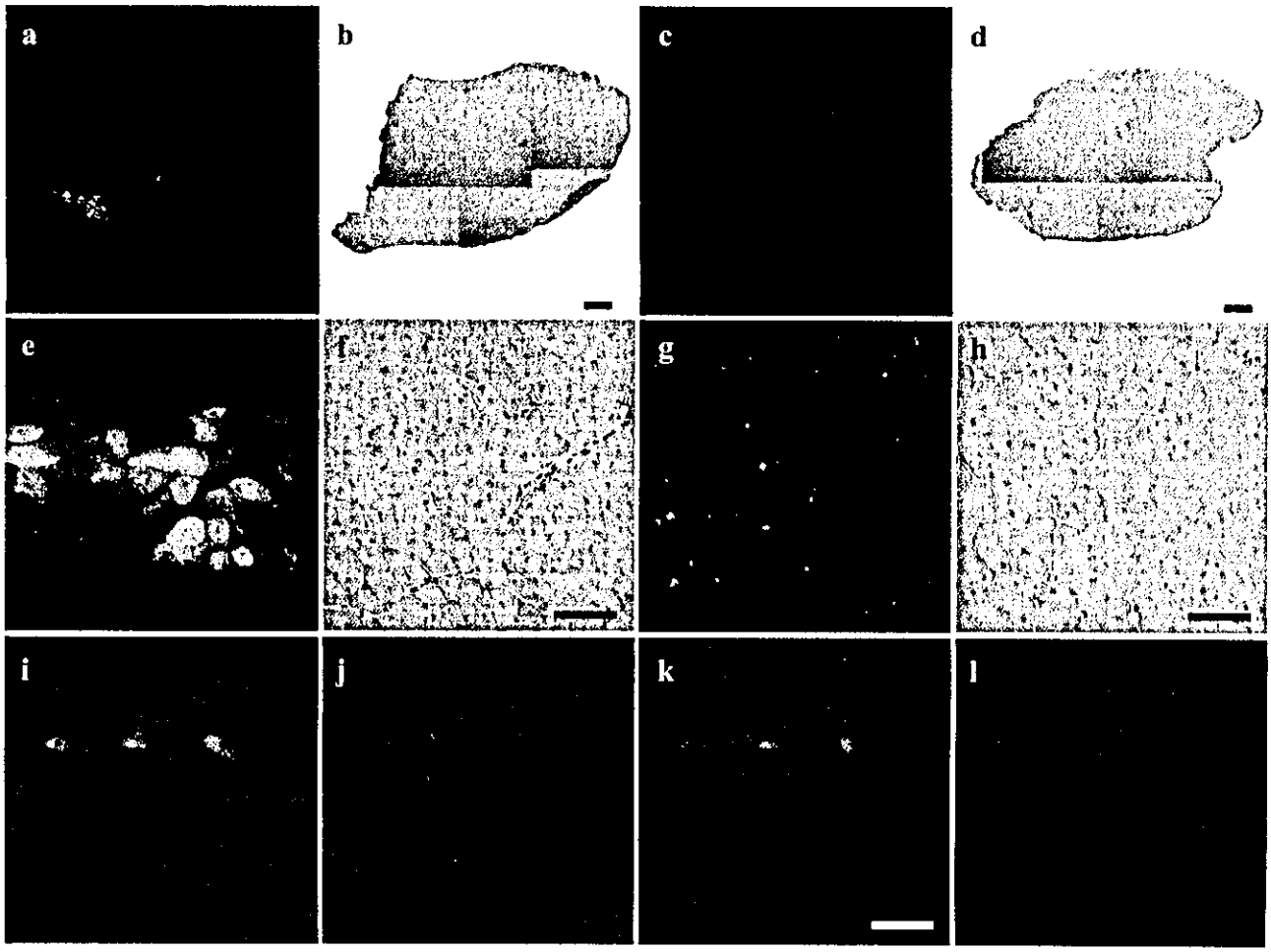

Fig. 3. SM/C-2.6-positive cells differentiate into myofibers in vivo. SM/C-2.6-positive and negative single cells from adult GFP-transgenic mice were obtained by cell sorting, and each muscle cell population was injected intramuscularly into the TA muscles of *mdx* mice. Two weeks later, muscles were isolated and cryosections were examined histologically (GFP: a, c, e, g, i, k; H–E: b, d, f, h). The positive fraction gave rise GFP^+ myofibers (a and e) with central nuclei, whereas the negative fraction did not (c and g). e–h, higher magnifications of a–d. GFP^+-myofibers (i) express dystrophin (j) (k, i and j were merged). GFP-negative area showed no dystrophin expression (l). Scale bars: 250 μm (a–d), and 50 μm (e–l).

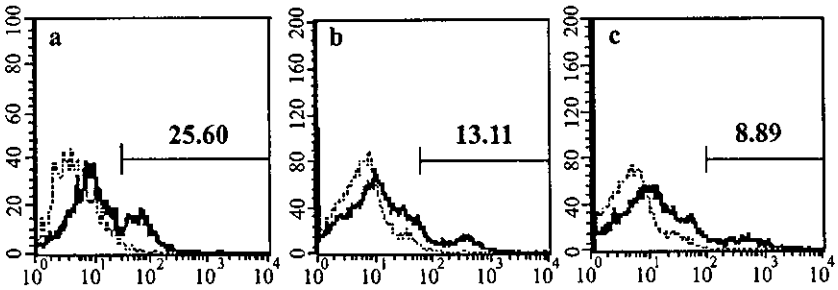

Fig. 4. Age-related changes in SM/C-2.6-positive satellite cells. Flow cytometric analyses of SM/C-2.6-positive cells in the muscles of mice at various ages. SM/C-2.6-positive cells in neonatal (day 2) thigh muscles (a), vastus lateralis and TA muscles from 4-week-old (b) to 8-week-old (c) mice are shown. The numbers of SM/C-2.6-positive cells decreases with age. The gates were set to exclude most of unstained cells. Percentages of unstained cells were equal in all panels.

herin, we compared SM/C-2.6 with M-cadherin expression in bone marrow cells. Approximately 10–15% of bone marrow cells express SM/C-2.6, but there are almost no SM/C-2.6/M-cadherin double positive cells (Fig. 5c). Similar to M-cadherin, we used flow cytometry to compare the expression of c-met and SM/C-2.6-reactive molecules on the mouse hepatocyte cell line NCTC1469. As shown in Fig. 5d, the NCTC1469 clone expresses c-met whereas it does not express SM/C-2.6-reactive molecules. The data definitively indicate that SM/C-2.6 detects neither M-cadherin nor c-met.

SM/C-2.6-positive cells express CD34 but not Sca-1, c-kit, or CD45

To investigate the expressions of several surface marker molecules on SM/C-2.6-positive cells, we analyzed adult muscle-derived mononuclear cells by flow cytometry. SM/C-2.6-positive cells did not co-express Sca-1, c-kit, or CD45 (Figs. 6a–c). However, all SM/C-2.6-positive cells (approximately 10% of muscle-derived mononuclear cells) co-expressed CD34 (Fig. 6d), and significant numbers of $CD34^+$ but SM/C-2.6-negative cells were also found.

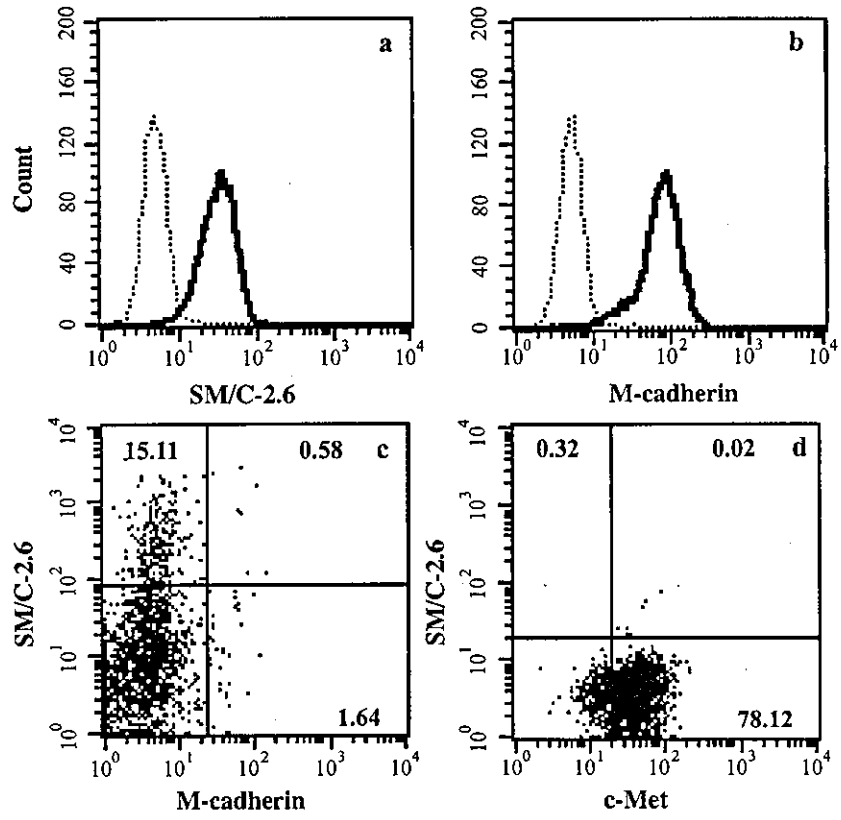

Fig. 5. SM/C-2.6 detects neither M-cadherin nor c-met. The SM/C-2.6-reactive molecule (a, c) and M-cadherin (b, c) are expressed on both C2/4 (a, b) and bone marrow cells (c). Two-color flow cytometry of bone marrow cells showed the SM/C-2.6-positive bone marrow cells do not express M-cadherin. A hepatocyte cell line, NCTC1469, expresses c-met but not the SM/C-2.6-reactive molecule (d). These data indicate that SM/C-2.6 detects neither M-cadherin nor c-met, which are known surface markers of satellite cells.

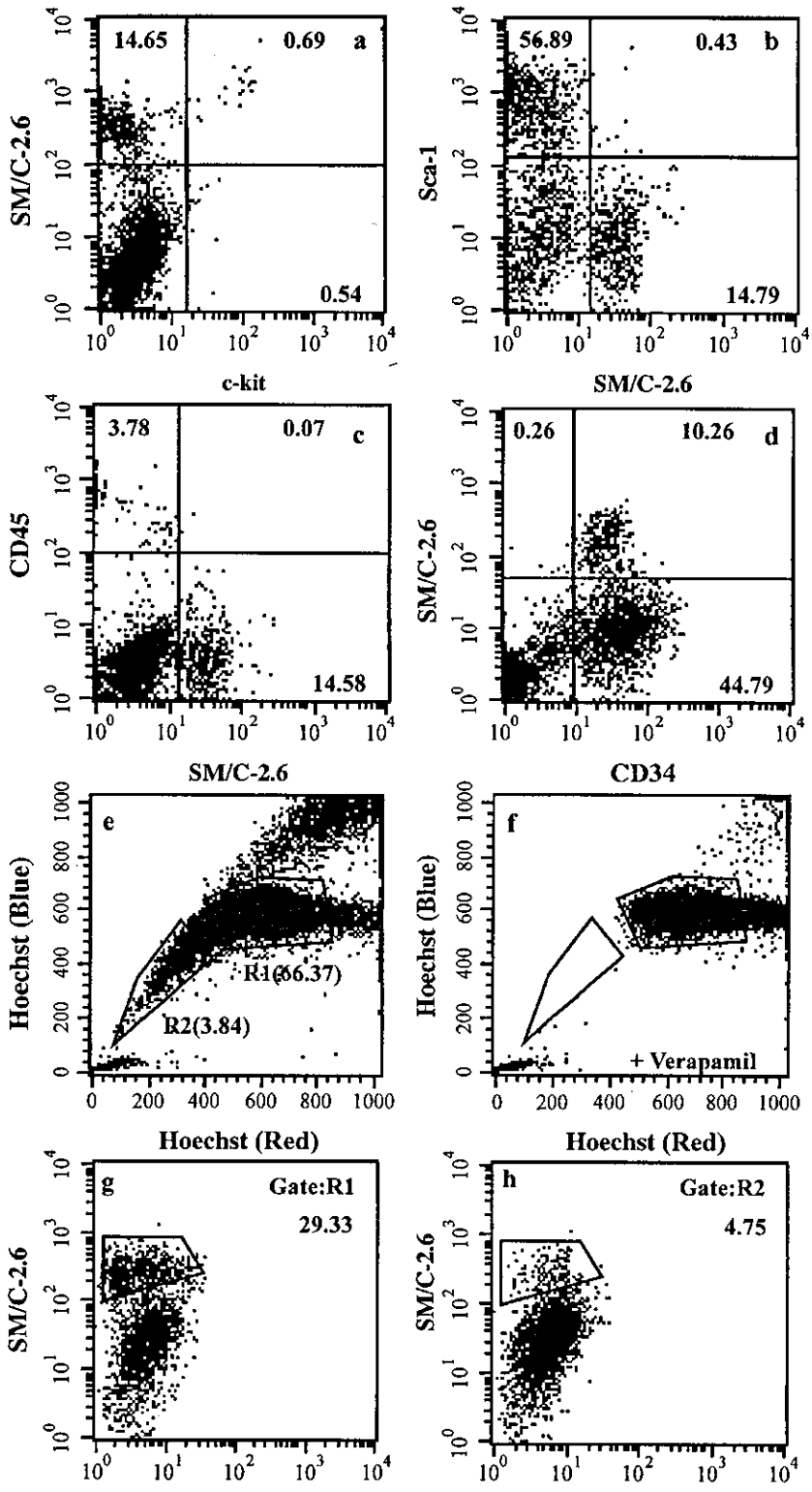

Fig. 6. Satellite cells are Sca-1$^-$, c-kit$^-$, CD45$^-$, CD34$^+$, and are included in the muscle MP fraction. Various surface markers on satellite cells were examined (a–d). SM/C-2.6-positive satellite cells are Sca-1$^-$ (a), c-kit$^-$ (b), CD45$^-$ (c), and CD34$^+$ (d). Muscle SP and MP fractions were separated by FACSVantageSE with (f) or without (e) verapamil. SM/C-2.6-positive cells among SP (3.84%) and MP (66.37%) cells were separated by flow cytometer. MP and SP include 29.33% (g) and 4.75% (h) SM/C-2.6-positive cells, respectively. This suggests that SM/C-2.6-positive satellite cells are mainly included in the muscle MP fraction.

Satellite cells are included in the fraction of muscle main population

Muscle-derived satellite cells can be isolated in the SP fraction by using the Hoechst-dye staining method, and the cells actively participated in myotube formation in the irradiated recipients [26]. Very recently, it was reported that hematopoietic stem cells from muscle SP are of hematopoietic origin [39]. On the other hand, muscle SP cells exhibit the potential to give rise to both myocytes and satellite cells after intramuscular transplantation [29]. We then investigated whether or not the SM/C-2.6-positive cells in adult skeletal muscle are found in the muscle SP fraction. As shown in Fig. 6e, muscle-derived mononuclear cells include 3% SP and a large number of MP cells. The SP fraction disappeared in cells treated with verapamil (Fig. 6f). The MP and SP fractions were gated (Fig. 6e, R1 and R2) and the SM/C-2.6-positive cells were examined. The gated MP fraction contained approximately 30% SM/C-2.6-positive cells (Fig. 6g) but the level was only 5% in the SP fraction (Fig. 6h). The results suggest that satellite cells are mainly included in the MP fraction.

Taken together, the results indicate that skeletal muscle quiescent satellite cells are Sca-1$^-$, c-kit$^-$, and CD45$^-$, but CD34$^+$, and are found in the muscle MP fraction.

Discussion

Muscle satellite cells are known as a key player in the skeletal muscle regeneration. Satellite cells are characterized by several significant features including histological location, electron micrographic characteristics in skeletal muscle, morphological change under physiological or pathological conditions, and the presence of a few specific marker proteins [14]. M-cadherin has been detected in the satellite cells of muscle [40]. Although several methods have been developed to isolate muscle satellite cells from enzymatically digested muscles [17–21], there is no definitive technique to isolate them from fresh muscle. In the present study, we aimed to purify skeletal muscle quiescent satellite cells using a mAb specific for them and to determine the surface phenotype. By immunizing rats with a C2/4 myoblast cell line (a subline of C2C12), we successfully established a novel mAb, SM/C-2.6, that detects muscle satellite cells by immunohistochemical and single fiber methods (Fig. 1B). By using FACS technique, we isolated SM/C-2.6-positive cells from mouse skeletal muscles and demonstrated that these cells differentiated into myotube or muscle fibers both in vivo and in vitro. SM/C-2.6-positive cells were detected in higher numbers in the neonatal muscle (postnatal day 2) than adult (4 week- or 8 week-old). This is consistent with earlier histological observations [14]. As shown in Figs. 2 and 3, FACS-sorted SM/C-2.6-positive cells became desmin$^+$ and MyoD$^+$ under proliferating or differentiating culture conditions. This is in good agreement with earlier studies that showed satellite cells become desmin$^+$ and MyoD$^+$ after muscle injury [41–44] or during short-term culture in vitro [45–47].

M-cadherin expression is restricted to satellite cells postnatally, and it is thought to be one of the proteins that define muscle satellite cells [40]. It is also known that hepatocyte growth factor activates quiescent skeletal muscle satellite cells in vitro [48], and that c-met, a receptor molecule for the factor, is expressed on quiescent satellite cells [49,50]. To investigate whether SM/C-2.6 detects these molecules, we compared the reactivity of SM/C-2.6 with the expressions of c-met in bone marrow cells or in a mouse hepatocyte cell line, NCTC1469. As clearly shown in Fig. 5, SM/C-2.6 detects neither M-cadherin nor c-met. Blanco-Bose et al. [51] reported that α7 integrin was useful for purification of myoblasts from cultured cells. However, α7 integrin is not likely the antigen recognized by SM/C-2.6 because α7 integrin is also expressed on myofibers [52–54]. We are now attempting to identify the reactive molecule.

Gussoni et al. [26] reported that muscle contains hematopoietic stem cells as well as muscle progenitor cells. Although the myogenic potential is highly enriched in muscle MP cells, SP cells with surface markers Sca-1$^+$, Lin$^-$, c-kit$^-$, CD45$^-$, and CD43$^-$, characterized from their efflux of Hoechst dye, are also incorporated into regenerated muscle fibers. The authors showed that the frequency of muscle progenitor cells is much lower than that of hematopoietic cells in muscle SP cells. McKinney-Freeman et al. [39] then showed that Sca-1$^-$ or CD45$^-$ cells give rise to donor-derived muscle fibers when they are injected into mouse muscle. Although it remains controversial, the data suggest that muscle-derived SP cells may not include sufficient muscle satellite cells. Rather, muscle SP cells are mainly composed of hematopoietic stem cells and differentiate into blood cells in the irradiated host. It is possible that they colonize in the muscle and differentiate into muscle satellite cells [29]. As described here, we have found that SM/C-2.6-positive cells in muscle MP cells, while SP cells contain few SM/C-2.6-positive cells. The results suggest that muscle quiescent satellite cells are a different population from SP cells of hematopoietic potential.

Sca-1 and c-kit are well-known surface markers of hematopoietic stem cells [55,56], and CD45 has been found in cells of hematopoietic origin but not on any non-hematopoietic cells [57]. CD34 is also known to be expressed on mouse hematopoietic stem cells [58,59]. As shown here, muscle-derived SM/C-2.6-positive cells do not co-express Sca-1, c-kit, or CD45 (Figs. 6a–c). On the other hand, all SM/C-2.6-positive cells (approximately 10% of muscle-derived mononuclear cells) co-express CD34 (Fig. 6d), and significant numbers of CD34-positive but SM/C-2.6-negative cells are also found. The expression of CD34 on SM/C-2.6-positive satellite cells is in agreement with earlier studies by Beauchamp et al. [60], in which they showed by a single fiber analysis that dormant satellite cells express

CD34 but not Sca-1 or CD45. The authors, however, reported in the paper that approximately 15–20% of satellite cells were negative for CD34 or M-cadherin staining, suggesting heterogeneity of satellite cells. The discrepancy in the CD34 expression on satellite cells remains to be investigated.

Because SM/C-2.6-negative cells give rise to few muscle fibers either in vitro or in vivo (Figs. 2 and 3), we conclude that SM/C-2.6 is a definitive marker of muscle satellite cells, which have the surface markers Sca-1$^-$, c-kit$^-$, CD45$^-$, and CD34$^+$. The characterization of the SM/C-2.6-reactive molecule will provide a powerful tool for understanding muscle-specific stem cell biology and helps us develop cell-base gene therapy or stem cell transplantation therapy for muscular dystrophies.

Acknowledgments

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Research report

Identification and characterization of ε-sarcoglycans in the central nervous system☆

Akiyo Nishiyama[a,b], Takeshi Endo[b], Shin'ichi Takeda[a], Michihiro Imamura[a,*]

[a] *Department of Molecular Therapy, National Institute of Neuroscience, NCNP, 4-1-1 Ogawahigashi-cho, Kodaira, Tokyo 187-8502, Japan*
[b] *Graduate School of Science and Technology, Chiba University, Yayoi-cho, Inage, Chiba 263-8522, Japan*

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Abstract

α-, β-, γ-, and δ-Sarcoglycans (SGs) are transmembrane glycoprotein components of the dystrophin-associated protein (DAP) complex, which is critical for the stability of the striated muscle cell membrane. ε-SG was found as a homologue of α-SG, but unlike other SG members, it is ubiquitously expressed in various tissues as well as in striated muscle. Moreover, mutations in the *ε-SG* gene cause myoclonus-dystonia, indicating the importance of ε-SG for the function in the central nervous system. To gain insight into the role of ε-SG, its expression and subcellular distribution in mouse tissues and especially in the mouse brain were investigated. Analysis by reverse transcription-polymerase chain reaction showed four splice variants of ε-SG transcripts in the mouse brain, two of which are major transcript forms. One is a conventional form including exon 8 (ε-SG1), and the other is a novel form excluding exon 8 but including a previously unknown exon, 11b (ε-SG2). Immunoblot analysis using various mouse tissues indicated a broad expression pattern for ε-SG1, but ε-SG2 was expressed exclusively in the brain. Therefore, both ε-SG isoforms coexist in various regions of the brain. Furthermore, these isoforms were found in neuronal cells using immunohistochemical analysis. Subcellular fractionation of brain homogenates, however, indicated that ε-SG1 and ε-SG2 are relatively enriched in post- and pre-synaptic membrane fractions, respectively. These results suggest that the two ε-SG isoforms might play different roles in synaptic functions of the central nervous system.

Theme: Cellular and molecular biology
Topic: Gene structure and function: general

Keywords: ε-Sarcoglycan; Dystrophin-associated protein; Muscular dystrophy; Myoclonus-dystonia; Brain

1. Introduction

Sarcoglycans (SGs) are essential constituents of the dystrophin-associated protein (DAP) complex, a large, membrane-associated protein architecture that is critical for the integrity of striated muscle fibers. The DAP complex consists of many proteins, including syntrophins (α1, β1, and β2), dystrobrevins, dystroglycans (α and β), SGs (α, β, γ, and δ), and sarcospan, that directly or indirectly associate with dystrophin [13,42,48]. Dystrophin, an actin-binding cytoskeletal protein, associates with the muscle plasma membrane via β-dystroglycan, which in turn binds to α-dystroglycan. α-Dystroglycan tightly associates with the laminin-α2 chain, a major component of the basal lamina, indicating that the DAP complex links extracellular matrix to intercellular cytoskeletal actin. The dystrophin-DAP complex is thought to function in protecting the plasma membrane of striated muscle fibers from contraction-induced mechanical stress by linking the molecules [42,43].

α-, β-, γ-, and δ-SGs are membrane-spanning glycoproteins that comprise a subcomplex within the DAP complex and associate with the other membranous subcomplex, which is composed of α- and β- dystroglycans [49]. A defect in any one of these four SGs disrupts the entire SG complex in the striated muscle

☆ The cDNA sequences of mouse and human ε-SG2 have been submitted to the DDBJ (DNA Data Bank of Japan) with accession numbers AB117975 and AB117974, respectively.

* Corresponding author. Tel.: +81-42-346-1720; fax: +81-42-346-1750.
E-mail address: imamura@ncnp.go.jp (M. Imamura).

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cell membrane and leads to limb-girdle muscular dystrophies [4,31,36,38,40,45]. Analyses of striated muscle of SG-deficient animals showed that the loss of a SG complex made the molecular interaction between α- and β- dystroglycans and between dystrophin and β-dystroglycan fragile [1,16,21]. These findings revealed that the SGs are functional only when they exist as a complex, and that they play a role in reinforcing the molecular linkage between the extracellular matrix and cytoskeletal actin. In addition to the structural role, the SG complex has been suggested to play a role in scaffolding for signal-transduction cascades, but its precise mechanism remains unknown [50]. Dystroglycans and the cytoplasmic members of DAPs, syntrophins and dystrobrevins, are expressed not only in muscle but also in various tissues, i.e., kidney, liver, lung, intestine and brain [3,35]. Recently, these proteins and dystrophin isoforms were shown to form complexes without SG complex in the central nervous system [8,37]. Little is known about their functional roles.

ε-SG, a type I transmembrane glycoprotein, was found as a homologue of α-SG [14,33]. In contrast to the expression of α-SG, which is specific to striated muscle, ε-SG is widely expressed in a variety of tissues including striated muscle, smooth muscle, lung, liver, kidney, spleen, testis, sciatic nerve, and brain [14,20]. ε-SG can form complexes with β-, γ-, and δ-SGs in skeletal [32] and smooth muscle cells [47] and with β- and δ-SGs in the Schwann cells surrounding peripheral nerve fibers [20]. Two ε-SG signals were detected in the brain by immunoblot analysis [14,20], but the localization and function of ε-SG have not been identified yet.

Recently, mutations in the human *ε-SG* gene have been shown to be associated with myoclonus-dystonia (M-D) [51]. M-D is a movement disorder characterized by rapid muscle contractions (myoclonus) and sustained twisting and repetitive movements, resulting in abnormal postures (dystonia). In addition to motor features, psychiatric symptoms, i.e., panic attacks, obsessive–compulsive behavior, or alcohol dependence, are reported in several M-D families [23,46]. These findings suggest that ε-SG has a key function in the central nervous system. Because a missense mutation in the *D2 dopamine receptor* gene is reportedly associated with M-D [23], it is intriguing to investigate the ε-SG expression in neuronal cells including dopaminergic neurons.

In this study, we found two ε-SG isoforms due to alternative splicing expressed in the mouse brain. One was an already reported conventional form; the other was a novel isoform specific to brain. Biochemical fractionation of mouse brains revealed that these two isoforms localized in different subcellular fractions. Furthermore, we clearly showed that the ε-SGs are broadly expressed in neuronal cells including dopaminergic neurons by immunocytochemical study. Our results provide the molecular basis for understanding the role of ε-SG in the central nervous system.

2. Materials and methods

2.1. Cloning of brain ε-SG cDNAs

The full-length mouse ε-SG cDNAs were amplified from a brain single-strand cDNA library (CeMines, Evergreen, CO, USA) by polymerase chain reaction (PCR) using the following set of oligonucleotide primers: 5′-GGAAAGGGTCGGGGGACACTC-3′ (nucleotide position, 19-39) and 5′-TGCGTAACCGATGTCAGGAAA-3′ (1392-1372) [14]. The amplification was carried out using LA-Taq polymerase (Takara Bio, Shiga, Japan) for 30 cycles, each cycle consisting of 94 °C for 1 min, 55 °C for 1 min, and 72 °C for 3 min.

The full-length human ε-SG cDNAs were obtained by reverse transcription-PCR (RT-PCR) using human cerebellum mRNA (Clontech, Palo Alto, CA, USA). The RT reaction was carried out with 1 μg of the poly A^+ RNA with a oligonucleotide reverse primer complementary to the sequence in the 3′-untranslated region of human ε-SG mRNA (5′-TCATGCATTATTGGAAGAGAAAA-3′, 1440-1418, [33]). The resulting single-strand cDNAs were used as the template for PCR amplification. The amplification was performed under the same conditions described above using a forward primer (5′-GTGCTTGGACGGGACAGG-GTC-3′, 77-97, [33]) in addition to the reverse primer used for the RT reaction (1440-1418).

The obtained full-length cDNAs of mouse and human were subcloned into a pCR2.1 vector (Invitrogen Life Technologies, Carlsbad, CA, USA), and the isolated clones were sequenced using an ABI377 sequencer (Applied Biosystems, Foster City, CA, USA). A homology search of the cDNA sequences (Genebank) was performed by using the online program 'BLAST the Mouse Genome' (NCBI; http://www.ncbi.nlm.nih.gov/genome/seq/MmBlast.html). A protein domains search of ε-SG was performed by using online software PROSITE (http://kr.expasy.org/site/support).

2.2. Structural analysis of ε-SG transcripts

Structural analysis of ε-SG transcripts was carried out in two steps, the RT-PCR to isolate full-length ε-SG from mouse tissues and the following nested PCR of the 3′-regions of the full-length cDNAs.

RT-PCR: Total RNA was prepared from 14 tissues of C57BL/6J adult mice, i.e., brain, heart, skeletal muscle, lung, pancreas, liver, kidney, spleen, small intestine, colon, testis, ovary, prostate and thymus, by use of TRIZOL reagent (Invitrogen Life Technologies). RT reactions were performed with 1 μg of the total RNA using a 21-mer oligonucleotide reverse primer complementary to a sequence in the 3′-untranslated region of mouse ε-SG mRNA (5′-TGCGTAACCGATGTCAGGAAA-3′, 1392-1372 [14]). The resulting amplified single-strand cDNAs were used as the template for PCR amplification. The PCR was carried out under the same conditions described above with the 21-

mer forward primer (nucleotide position 19-39 [14]). The PCR products were separated by electrophoresis on agarose gel (1% agarose), and the 1.4-kbp full-length ε-SG fragments were purified by Wizard® SV Gel and PCR Clean-Up System (Promega, Madison, WI, USA).

Nested PCR: The inclusion or exclusion of exon 8 and 11b was examined by nested PCR of the purified full-length ε-SG cDNAs using following primer sets: 5′-GCTTATATCATGTGCTGCCGA-3′ (976-996) and 5′-GGGCCATGCAATCTCTCTGTT-3′ (1119-1099) [14] for exon 8 and 5′-AACTACGACAGCACCAACATG-3′ (1183-1203) and 5′-GTGAGACACGGCTGCAGCAGT-3′ (1324-1344) [14] for exon 11b. Amplification of the long region containing both exons 8 and 11b was carried out using the above forward primer (976-996) for exon 8 and the reverse primer (1324-1344) for exon 11b. The resulting PCR products were separated by polyacrylamide gel (8%) electrophoresis and stained with ethidium bromide (EtBr). The EtBr signals were detected on image analyizer (Lumi-Imager™ F1; Roche Diagnostics, Penzsberg, Germany) and quantified using the computer software, Lumi-Analyst 3.1 (Roche Diagnostics).

Structural analysis of the 3′ region of human ε-SG transcripts was carried out by PCR using first strand cDNAs from brain, heart, skeletal muscle, lung, pancreas, liver, kidney, spleen, small intestine, colon, testis, ovary, prostate and thymus (Clontech) with primer sets: 5′-GCTTATATCATGTGCTGCCGA-3′ (1045-1065) and 5′-AGGGTGGAACACAGGAAGCGT-3′ (1215-1195) [33] for exon 8 and 5′-ACAGACAACTATGATAGCACA-3′ (1246-1266) and 5′-TTCAGTCAGTTTTCTTTCTTCAG-3′ (1372-1350) [33] for exon 11b. Amplification of the region containing both exon 8 and 11b was performed using the above forward primer (1045-1065) and the reverse primer (1372-1350).

2.3. Antibodies

Mouse monoclonal antibodies against SNAP-25, PSD-95, and eNOS were purchased from BD Transduction Laboratories (San Diego, CA, USA). The other mouse monoclonal antibodies, anti-synaptophysin and Cy3-conjugated anti-glial fibrillary acidic protein (GFAP) were purchased form Sigma (St. Louis, MO, USA).

A rat monoclonal antibody against laminin-α2 chain was purchased from Alexis Biochemicals (Laufelfingen, Switzerland). Affinity-purified sheep antibody against tyrosine hydroxylase (TH) and rabbit antibody against GFAP were purchased from Chemicon International Lab (Temecula, CA, USA).

Affinity-purified rabbit antibody against the whole cytoplasmic region of ε-SG (Esg-Cyt antibody) was newly generated for the present study by the same method as previously described [20].

Rabbit antibodies against unique COOH-terminal sequences of ε-SG variants were raised against GST-fusion proteins. The 3′-terminal short cDNA fragment was amplified from each full-length ε-SG cDNA, including or excluding exon 11b, by PCR using the following oligonucleotide primer sets: 5′-TCATGCATTATTGGAAGAGAAAA-3′ (1440-1418) and 5′-ACAGACAACTATGATAGCACA-3′ (1246-1266) [33] for the cDNA with exon 11b and 5′-TCATGCATTATTGGAAGAGAAAA-3′ (1440-1418) and 5′-CAGAACTTGCCACATCAGACT-3′ (1291-1311) [33] for the cDNA without exon 11b. The amplification was carried out using Pyrobest (Takara) for 30 cycles, each cycle consisting of 98 °C for 10 s and 60 °C for 30 s. The amplified DNA fragments were subcloned into the pCR-Blunt vector (Invitrogen), and then the *Eco*RI-fragments of ε-SG variants were purified from a cloned pCR-Blunt plasmid and ligated into a pGEX expression vector (Amersham Biosciences K.K., Tokyo, Japan). Recombinant proteins were expressed as a fusion protein with GST in *E. coli* and purified from the soluble fraction of cell lysates on a glutathione-sepharose column as previously described [20]. These recombinant proteins were used as antigens. The antisera obtained were purified using affinity columns coupled with two kinds of synthetic peptides, i.e., CTGDFRLTTFQRFEVNGI-PEERKLTEAMNL (amino acids 399-427) for ε-SG including exon 11b (Esg-C2 antibody) and CGGTTGKWYP (amino acids 407-413 [33]) for the ε-SG excluding exon 11b (Esg-C1 antibody).

The antibody against the sequence encoded in exon 8 (Esg-E8 antibody) was purified from antiserum against the whole cytoplasmic region of ε-SG using an affinity column conjugated with the synthetic peptide, CGVEKRNMQTPDIQ (amino acids 321-333 [33]).

2.4. Fusion proteins

To examine the specific reactivity of the purified anti-ε-SG antibodies, cytoplasmic regions of ε-SG variants were generated as recombinant fusion proteins with GST.

Three kinds of cDNA fragment encoding cytoplasmic regions of ε-SG variants were amplified from full-length ε-SG cDNAs by PCR using the following oligonucleotide primers: 5′-GCTTATATCATGTGCTGCCGA-3′ (976-996 [14]) and 5′-GTGAGACACGGCTGCAGCAGT-3′ (1324-1344 [14]) for mouse ε-SG. The enzyme reaction, using Pyrobest (Takara), and expression and purification of GST-fusion proteins were carried out under the same experimental conditions described in "Antibodies".

2.5. Immunocytochemistry

Cryosections (14 μm) of mouse brain were used for immunofluorescence staining. The cryosections were mounted on slide glasses and fixed in cold acetone (−20 °C). After equilibration of the fixed sections with Tris-buffered saline (TBS), the sections were blocked in TBS containing 2% casein. Indirect immunofluorescence microscopy was performed as previously described [20], using the

following primary antibodies at appropriate dilutions: affinity purified Esg-Cyt rabbit antibody at 1:1000, anti-TH sheep antibody at 1:200, anti-laminin-α2 chain rat antibody at 1:100, and Cy3-conjugated anti-GFAP mouse antibody at 1:1000. As secondary antibodies, Alexa488-conjugated anti-rabbit IgG (1:600), Alexa568-conjugated anti-sheep IgG (1:1000), and Alexa568-conjugated anti-rat IgG (1:1000) antibodies (Molecular Probes, Eugene, OR, USA) were used. A fluorescent Nissl stain was performed using NeuroTrace 640/660 (Molecular Probes) according to the manufacturer's protocol. Fluorescence signals on cryosections were observed using a confocal laser scanning microscope (Leica TCS SP; Leica, Heidelberg, Germany).

2.6. Subcellular fractionation

Biochemical fractionation of mouse brain homogenate was performed as described by Huttner et al. [18] and Kahle et al. [22]. Cerebellum-excised mouse brains were homogenized in ice-cold Hepes buffer (4 mM Hepes-NaOH, pH 7.3, and a protease inhibitor cocktail, 0.5 mM PMSF) containing 320 mM sucrose using a Dounce homogenizer. The brain homogenate (H) was centrifuged at $1000 \times g$ to remove nuclei and large debris (P1). The supernatant (S1) was centrifuged at $12,500 \times g$ to obtain a crude synaptosomal fraction (P2) and subsequently lysed hypoosmotically and centrifuged at $25,000 \times g$ to pellet a synaptosomal membrane fraction (LP1). Then the resulting supernatant (LS1) was centrifuged at $165,000 \times g$ to obtain a synaptic vesicle-enriched fraction (LP2). Concurrently, the supernatant (S2) of the crude synaptosomal fraction (P2) was centrifuged at $165,000 \times g$ to obtain a cytosolic fraction (S3) and a light membrane/microsome-enriched fraction (P3; hereafter referred to as light membrane). A postsynaptic density fraction (PSD) was prepared by washing the LP1 with Hepes-buffered solution containing 1% TritonX-100 according to the method of Phillips et al. [44].

2.7. Other procedures

Purification of capillary endothelial cells was performed using BS-1 lectin beads according to the method of Da Silva-Azevedo et al. [9]. SDS-polyacrylamide electrophoresis (SDS-PAGE) and protein transfer to the PVDF membrane were performed as described by Laemmli [26] and Kyhse-Anderson [25], respectively. Immunoreactive protein bands in the immunoblotting were visualized using a chemiluminescence detection system (ECL; Amersham Biosciences K.K.). Protein concentration was determined using Protein assay (Bio-Rad Laboratories, Hercules, CA, USA) with bovine serum albumin as a standard. All animal handling procedures were in accordance with a protocol

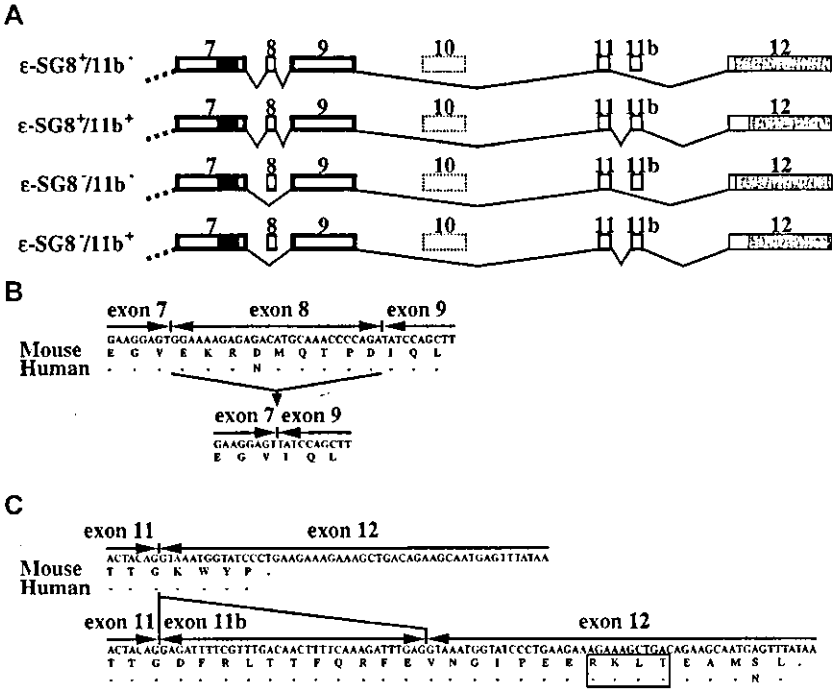

Fig. 1. Structures of ε-SG splice variants isolated from the mouse brain. (A) The exon organization of four ε-SG transcripts is schematically represented. Their 3′-terminal structures, corresponding to the region from exon 7 to exon 12, are shown. There was an alternative splicing around exon 8 and another alternative splicing around a newly found exon, 11b. The four resulting clones are designated ε-SG8$^+$/11b$^-$, ε-SG8$^+$/11b$^+$, ε-SG8$^-$/11b$^-$, and ε-SG8$^-$/11b$^+$. The black box in exon 7 indicates the region encoding the transmembrane domain. The shaded box in exon 12 indicates the untranslated region. The number of exons is given according to the human *SGCE* gene [33], although the sequence corresponding to exon 10 of the *SGCE* gene has not been found in the mouse genome database. (B) and (C) Represent the deduced amino acid sequences from the ε-SG variants without exon 8 and with the insertion of the newly found exon 11b, respectively. Identities between the mouse and human sequences are indicated by *dashes*. A possible site of phosphorylation by cyclic nucleotide-dependent protein kinases is boxed.

approved by the National Institute of Neuroscience, NCNP, Japan.

3. Results

3.1. Identification of variants of ε-SG transcript in the brain

Previous immunoblot studies showed that ε-SG was widely expressed in a variety of mouse tissues as a 46 kDa protein. However, in the brain, signal(s) other than the 46 kDa ε-SG were detected [14,20]. This observation implies the possibility of a novel ε-SG isoform in the brain. To elucidate the presence of the brain-specific isoform of ε-SG, we searched for variants of ε-SG transcripts in the mouse brain.

We obtained cDNA clones having the entire coding region of ε-SG from mouse brain by RT-PCR. Analysis of their sequences showed that ε-SG transcripts were variable at two sites of the 3′ terminal region (Fig. 1). One variation is the inclusion or exclusion of exon 8, and the other is the inclusion or exclusion of a novel sequence between exon 11 and exon 12 (Fig. 1C). A homology search of the sequence in the mouse genomic database (Genebank) found the same sequence in intron 11 of the mouse *ε-SG* gene (*Sgce*), where splice-donor and -acceptor roles have been completely maintained (data not shown). Therefore, we numbered the new sequence as exon 11b, and the resulting four transcripts were designated as ε-SG8$^+$/11b$^-$, ε-SG8$^+$/11b$^+$, ε-SG8$^-$/11b$^-$ and ε-SG8$^-$/11b$^+$. In the primary structure, the exclusion of exon 8 is predicted to cause an in-frame deletion of 9 amino acids, while the inclusion of exon 11b causes the addition of 27 amino acids at the C-terminal (Fig. 1B,C). We also obtained the same results from human brain and the genomic database (Fig. 1). We numbered the exons and introns of *Sgce* according to a previous work on the human *ε-SG* gene (*SGCE*) [33].

Among the four ε-SG variants, one transcript that contains exon 8 but lacks exon 11b (ε-SG8$^+$/11b$^-$) has been already reported [14,33]. To clarify whether the exclusion of exon 8 and inclusion exon 11b occur specifically in the brain, we analyzed the 3′ structures of ε-SG transcripts in a variety of tissues. We initially amplified the full-length ε-SG transcripts from the tissues by RT-PCR and then performed second PCR with the same amount of full-length ε-SG cDNA to verify the presence of exon 8 or exon 11b. The second PCR, to verify whether transcripts have exon 8 or not, amplified the 144 bp fragment containing exon 8 from all tissues, but the 117 bp fragment lacking exon 8 was found mainly in brain, as shown in Fig. 2B. On the other hand, the PCR amplified the 197 bp-fragment containing exon 11b only from the brain, while the exon 11b-lacking 162 bp-fragment was amplified from all tissues examined.

Further, we performed RT-PCR analysis to clarify the combination of two alternative splicings, exon 8 and 11b. The sizes of PCR fragments comprising exon 8$^+$/11b$^-$, exon 8$^+$/11b$^+$, exon 8$^-$/11b$^-$ and exon 8$^-$/11b$^+$ were 369, 404, 342 and 377 bp, respectively. The 369- and 377-bp fragments were the major products in the brain and constituted 90% of the total product. The 369-bp fragment corresponded to a previously reported transcript, containing exon 8, but lacking

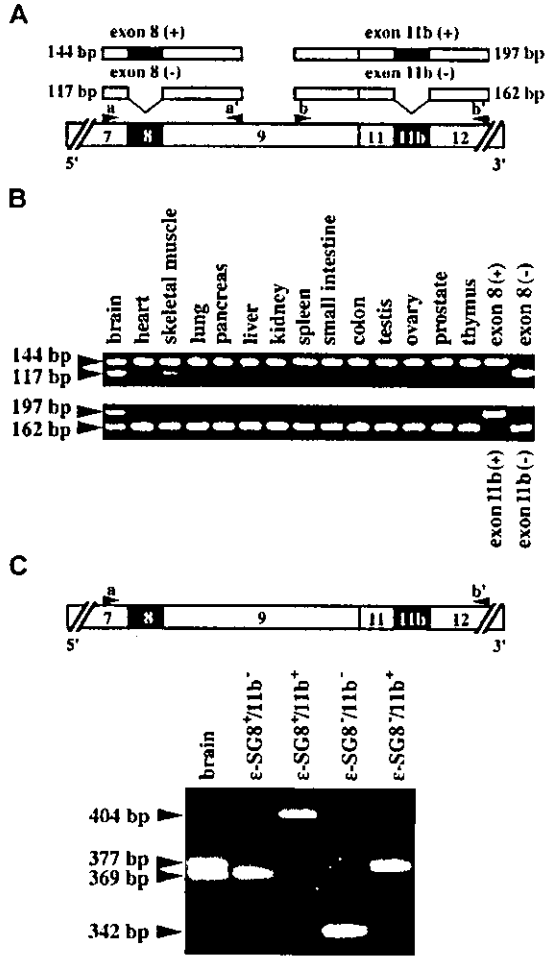

Fig. 2. Tissue expressions of splice variants of ε-SG transcripts. (A) Schematic representation of PCR products amplified from ε-SG splice variants. To examine the effects of alternative splicing of exon 8 and 11b on ε-SG transcripts in mouse various tissues, PCR analysis was performed using oligonucleotide primer sets (a and a′, and b and b′). The 3′-terminal structure of ε-SG, corresponding to a segment from exon 7 to the end of exon 12, is schematically represented at the bottom of the panel. (B) Expression of ε-SG splice variants in mouse tissues. First, cDNAs that cover the entire length of ε-SG were amplified from total RNAs of 14 different mouse tissues by RT-PCR. To analyze the inclusion or exclusion of exon 8 and exon 11b, respectively, a second PCR was performed using the primer sets described in (A) (a and a′, and b and b′). The resulting PCR products were separated by polyacrylamide gel (8%) electrophoresis. The 144 bp and 117 bp fragments in the upper panel indicate the inclusion or exclusion of exon 8. The 197 bp and 162 bp in the lower panel indicate the inclusion or exclusion of exon 11b. The right two lanes in each panel show the PCR products from the cloned ε-SG cDNAs including or excluding exon 11b and exon 8. (C) Combinations of the two alternative splicings were analyzed. First, cDNA that covers the entire length of ε-SGs was amplified from the mouse brain total RNA by RT-PCR, then the second PCR was performed using the primer set, a and b′, described in panel (A). The resulting DNA fragments are shown in the left lane as brain. The four right lanes indicate PCR products with the primer set using four cloned types of ε-SG cDNAs (see Fig. 1). The sizes of the PCR products comprising ε-SG8$^+$/11b$^-$, ε-SG8$^+$/11b$^+$, ε-SG8$^-$/11b$^-$ and ε-SG8$^-$/11b$^+$ were 369, 404, 342 and 377 bp, respectively.

exon 11b (ε-SG8$^+$/11b$^-$), while another 377-bp fragment was a novel transcript containing exon 11b, but lacking exon 8 (ε-SG 8$^-$/11b$^+$).

3.2. Identification of protein products from ε-SG transcripts

We generated three antibodies, Esg-C1, Esg-C2, and Esg-E8, that recognize variant-specific C-terminal structures

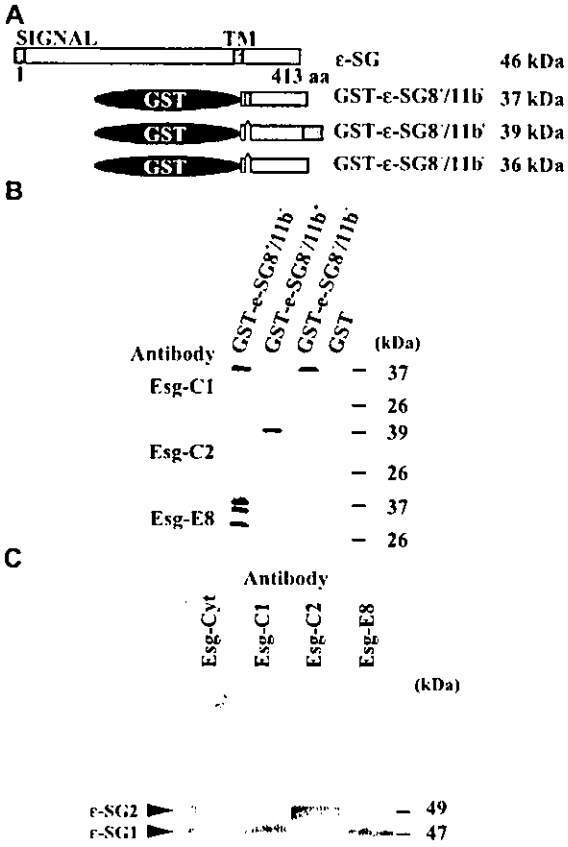

Fig. 3. Identification of protein products of ε-SG transcript variants in the mouse brain. (A) Schematic representation of GST-ε-SG fusion proteins that were used for testing immunoreactivities of antibodies, Esg-C1, Esg-C2, and Esg-E8. The shaded boxes in the N-terminal of ε-SG8$^+$/11b$^-$ and the C-terminal of ε-SG8$^-$/11b$^+$ indicate the peptide structures produced by the inclusion of exon 8 and exon 11b, respectively. (B) Specific reactivities of Esg-C1, Esg-C2, and Esg-E8 antibodies to ε-SG variants. Immunoblotting of GST-ε-SG-fusion proteins showed that Esg-C1 and Esg-C2 antibodies recognize the C-terminal of ε-SG excluding and including exon 11b, respectively. Esg-E8 was shown to recognize the ε-SG inclusion of exon 8. Note that Esg-E8 antibody recognizes degradation products of GST-ε-SG8$^+$/11b$^-$ protein. (C) Expression of two ε-SG isoforms in adult mouse brain. Ten micrograms of tissue lysate were separated on SDS-PAGE (9% polyacrylamide gel) and transferred onto polyvinylidene difluoride (PVDF) membranes. The membranes were sequentially treated with affinity-purified rabbit antibodies, Esg-C1, Esg-C2, and Esg-E8, and a horseradish peroxidase (HRP)-conjugated anti-rabbit secondary antibody. Immunostained bands were detected using a chemiluminescence detection system. The staining pattern of the antibody against the whole cytoplasmic region of ε-SG is shown in the left lane as Esg-Cyt.

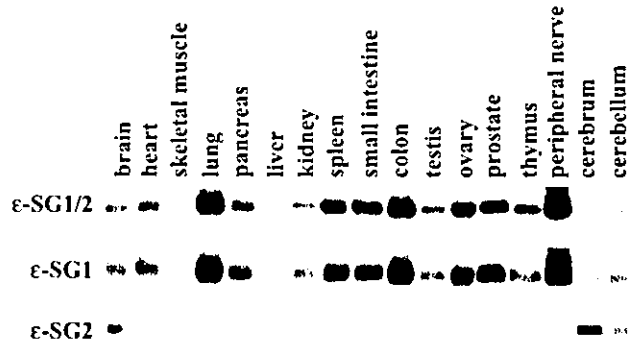

Fig. 4. Tissue expression of ε-SG1 and ε-SG2. Expression of the two ε-SG isoforms, ε-SG1 and ε-SG2, was examined in fifteen mouse tissues by immunoblotting. Ten micrograms of tissue lysates were separated on 9% SDS-PAGE and stained with the antibodies Esg-C1 and Esg-C2. The upper panel, indicated as ε-SG1/2, shows the staining pattern with Esg-Cyt antibody.

of ε-SG. Esg-C1 recognizes the C-terminal of ε-SG, which is the product of transcripts including exon 12, but lacking exon 11b. Esg-C2 recognizes the C-terminal of the other ε-SG, which is the product of transcripts including exon 11b and 12. Esg-E8 recognizes ε-SG, corresponding to transcripts that include exon 8 (Fig. 3B).

Immunoblotting of the mouse brain lysate with an antibody against the whole cytoplasmic region, Esg-Cyt, showed 47 and 49 kDa bands (Fig. 3C). Esg-C1 and Esg-E8 antibodies reacted to the 47 kDa band but not the 49 kDa, while Esg-C2 antibody reacted to the 49 kDa band but not the 47 kDa. These results indicated that two ε-SG isoforms are expressed mainly in the mouse brain. One is a conven-

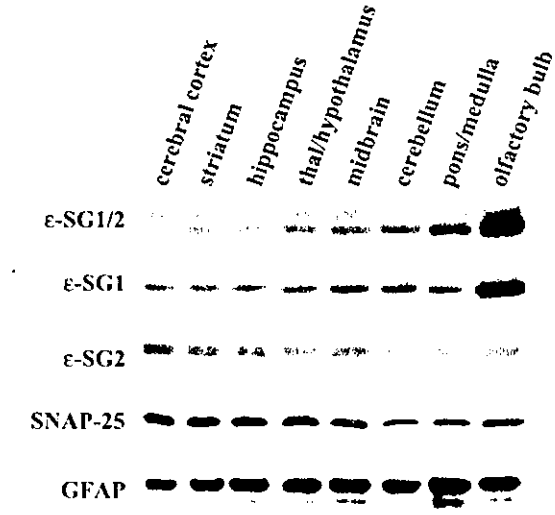

Fig. 5. Regional distribution of ε-SG1 and ε-SG2 in adult mouse brain. Adult mouse brains were separated into eight regions and homogenized in lysis buffer. These lysates were separated by SDS-PAGE (9% polyacrylamide gel) and immunostained with the antibodies Esg-C1 and Esg-C2. The upper panel (ε-SG1/2) shows the staining pattern with the Esg-Cyt antibody. The panels indicated as SNAP-25 and GFAP show the relative amounts of neuronal cells and astrocytes in each brain region. The thal/hypothalamus and pons medulla indicate the regions including the thalamus and hypothalamus, and pons and medulla oblongata, respectively.

tional 47 kDa isoform derived from a transcript encoding exon 12 but not exon 11b, another is a novel 49 kDa isoform derived from a transcript encoding exon 11b, but not exon 8. We designated the former ε-SG1 and the latter ε-SG2.

The analysis of tissue expression with Esg-C1 and Esg-C2 antibodies showed that ε-SG1 was widely expressed in a variety of tissues, including brain, heart, skeletal muscle, lung, pancreas, liver, kidney, spleen, small intestine, colon, testis, ovary, prostate, thymus, peripheral nerve, while ε-SG2 was detected only in brain (Fig. 4).

3.3. Regional distribution of ε-SG1 and ε-SG2 in the mouse brain

We further examined the expression of the ε-SGs in eight regions of the mouse brain. Immunoblotting with Esg-C1 and Esg-C2 antibodies detected ε-SG1 and ε-SG2 in all regions examined: the cerebral cortex, striatum, hippocampus, thalamus/hypothalamus, midbrain, cerebellum, pons/medulla oblongata, and olfactory bulb (Fig. 5). The expression of ε-SG1 was more prominent in the olfactory bulb, while the expression of ε-SG2 was less abundant in the cerebellum, pons/medulla oblongata, and olfactory bulb.

3.4. Localization of ε-SG in the mouse brain

To identify the localization of ε-SGs, we performed immunocytochemical studies with the Esg-Cyt antibody. ε-SG immunoreactivity was clearly observed throughout the brain, but its signal is relatively high in olfactory bulb, cerebral cortex, hippocampus, pons, and cerebellar cortex (Fig. 6A). The ε-SG immunoreactivity partially overlapped

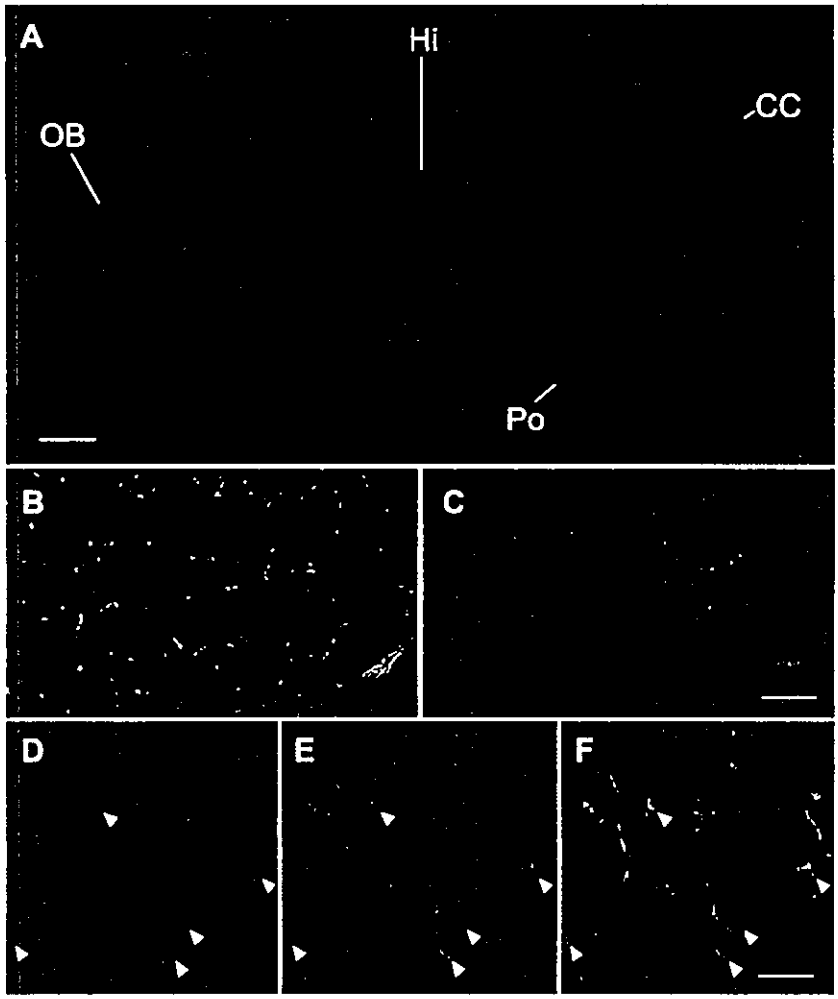

Fig. 6. Distribution of ε-SGs in adult mouse brain. Parasagittal cryosections of adult mouse brain were reacted with the Esg-Cyt antibody. The ε-SG immunoreactivity was visualized using Alexa488-conjugated secondary antibody (green). (A) Immunoreactivity of ε-SGs in a whole parasagittal section of mouse brain. The signals in the olfactory bulb (OB), hippocampus (Hi), pons (Po), and cerebellar cortex (CC) were intense. (B) and (C) Indicate the double-stain patterns of the dentate gyrus with Esg-Cyt rabbit antibody (green) and anti-lamini-α2 chain rat antibody (red) or Cy3-conjugated anti-GFAP mouse antibody (red), respectively. Note that the red fluorescence of lamini-α2 signals are seen as orange or yellow because of colocalization with the green signal of ε-SGs. (D–F) Higher magnification of a hippocampal CA2 region that was double-stained with Esg-Cyt (D) and Cy3-anti-GFAP antibody (E), and their merged image (F). Arrowheads indicate astrocytes showing immunoreactivity of ε-SGs. Scale bar = 1 mm for A, 100 μm for B and C, 50 μm for D–F. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

with capillary vasculature stained with an antibody against laminin-α2 chain, a component of basal lamina surrounding micro-capillaries (Fig. 6B), whereas the localization of ε-SG was different from that of GFAP, a marker of astrocytes (Fig. 6C). In a higher magnification, however, a faint signal was detected in some astrocytes (Fig. 6D–F). Double-staining analysis with the Esg-Cyt antibody and fluorescent Nissl stain showed that ε-SGs expressed in neuronal cells within the olfactory bulb, hippocampus, pons, and cerebellar cortex, and localized along their cell bodies (Fig. 7). Furthermore, ε-SG immunoreactivity was detected in the cells expressing tyrosine hydroxylase (TH) within the sub-

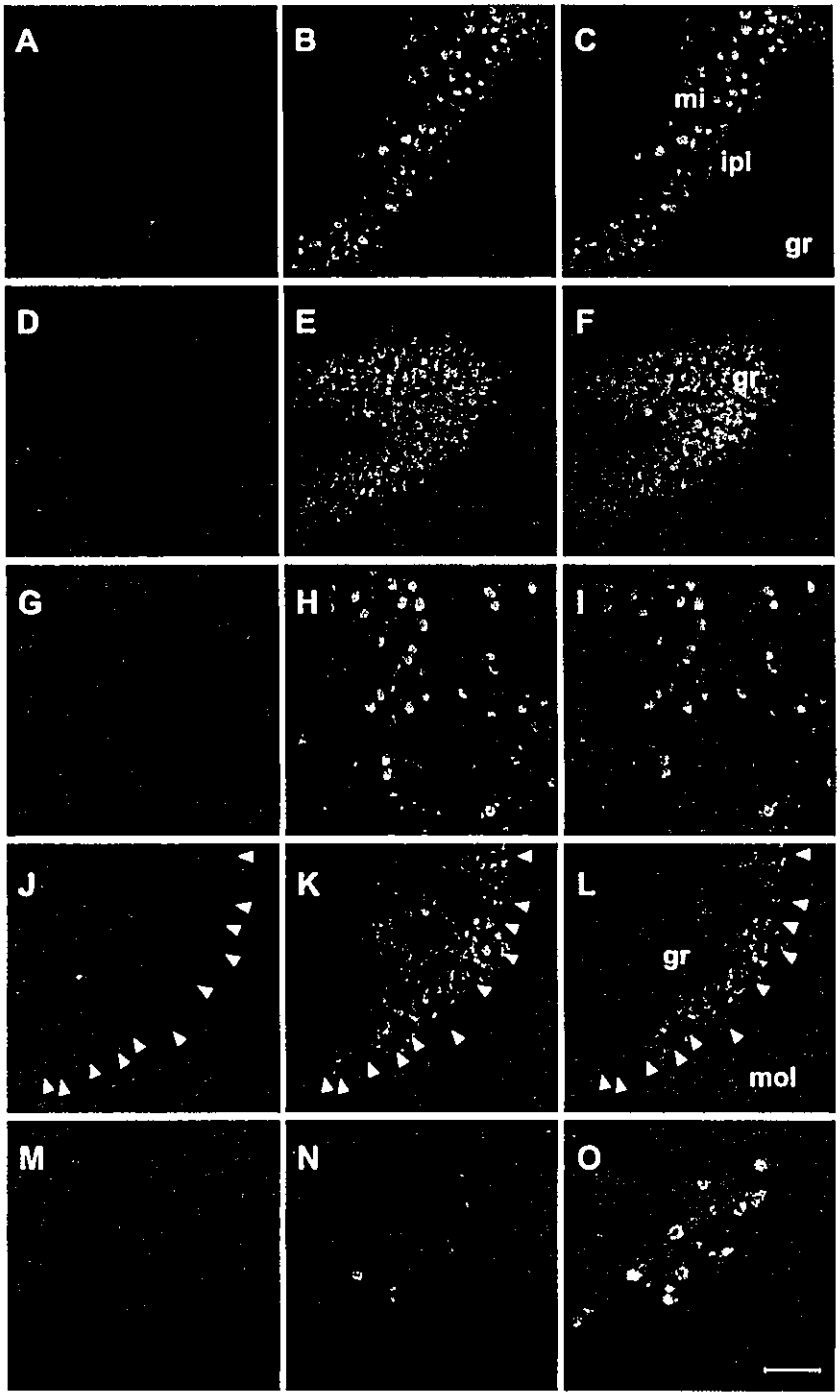

Fig. 7. Localization of ε-SGs in neuronal cells. Double-staining of mouse brain cryosections using Esg-Cyt antibody (A, D, G, J, M) and NeuroTrace™ fluorescent Nissl stain (B, E, H, K) was performed. The figures focus on the regions of the olfactory bulb (A–C), dentate gyrus (D–F), pons (G–I), and cerebellar cortex (J–L). In the staining of the substantia nigra (M–O), anti-TH sheep antibody was used instead of fluorescent Nissl stain and visualized by an Alexa568-secondary antibody (N). All the right-hand panels (C, F, I, L, O) are merged images of the two preceding panels. Arrowheads in panels J–L indicate Purkinje cells. mi, mitral cell layer; ipl, internal plexiform layer; gr, granular cell layer; mol, molecular cell layer. Scale bar = 50 μm.

stantia nigra, indicating that ε-SG is expressed in dopaminergic neurons (Fig. 7M–O). Neither Esg-C1 nor Esg-C2 antibody was available for immunocytochemical study.

3.5. Subcellular localization of ε-SG isoforms in the mouse brain

We examined the expression pattern of ε-SG1 and ε-SG2 in various subcellular compartments of mouse brain to elucidate their roles in the central nervous system.

Fig. 8 shows the brain subcellular fractions prepared according to the procedure of Huttner et al. [18]. We first examined the distribution of several neural membrane markers, such as a marker for synaptic vesicles, synaptophysin; one for pre-synaptic membranes, SNAP-25; and one for post-synaptic membranes, PSD-95. Synaptophysin was remarkably enriched in the LP2 fraction but not in LP1 and PSD fractions, whereas PSD-95 was enriched in LP1 and PSD fractions but not in the LP2 fraction. These results were consistent with previous reports [12]. On the other hand, SNAP-25 was found in LP1 as well as the LP2 fraction, but not found in the PSD fraction. We then examined the expression of ε-SG1 and ε-SG2. ε-SG1 was mainly present in P2 and P3 fractions, but more concentrated in LP1 than in the LP2 fraction. ε-SG2 was also concentrated in P2 and P3 fractions, but distributed equally in LP1 and LP2 fractions. Neither isoform was enriched but certainly existed in the PSD fraction.

We further analyzed the expression of ε-SG isoforms in the brain capillary endothelial cell fraction purified with BS-1 lectin beads [9] (Fig. 8C). In the isolated endothelial cells, we were able to rule out the expression of a neuronal marker

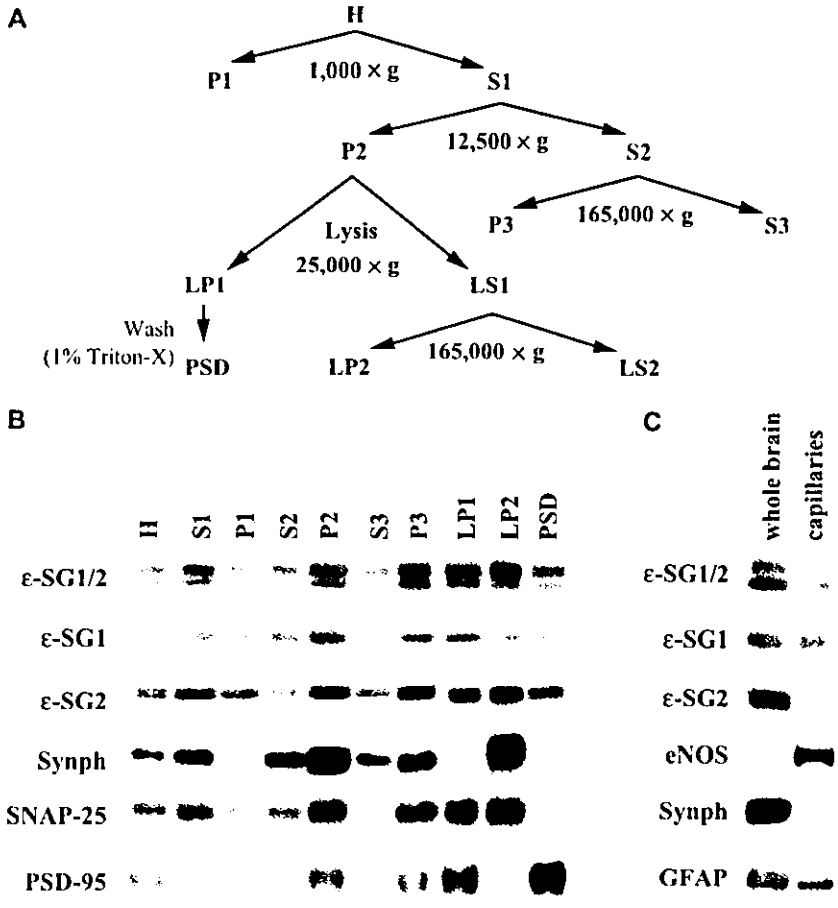

Fig. 8. Subcellular localization of ε-SG1 and ε-SG2 in adult mouse brain. (A) Schematic of the biochemical fractionation. The subcellular fractionation of mouse brain was carried out according to the procedure of Huttner et al. [18]. Fractions are as follows: H, total brain homogenates; P1, nuclei and large debris; P2, a crude synaptosomal fraction; P3, a light membrane/microsome-enriched fraction; LP1, a synaptosomal membrane fraction; LP2, a synaptic vesicle-enriched fraction. Each of the supernatants is designated S1, S2, or S3. A post-synaptic density fraction (PSD) was prepared from LP1 according to the method of Phillips et al [44]. (B) Detection of ε-SG isoforms in subcellular fractions from adult mouse brain. The isolated biochemical fractions were separated by SDS-PAGE (9% polyacrylamide gel) and then blotted with the antibodies, Esg-C1 (ε-SG1), Esg-C2 (ε-SG2), or Esg-Cyt (ε-SG1/2). Subcellular compartments were identified by detection of resident marker proteins with the corresponding antibodies. These markers are synaptophysin (Synph) for synaptic vesicles, SNAP-25 for pre-synaptic membranes, and PSD-95 for post-synaptic membranes. (C) Detection of ε-SG1 in brain capillaries. The capillary endothelial cells were isolated from the mouse brain by BS-1 lectin-beads [9], and the expression of ε-SG1 and ε-SG2 in the cells was analyzed by immunoblotting. Ten micrograms of proteins of mouse whole brain and the isolated capillaries were used for the analysis. eNOS, endothelial nitric oxide synthase, is a marker for endothelial cells.

(synaptophysin), but did detect an astrocyte marker (GFAP), indicating a close association of astrocytes with capillary endothelial cells. Immunoblotting using Esg-C1 and Esg-C2 antibodies clearly found ε-SG1, but not ε-SG2, in the cells. This result revealed that ε-SG1 is predominantly expressed in capillary endothelial cells and astrocytes.

4. Discussion

Mutations in the *ε-SG* gene (*SGCE*) cause M-D, indicating the functional importance of ε-SG in the central nervous system [51]. Despite much work on *SGCE* mutations in M-D families, very little is known about the localization and function of the protein product of *SGCE* in the central nervous system. In the present study, we found two isoforms of ε-SG in the mouse brain and investigated their distribution and localization.

We have shown the expression of two ε-SG isoforms in the mouse brain. One is identical to the ε-SG (ε-SG8$^+$/11b$^-$) that was initially discovered by cDNA cloning of mouse lung [14], and the other is a novel isoform excluding exon 8 and including exon 11b (ε-SG8$^-$/11b$^+$). We propose to designate the former ε-SG1 and the latter ε-SG2. The same results were obtained from human brain on mRNA and protein levels. In addition, ε-SG8$^-$/11b$^-$ type transcripts were markedly expressed in human brain (data not shown). This finding suggested that ε-SG2 plays some specific role in the mammalian brain.

Previous immunocytochemical studies showed ε-SG expression in a variety of cell types, i.e., striated and smooth muscles, capillary blood vessels, Schwann cells in peripheral nerves, alveoli and bronchioles in lung, and glomerular mesangium in kidney [14,20]. The present study showed that ε-SGs are widely distributed throughout the brain and that they are expressed in neuronal and non-neuronal cells including capillary endothelial cells and astrocytes. Immunolabeling of whole mouse brain sections revealed that the ε-SG expression was most marked in the neuronal cells within the olfactory bulb, hippocampus, cerebral cortex, pons, and cerebellar cortex. In almost all cases, ε-SG around cell bodies was more remarkable than that of fibrous structures.

Subcellular fractionation of brain homogenate suggested differential localization of ε-SG1 and ε-SG2 in synaptosomal membranes. We speculate that the two ε-SG isoforms, ε-SG1 and ε-SG2, play different roles at synapses in neurons, and this difference may relate to the structural difference of ε-SGs at their cytoplasmic domains (Fig. 1). Sequence analysis of this domain using the BLAST program (blastp) did not suggest any candidate gene, but a consensus sequence (Arg-Lys-Leu-Thr) for a phosphorylation site of cAMP- and cGMP-dependent protein kinase is present in the ε-SG2 C-terminal. To clarify the roles of ε-SG isoforms in the brain, it is important to search out proteins that interact with their unique cytoplasmic domains.

SGs (α, β, γ, and δ) are thought to function only when they form a subcomplex (SGC) within the dystrophin-DAP complex. ε-SG1 also has been shown to participate in forming SGCs in the smooth muscle and peripheral nervous system [20,47]. Therefore, the question arises whether the ε-SGs play a role as a constituent of the DAP complex that anchors dystrophin in the central nervous system or not. Several different promoters, scattered throughout the *dystrophin* gene, drive the tissue-specific expression of full-length dystrophins (427 kDa) and various short dystrophin isofroms including dystroglycan-binding sites, i.e., Dp260, Dp140, Dp116, and Dp71, in reference to their respective molecular sizes [5,11,17,27,30,35]. Among these dystrophins, full-length dystrophin (Dp427), Dp140, and Dp71 are expressed in the central nervous system. Dp427 is found almost exclusively in neurons in the cerebral cortex and cerebellar cortex, and localized along the plasma membrane of their perikaryons and the proximal dendrites [29,37]. It is also expressed in the hippocampal pyramidal cell layer but not in granule cells of the dentate gyrus. Within the cerebellar cortex, Dp427 is found in Purkinje cells but not in granule cells, Golgi cells, and basket cells. On the other hand, Dp140 is found in astrocytic processes throughout the neuropil, along penetrating microvasculature, and on the cells ensheathing olfactory neurons [30]. The major dystrophin isoform in the brain, Dp71, is expressed in the cerebral cortex, granule cells of the hippocampal dentate gyrus, olfactory bulb, and pituitary gland [34]. These brain dystrophins have been shown to form several types of complex with some dystrophin-accociated proteins, i.e., dystroglycans, syntrophins, and dystrobrevins [8,37]. However, to date, no dystrophin-DAP complex including an SGC has ever been found in the brain, although the expression patterns of the Dp427, Dp140, and Dp71 are totally overlapped with those of ε-SGs except for the neurons in the substantia nigra (Figs. 6 and 7). Besides ε-SGs, faint expression of β-, γ-, and δ-SG were found in whole brain materials at the transcriptional level [4,31,39,41]. We preliminarily tried to detect the SGs in the brain subcellular fractions containing ε-SGs by immunoblot, but found no evidence of their expression at the protein level (data not shown). In the central nervous system, especially in dorpaminergic neurons, the ε-SGs do not seem to form SGCs as a subcomplex of the dystrophin-DAP complex, but it is possible that the brain ε-SGs associate with other kinds of membrane proteins and/or cytoskeletal proteins in neuronal cells.

M-D is a movement disorder clinically characterized by myoclonus combined with dystonia. These abnormal movements can be caused by the pharmacological interference in dopaminergic and serotonergic neurotransmission. Indeed, dopa-responsive dystonia is caused by mutation in genes encoding enzymes of dopamine biosynthesis [19,24], and the transcript for *DYT1*, a gene responsible for early-onset torsion dystonia, is shown to be highly enriched in dopaminergic neurons in the substantia nigra [2]. Furthermore, a

point mutation in the gene for the dopamine D2 receptor was found in a family with M-D [23]. We demonstrated ε-SG expression in the dopaminergic neurons of the substantia nigra in mouse brain (Fig. 7). Biochemical fractionation of the brain homogenates suggested that some population of ε-SGs was present in synaptic membranes. These results raise the possibility that ε-SGs might be involved in the neuronal functions through dopaminergic transmission. However, besides the dopaminergic neurons, we detected ε-SG expression in neuronal cells in various brain regions (Figs. 6 and 7). Further studies for the expression of ε-SG among other types of neurons are necessary to elucidate the precise role of ε-SG in the central nervous system. A more recent study reported an M-D family with a novel mutation in the *SGCE* gene associated with epilepsy and/or electroencephalogram (EEG) abnormalities [15]. Interestingly, we found marked expression of ε-SGs in the cerebral cortex, hippocampus, and cerebellar cortex (Figs. 6 and 7), the location of lesions for some types of epilepsy [6,10,28]. It is therefore of interest to study the ε-SG expression in experimental models of epilepsy.

Disruption of the SGC including ε-SG1 does not produce obvious abnormalities in the peripheral nervous system [20], while it does induce vascular smooth muscle irregularities, which eventually cause cardiomyopathy [7]. Biochemical analysis for SGC formation [20] suggests that the loss-of-function mutations in the *SGCE* gene, reported in almost all M-D patients, would disrupt SGCs in the smooth muscle and Schwann cells. However, heart failure has not been reported in M-D patients, suggesting that differences exist between the pathophysiological mechanisms in the brain and smooth muscle in sarcoglycan deficiency.

In summary, we cloned and subsequently characterized two ε-SG isoforms, designated ε-SG1 and ε-SG2, in the brain. Our results strongly suggest that these isoforms play key functional roles in synaptic membranes of neuronal cells. Further investigation into the individual role of ε-SG isoforms would contribute to the understanding of the molecular mechanisms of M-D.

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α1-Syntrophin Modulates Turnover of ABCA1*

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Youichi Munehira‡§, Tomohiro Ohnishi‡§, Shinobu Kawamoto¶, Akiko Furuya¶, Kenya Shitara¶, Michihiro Imamura‖, Toshifumi Yokota‖, Shin'ichi Takeda‖, Teruo Amachi‡, Michinori Matsuo‡, Noriyuki Kioka‡, and Kazumitsu Ueda‡**

From the ‡Laboratory of Cellular Biochemistry, Division of Applied Life Sciences, Graduate School of Agriculture, Kyoto University, Kyoto 606-8502, Japan, the ¶Tokyo Research Laboratories, Kyowa Hakko Kogyo Company Limited, Machida, Tokyo 194-8533, Japan, and the ‖National Institute of Neuroscience, National Center of Neurology and Psychiatry, 4-1-1 Ogawa-higashi, Kodaira, Tokyo 187-8502, Japan

ABCA1 (ATP-binding cassette transporter A1) mediates the release of cellular cholesterol and phospholipid to form high density lipoprotein. Functions of ABCA1 are highly regulated at the transcriptional and post-transcriptional levels, and the synthesized ABCA1 protein turns over rapidly with a half-life of 1–2 h. To examine whether the functions of ABCA1 are modulated by associated proteins, a yeast two-hybrid library was screened with the C-terminal 120 amino acids of ABCA1. Two PDZ (PSD95-Discs large-ZO1) proteins, α1-syntrophin and Lin7, were found to interact with ABCA1. Immunoprecipitation revealed that α1-syntrophin interacted with ABCA1 strongly and that the interaction was via the C-terminal three amino acids SYV of ABCA1. Co-expression of α1-syntrophin in human embryonic kidney 293 cells retarded degradation of ABCA1 and made the half-life of ABCA1 five times longer than in the cells not expressing α1-syntrophin. This effect is not common among PDZ-containing proteins interacting with ABCA1, because Lin7, which was also found to interact with the C terminus region of ABCA1, did not have a significant effect on the half-life of ABCA1. Co-expression of α1-syntrophin significantly increased the apoA-I-mediated release of cholesterol. ABCA1 was co-immunoprecipitated with α1-syntrophin from mouse brain. These results suggest that α1-syntrophin is involved in intracellular signaling, which determines the stability of ABCA1 and modulates cellular cholesterol release.

Cholesterol is not catabolized in the peripheral cells and, therefore, is mostly released and transported to the liver for conversion to bile acids to maintain cholesterol homeostasis. The same pathway may also remove cholesterol that has pathologically accumulated in cells, such as at the initial stage of atherosclerosis. The assembly of high density lipoprotein (HDL)[1] particles by lipid-free apolipoproteins with cellular lipid has been recognized as one of the major mechanisms for the cellular cholesterol release (1, 2). ApoA-I-mediated cholesterol efflux is a major event in "reverse cholesterol transport," a process that generates HDL and transports excess cholesterol from the peripheral tissues, including the arterial wall, to the liver for biliary secretion. The importance of ABCA1 in this active cholesterol-releasing pathway for regulating cholesterol homeostasis became apparent with the finding that it is impaired in the cells from patients with Tangier disease, a genetic deficiency of circulating HDL (3, 4). Tangier disease is caused by mutations in ABCA1. ABCA1 mutations are also a cause of familial HDL deficiency and are associated with premature atherosclerosis (5, 6).

Cholesterol is a prerequisite for cells, but, at the same time, the hyper-accumulation of cholesterol is harmful to cells. Therefore, the expression of ABCA1 is highly regulated at both the transcriptional and post-transcriptional level. The transcription of ABCA1 is regulated by the intracellular oxysterol concentration via the LXR/RXR nuclear receptor (7), and the synthesized ABCA1 protein turns over rapidly with a half-life of 1–2 h (8–10). However, the post-translation regulatory mechanism of ABCA1 is unclear. We analyzed the associated proteins that could be involved in the post-translational regulation of ABCA1. By yeast two-hybrid screening with the C-terminal 120 amino acids of ABCA1, two PDZ (PSD95-Discs large-ZO1)-binding proteins, α1-syntrophin and Lin7, were found to interact with ABCA1. Immunoprecipitation confirmed the association of α1-syntrophin and ABCA1 via its C-terminal amino acids. The importance of this interaction in the regulation of ABCA1 function was examined.

EXPERIMENTAL PROCEDURES

Materials—The anti-ABCA1 monoclonal antibody KM3073 was generated against the first extracellular domain of the human ABCA1 protein in rats. Anti-ABCA1 monoclonal antibody KM3110 was generated against the C-terminal 20 amino acids of ABCA1 in mice. Anti-ABCA1 polyclonal antibody, previously described (11), was used for immunostaining. Affinity-purified antibody specific for α1-syntrophin was prepared using recombinant proteins. Human α1-syntrophin (amino acids 169–346) was fused to glutathione *S*-transferase (GST) in the pGEX vector (Amersham Biosciences) and to the maltose-binding protein (MBP) in the pMAL-c2 vector (New England Biolabs, Inc.). The GST-α1-syntrophin protein was used as an antigen. Obtained rabbit antiserum was affinity purified with the column coupled with the MBP-α1-syntrophin fusion protein. Anti-FLAG epitope monoclonal antibody M2 was purchased from Sigma. Human apoA-I was a gift from Dr. Shinji Yokoyama, Nagoya City University Graduate School of Medical Sciences.

Animals—16-week-old α1-syntrophin (−/−) (12) and wild-type C57BL/6 mice were used in this study. The animals were allowed *ad libitum* access to food and drinking water. Mice carrying mutations were identified by Southern blot analysis as described (12).

Yeast Two-hybrid Library Screening—The Matchmaker Two-hybrid

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§ These authors contributed equally to this work.

** To whom correspondence should be addressed. Tel.: 81-75-753-6105; Fax: 81-75-753-6104; E-mail: uedak@kais.kyoto-u.ac.jp.

[1] The abbreviations used are: HDL, high density lipoprotein; ABCA1, ATP-binding cassette transporter A1; HEK293, human embryonic kidney 293; LXR/RXR, liver X receptor/retinoid X receptor; PBS, phosphate-buffered saline; PDZ, PSD95-Discs large-ZO1.