Relationship Between Contact Inhibition and Intranuclear S100C of Normal Human Fibroblasts

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Abstract. Many lines of evidence indicate that neoplastic transformation of cells occurs by a multistep process. For neoplastic transformation of normal human cells, they must be first immortalized and then be converted into neoplastic cells. It is well known that the immortalization is a critical step for the neoplastic transformation of cells and that the immortal phenotype is recessive. Thus, we investigated proteins downregulated in immortalized cells by two-dimensional gel electrophoresis. As a result, S100C, a Ca$^{2+}$-binding protein, was dramatically downregulated in immortalized human fibroblasts compared with their normal counterparts. When the cells reached confluence, S100C was phosphorylated on threonine 10. Then the phosphorylated S100C moved to and accumulated in the nuclei of normal cells, whereas in immortalized cells it was not phosphorylated and remained in the cytoplasm. Microinjection of the anti-S100C antibody into normal confluent quiescent cells induced DNA synthesis. Furthermore, when exogenous S100C was compelled to localize in the nuclei of HeLa cells, their DNA synthesis was remarkably inhibited with increase in cyclin-dependent kinase inhibitors such as p16$^{INK4a}$ and p21$^{Waf1}$. These data indicate the possible involvement of nuclear S100C in the contact inhibition of cell growth.

Key words: immortalization of human cells • S100C protein • actin filaments • nuclear import • cell density-dependent growth arrest

Introduction

Many lines of evidence indicate that neoplastic transformation of cells occurs by a multistep process, which is clearly determined by the successive stages of aging, immortalization, and neoplastic transformation (Namba et al., 1996; Hayflick, 1997). It is well known that normal human diploid cells are extremely refractory to in vitro neoplastic transformation, because they cannot be easily immortalized. Once they are immortalized, they can easily undergo neoplastic transformation by treatment with carcinogenic agents, including chemicals, radiation, and oncogenes (Rhim et al., 1990; Namba et al., 1996). These facts indicate that cellular immortalization is an important early step of human carcinogenesis. However, the molecular mechanism responsible for cellular immortalization is still poorly understood.

Two-dimensional (2-D)\(^{1}\) PAGE is one of the powerful techniques for analyzing protein dynamics under various physiological conditions of cells. In this study, we used the 2-D PAGE technique to investigate the protein dynamics in normal and immortalized human fibroblasts in order to understand the mechanisms of cellular immortalization. We found that S100C (S100A11, calgizzarin; pI 6.2, molecular mass 11 kD) was dramatically downregulated in immortalized human fibroblasts as compared with their normal counterparts. S100C is a member of EF-hand type Ca$^{2+}$-binding protein of the S100 family and was first identified in chicken gizzard smooth muscle and has also been detected in several mammalian species and tissues (Watanabe et al., 1991; Tanaka et al., 1995; Schnekess and Walsh, 1997). It has

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\(^{1}\)Abbreviations used in this paper: 2-D, two-dimensional; BrdU, bromodeoxyuridine; CBB, Coomassie brilliant blue; GST, glutathione S-transferase; NLS, nuclear localization signal; PVDF, polyvinylidene difluoride filter.
been suggested that the S100 family, including S100C, plays important roles in cell cycle regulation, differentiation, growth, and metabolic control (Ailen et al., 1996; Marti et al., 1996; Scotto et al., 1998). Many studies have been carried out to determine the functions of S100C in vivo and in vitro; however, little is known about its precise intracellular functions. The purpose of this study was to investigate the biological functions of S100C in normal fibroblasts and their immortalized cells.

### Materials and Methods

#### Cell Culture, 32P Labeling, Bromodeoxyuridine (Brdu) Labeling, and [3H]Thymidine Incorporation

Normal human fibroblast strains (KMS-6, OUMS-36, and OUMS-24) and their immortalized cell lines (KMS-6-DU, OUMS-1, and OUMS-24F) were cultured in a 5% CO2 incubator at 37°C. MEF (Nissui) supplemented with 10% FBS (Intergen Co.) was used. Characteristics of these cell lines have been described elsewhere (Namba et al., 1985, 1988; Bai et al., 1993).

32P-labeling of cells was performed as described previously (Kondo et al., 1993). In brief, cells were incubated in a phosphate-free medium for 2 h and then labeled with 32Porthophosphate at a dose of 100 mCi/ml (ICN) at 37°C for 6 h. For phosphorylation of recombinant S100C in a cell-free system, confluent normal KMS-6 cell pellets were lysed in 500 μl of detergent disruption buffer (0.5% NP-40, 2.5 mM DTT, 15% glycerol, 1 mM NaF, 0.1 mM Na3VO4, 135 mM KCl, 100 μM CaCl2, 1 μg/ml leupeptin, 1 μg/ml aprotinin, 50 mM Tris-HCl, pH 7.4). Supernatants were separated by a 20-min centrifugation at 15,000 rpm, and protein contents were adjusted to 1 mg/ml. Purified recombinant glutathione S-transferase (GST)-S100C (1 μg) and [γ-32P]ATP (1 μCi) were added to the supernatants and incubated for 25 min at 25°C. 32P-labeled GST-S100C in cell lysates was obtained by glutathione-agarose affinity chromatography. 32P-labeled S100C was cut off by treatment of the 32P-labeled GST-S100C with bovine thrombin and then subjected to the SD PAGE. DNA synthesis was assessed by BrdU (Sigma) (Dover and Patel, 1994) or [3H]thymidine uptake. Detection of the BrdU was carried out using mouse anti-BrdU antibody (Neomarkers) as the primary antibody and FITC-conjugated goat anti-mouse IgG antibody (Sigma) as the secondary antibody. To assay [3H]thymidine incorporation, trypsized cells were plated in 24-well plates at a density of 5 × 104 cells/ml and cultured overnight at 37°C in MEM supplemented with 10% Tet-cycline system-approved FBS (GIBCO BRL) according to the manufacturer's instructions. A 48 h, stably transfected clones were selected by hygromycin B (200 μg/ml) in MEM supplemented with 10% Tet system approved FBS (Clontech) and doxycycline (1 μg/ml).

#### 2-D Gel Electrophoresis

Protein sampling and isoelectric focusing separation with immobilized pH gradient (pH, 4.0–7.0) gels (IPG; A mersham Pharmacia Biotech) were performed as described previously (Kondo et al., 1998a). A 2D gel equilibration with SDS, the IPG gels were placed directly onto 15% tricine SDS-polyacrylamide slab gels and run with a vertical electrophoresis system (Nihon Eido). Owing to the nature of this system, we used two types of running buffer for electrophoresis, i.e., a top running buffer (0.1 M tricine, 0.1% SDS, 0.1 M Tris, pH 8.2) as a cathode and a bottom running buffer (0.2 M Tris, pH 8.9) as an anode.

#### Protein Sequencing

Comassie brilliant blue (CBB)-stained protein on a polyvinylidene difluoride filter (PVDF) membrane was digested with 1 pmol of V8 endopeptidase (Achromobacter protease I; WAKO). Some peptide fragments eluted from the PVDF membrane were separated on a C18 column (YM-C-pack ODS-A, 150 mm x 6.0 mm ID; A mersham Pharmacia Bio tech) by HPLC, with monitoring of their absorbance at 210 nm. The separated peptides were subjected to NH2-terminal sequencing on a M odel 491 peptide sequencer (Applied Biosystems). For NH2-terminal sequencing of phosphopeptide, the spot of phosphopeptide on a TLC plate was scraped off and extracted with electrophoresis buffer (formic acid/acetate acid/double-distilled water (DDW), 1:3:16). A 0.5 g dry extractions was dried and subjected to tricine SDS-PAGE, and blotted onto a PVDF membrane. The peptide band was cut-off from the CBB-stained PVDF membrane, and the peptide sequence was analyzed by the peptide sequencer.

#### Antibody to Recombinant Human S100C Protein

Echerichia coli (E. coli NM 522) cells were transformed by the procaryotic expression vector pGEX-2T-S100C. Purification of the GST-S100C fusion protein in transformed cell extracts was performed by glutathione-agarose affinity chromatography using a Sephadex 4B column (A mersham Pharmacia Biotech). A 2D gel analysis of the GST-S100C fraction with a dialysis buffer (150 mM NaCl, 1.5 mM KCl, 20 mM Tris, pH 7.4), bovine thrombin was added to the GST-S100C solution at a concentration of 1:200 (w/v). The mixture was incubated at 37°C for 60 min to complete the proteolysis reaction, and then S100C protein was isolated from the protein mixture by chromatography with a Sephadex 4B column. For preparation of anti-human S100C antibody, rabbits were immunized three times for 2 mo with the human recombinant S100C (each at 1 mg per animal). Immune serum was collected from each rabbit and the IgG fraction was isolated by salting-out. We confirmed that anti-S100C antibody reacted specifically with human S100C (11 KD) on Western blot.
Immunocytochemistry
To visualize S100C and actin filaments simultaneously, cells were treated with rabbit anti-S100C antibody at 37°C for 1 h and treated with BODIPY 558/568-conjugated phalloidin (a specific probe for actin filaments; Molecular Probes, Inc.) under the same conditions reported previously (Sakaguchi et al., 1998, 1999; Kondo et al., 1998b). Then, cells were treated at 37°C for 1 h with a secondary antibody and FITC-conjugated goat anti-rabbit IgG antibody (Sigma).

Immunostaining of Exogenously Added S100C
Total cell lysates were prepared by homogenizing normal and immortalized cells at various stages in a homogenizing buffer (10 mM KCl, 3 mM MgCl₂, 10 μg/ml leupeptin, 10 μg/ml aprotinin, and 200 μg/ml phenylmethylsulfonyl fluoride, 10 mM HEPES, pH 7.0). Confluent normal and immortalized cells on coverslips were permeabilized with digi- tonin (Mitsui and Parnaik, 1995; Y. Okaya et al., 1999) and then incubated with normal or immortalized cell extracts that were treated with or not treated with alkaline phosphatase from Escherichia coli (WAKO) at 37°C for 15 min. Thereafter, the cells were immunostained for S100C as described above.

Immunoprecipitation and Immunoblotting
Total cell lysates were prepared by homogenizing normal and immortalized cells at various stages with a cell lysis buffer (300 mM NaCl, 1% Triton X-100, 1 mM CaCl₂, 10 μg/ml leupeptin, 10 μg/ml aprotinin, and 200 μg/ml phenylmethylsulfonyl fluoride, 10 mM TRIS, pH 7.3). Subfractionation of the total cell lysates was carried out basically as described previously (Lindeman et al., 1997). In brief, the total cell lysates, soluble, and nuclear fractions were cleared by treatment with excess of protein A-Sepharose (Sigma). Cleared cell samples were incubated with rabbit anti-S100C antibody at 4°C for 60 min followed by protein A, and the immunoprecipitates were resolved on tricine SDS-PAGE and transferred onto nitrocellulose mem- branes (A merham Pharmacia Biotech). Immunoblotting of the membranes was performed as reported previously (Sakaguchi et al., 1999) using rabbit anti-S100C antibody or rabbit anti-actin antibody followed by HRP-conjugated goat anti-rabbit IgG antibody (MBL). Then, S100C and actin were detected by the enhanced chemiluminescence system (A merham Pharmacia Biotech). Native polyacrylamide gel electrophoresis analysis was performed as reported previously (Tom et al., 1996). In brief, the total cell lysates were resolved in 4% native polyacrylamide gels at 4°C and then immunoblotted with rabbit anti-S100C antibody as described above.

Cosedimentation Assay
To examine binding of S100C to purified actin filaments, a simple high-speed cosedimentation assay was performed as described previously (Gonzalez et al., 1998). Purified monomeric actin (G-actin, 10 μM; Sigma) was incubated with recombinant GST-S100C (10 μM) or GST (10 μM) in an actin polymerization buffer (2 mM MgCl₂, 100 mM KCl, 0.1 mM ATP, 10 mM HEPES, pH 7.3) containing various concentrations of Ca²⁺ at room temperature for 60 min to complete actin polymerization. A association of recombinant S100C with polymerized actin filaments was determined by a sedimentation assay with ultracentrifugation at 126,000 g for 20 min in a Beckman Airfuge. Equal volumes of the pellet and supernatant from each reaction mixture were subjected to SDS-PAGE. The amounts of GST-S100C and actin were then quantified by densitometry of the stained gels.

DNase I Affinity Chromatography
A flii-Gel 10 (Bio-Rad) coupled with D Nase I, which specifically binds to G-actin, was used to examine the interaction of G-actin with GST-S100C. G-actin (10 μM) bound D Nase I affinity beads and various concentrations of GST-S100C (1-100 μM) in a hypoxicen strength buffer (0.1 mM ATP, 10 mM HEPES, pH 7.3) were incubated for 2 h at room temperature in the presence of 1 mM Ca²⁺. After the incubation, the beads were washed three times with the same buffer, resuspended in the electrophoresis sample buffer, and analyzed by SDS-PAGE.

2-D Separation of S100C Phosphopeptides
³²P-labeled phosphopeptide mapping was performed essentially as described previously, with a minor modification (Fackler et al., 1990). In brief, bands containing ³²P-labeled cellular S100C or recombinant S100C were excised from the dried SD S-polyacrylamide gel, rehydrated, and digested in 50 mM NH₄CO₃ buffer, pH 8.3, containing l³³P-labeled endopeptidase for 16 h at 37°C. The ratio (mol/mol) of l³³P-labeled endopeptidase and S100C was 1:100. A fter centrifugation of the excised gel suspension, the supernatant was collected and lyophilized. The lyophilized sample was dissolved in 1 ml D D W and relyophilized. This process was repeated five times to completely remove NH₄CO₃. The finally lyophilized samples were dissolved in 5 μl of l³³P-labeled endopeptidase buffer (formic acid/acetic acid/ D D W, 1:3:16) and applied to thin layer plates (A merham Pharmacia Biotech). Electrophoresis was carried out in the first dimension at 1,000 V for 30 min with cooling at 4°C. A fter drying, the plate was chromatographed for 3-4 h in the second dimension in n-butanol/pyridine/acetic acid/D D W (6:5:5:1:4) until the leading edge of the solvent had reached 1-2 cm from the top.

Phosphoamino Acid Analysis
L³³P-labeled endopeptide digests of ³²P-labeled intracellular S100C and recombinant S100C were incubated in 100 μl of 6 N HCl at 105°C for 60 min as described previously (Fackler et al., 1990). The samples were concentrated by a Speed VAC concentrator and dissolved in 5 μl of D D W containing standards (each 1 mg/ml of cold phosphoserine, phosphothreono- nine, and phosphotyrosine). Electrophoresis was carried out at 1,000 V for 50 min with cooling at 4°C using a pyridine/acetic acid/D D W (1:10:189) electrophoresis buffer. A fter drying the plates, the standards were identi- fied with ninhydrin spray (Sigma). Then, ³²P-labeled phosphoamino acids were visualized by autoradiography.

Microinjection of S100C Expression Vector or Rabbit Anti–human S100C Antibody
The plasmid pT Racer-E FA-S100C was microinjected at a dose of 500 cop- ies per nucleus into immortalized cells grown on coverslips. A fter 24 h, cells were fixed and observed under a fluorescence microscope. NBD fluo- ride (Molecular Probe), an amine reactive fluorescent probe, was conjugated with purified recombinant S100C according to the manufacturer's recommended protocol. The S100C-NBD fluoride (5 mg/ml) was microinjected into the cytoplasm of normal semiconfluent fibroblasts at a dose of 50 fl per cell, and the injected cells were incubated at 37°C for 2 h and then observed under a fluorescent microscope. For microinjection of rabbit anti-S100C antibody, normal cells were plated on coverslips. A fter reaching confluence, the cells were further maintained for 2 wk with three changes of the medium. A fter confirmation that the cells did not incorpo- rate any BrdU, rabbit anti-S100C antibody (5 mg/ml) was microinjected into the cytoplasm at a dose of 50 fl per cell, and the injected cells were incubated at 37°C for 24 h. Localization of rabbit anti-S100C antibody in the injected cells was detected with TRITC-conjugated goat anti-rabbit IgG antibody (Sigma). Then, DNA synthesis in the injected cells was assessed by BrdU staining.

Results

S100C in Human Fibroblasts
In analysis using semiconfluent cells by 2-D gel electrophoresis, several hundred proteins were detected per silver-stained gel. Numerous differences in the protein expression levels were observed between normal and immortalized cells (Fig. 1 a). We noticed a spot of low-molecular weight protein that was downregulated in immortalized KMST-6 cells as compared with their normal counterparts (Fig. 1 a, arrows). The isoelectric point and molecular mass of the protein were 6.2 and 11 kD, respectively. The amino acid sequence of the protein was then determined. Nine peaks were obtained by H P L C separa- tion of the l³³P-labeled endopeptidase digests, and four (Nos. 2, 3, 8, and 9) of them were sequenced (Fig. 1 b). A t the top of Fig. 1 c, the sequences of the four peptides (Nos. 2, 3, 8, and 9) are shown. These sequences completely correspond to the underlined sequences of the full-length human...
S100C (bottom of Fig. 1 c). As a result, the amino acid sequences of the four peptides were completely coincident with the partial sequence of human S100C protein (Fig. 1 c). Thus, we concluded that this protein was the human S100C protein.

To determine the biological functions of S100C, we built up a monospecific polyclonal antibody to human S100C (Fig. 1 d). Western blot analysis with the antibody showed that expression of the S100C protein was lower in immortalized fibroblast cell lines (KMST-6, SUSM-1, OUMS-24F) than in normal human fibroblast strains (KMS-6, OUMS-36, OUMS-24) at semiconfluence (Fig. 1 e). In addition, we found that the expression of the protein increased in parallel to cell density in both normal and immortalized cells (Fig. 1 f).

**Localization of S100C in Cells**

We next examined the subcellular distribution of S100C in normal and immortalized cells at low and high cell densities using the rabbit anti-S100C antibody. Immunoblot analyses showed that S100C was predominantly present in the soluble fractions from normal and immortalized cells at semiconfluence (Fig. 2 a). Interestingly, S100C accumulated in the nuclei of normal cells when they reached confluence, whereas it remained in the cytoplasm of immortalized cells even after confluence (Fig. 2 a). No difference in the cDNA sequence of S100C was observed between normal KMS-6 and immortalized KMST-6 cells (data not shown), indicating that different localization of S100C in normal and immortalized cells at confluence was not due to the S100C gene mutation.

Although it has been proposed that S100C can associate with actin cytoskeletal protein in vitro (Naka et al., 1994), it is still unclear whether the association actually occurred in human fibroblasts. For this point, the interaction between S100C and actin filaments in cells was further evaluated by GST fusion protein binding and immunoprecipitation assays. By loading extracts of normal and immortalized cells onto a column filled with glutathione beads coupled with GST-S100C fusion protein (Fig. 2 b, top right) or GST alone (Fig. 2 b, top left), we detected a protein with a mo-
lecular mass of 42 kD in eluates from the GST-S100C column (Fig. 2 b, top right) but not from the control GST column (Fig. 2 b, top left). Western blot analysis showed that the GST-S100C binding protein (42 kD) was actin (Fig. 2 b, bottom right). When whole cell lysates from normal and immortalized cells at semiconfluence and confluence were immunoprecipitated with rabbit anti-S100C antibody, actin was coprecipitated with S100C in these lysates (Fig. 2 c). In contrast, neither S100C nor actin was detected in immunoprecipitates prepared with preimmune serum (data not shown). A tin bound to S100C was detected in the soluble fractions from both normal and immortalized cells at semiconfluent and confluent stages but not in the nuclear fractions (Fig. 2 d). These results clearly show that S100C associates with actin filaments in the cytoplasm but not in the nucleus of both types of cells independently of cell density.

Immunofluorescence staining of normal and immortalized semiconfluent cells showed that S100C was distributed in the cytoplasm (Fig. 3, a and b). At confluence, intranuclear distribution of S100C was observed in normal cells but not in immortalized cells (Fig. 3, c and d). Preincubation of anti-S100C antibody with the purified recombinant S100C protein diminished the immunostaining of S100C (Fig. 3, a-# and c-#). In addition, the cells were not stained with preimmune serum, and this distribution pattern was reproduced with different fixations, such as methanol and acetone fixations (data not shown). These results indicated that the S100C immunostain pattern was specific.

Immunofluorescence staining also demonstrated that S100C was colocalized with actin stress fibers (Fig. 3, e, f, e-a', and f-b'). In addition, a clear colocalization pattern of S100C with actin filaments in normal and immortalized cells by immunoprecipitation assay. Whole cell lysates (c), and soluble (S) and nuclear (N) fractions (d) from normal and immortalized cells were immunoprecipitated with rabbit anti-S100C antibody (c, top; d, top). Total amounts of actin in whole cell lysates were determined by Western blot analysis using rabbit anti-actin antibody (c, bottom).

Figure 2. Association of S100C with actin filaments. (a) Subcellular distribution of S100C and actin filaments in soluble and nuclear fractions was determined by Western blotting. (b) Silver staining of GST-S100C (right) or GST (left) binding proteins in normal (lane 1) and immortalized cells (lane 2). A arrowhead indicates a 42-kD protein that was coprecipitated with GST-S100C, but not GST alone. This protein was identified as actin by Western blotting using rabbit anti-actin antibody (b, bottom). (c and d) Association of S100C with actin filaments in normal and immortalized cells at semiconfluent and confluent stages was immunoprecipitated with rabbit anti-S100C antibody (c, middle and bottom; d, bottom) and rabbit anti-S100C antibody (c, top; d, top). Total amounts of actin in whole cell lysates were determined by Western blot analysis using rabbit anti-actin antibody (c, bottom).
Interaction of S100C with Actin Filaments In Vitro and In Vivo

By coimmunoprecipitation and affinity chromatography, we demonstrated that endogenous S100C actually binds to actin. However, it is not clear what type of actin, for example, G-actin (monomeric actin) or F-actin (actin filaments), associates with S100C. In addition, it remains to be determined whether interaction of S100C with actin is direct but mediated via an unidentified linker protein(s). Thus, we further investigated the in vitro interaction between S100C and actin filaments by cosedimentation assay.

As shown in Fig. 4 a, when affinity-purified GST-S100C was added to G-actin before its polymerization reaction, GST-S100C was directly incorporated into actin filaments assembled in a Ca\(^{2+}\)-dependent manner, whereas S100C-GST failed to bind to actin filaments in the absence of Ca\(^{2+}\). GST alone was never incorporated into actin filaments. Interaction of S100C-GST with G-actin was evaluated by a coprecipitation assay using G-actin-bound DNase I affinity beads in the presence of 1 mM Ca\(^{2+}\). Fig. 4 b shows that G-actin alone did not associate with GST-S100C even though excessive amounts of S100C-GST were added to the mixture. If S100C and DNase I have the same or overlapping binding sites on the actin monomer, binding of S100C to G-actin may not be observed. This possibility remains to be determined. To decide the molar ratio of an S100C–actin filaments complex, densitometric analysis of the in vitro-assembled complex was done, and the results are shown in Fig. 4 c. The amount of GST-S100C that bound to actin filaments increased in parallel with the amount of GST-S100C added, and the mol:mol ratio of GST-S100C and actin filaments was ~1:1. To further examine the interaction of S100C with actin filaments in cells, recombinant S100C labeled with a fluorescent probe was microinjected into the cytoplasm of normal semiconfluent fibroblasts. After 2 h of incubation, the injected exogenous S100C coexisted with actin filaments in a meshwork structure in the cytoplasm (Fig. 4 d). These results coincide well with the immunofluorescent staining patterns of the endogenous S100C in cells (Fig. 3, e and e-a). Thus, we concluded that S100C directly interacted with actin filaments in a Ca\(^{2+}\)-dependent manner.

Figure 3. Subcellular localization of S100C in normal KMS-6 and immortalized KMST-6 cells at semiconfluent and confluent stages. S100C was visualized by immunofluorescence staining. (a-d) Normal (a and c) and immortalized cells (b and d) were stained at semiconfluence (a and b) or at confluence (c and d). S100C was detected in the nuclei of normal cells at confluence. Preincubation of anti-S100C antibody with recombinant S100C diminished the immunostaining (a# and c#). (e-j) Double immunofluorescence stainings were performed in normal cells with rabbit anti-S100C antibody (e, e-a’, g, and i) and BODIPY 558/568-conjugated phalloidin (f, f-b’, h, and j). S100C and actin were identified by fluorescence-labeled second antibodies, FITC (green) for S100C, and BODIPY 558/568 (red) for actin, respectively. In interphase cells, the interaction of S100C with actin filaments (e and f) was visualized in cytoplasmic domains (enlarged view of e and f, e-a’, e-b’, and f-b’). After allowing the cells to attach to and spread on coverglasses for 1 h, S100C (g and i) and actin filaments (h and j) were stained in the cells. A rows show colocalization of S100C and actin filaments at the leading edges of filopodia (g and h) and lamellipodia (i and j). (k-n) Immortalized cells with immunofluorescence staining (k, m, and n, pTracer-S100C cDNA) or empty vector (l, pTracer). S100C-expressing (k and m) and -nonexpressing cells (l) were detected by a GFP marker (green) inserted in pTracer, and actin in the cells injected with pTracer-S100C (m) was visualized by BODIPY 558/568-conjugated phalloidin staining (n, red). S100C-expressing cells display a drastic morphological change accompanied by the formation of cell protrusions (k and m) with remarkable accumulation of actin filaments (n, arrows). Bars: 20 μm (b, d, f, i, and m); 5 μm (f-b’); 10 μm (j).
Movement of S100C into Nuclei of Normal Cells at Confluence

The nuclear localization of S100C in permeabilized normal cells was not affected by the addition of extracts of immortalized cells at semiconfluent (Fig. 5, panel I) and confluent stages (Fig. 5, panel II). When immortalized confluent cells were permeabilized with digitonin and incubated with the extracts of normal semiconfluent cells, S100C still remained in the cytoplasm (Fig. 5, panel III). However, S100C in immortalized confluent cells moved into the nuclei when the cells were permeabilized and incubated with the extracts of normal confluent cells (Fig. 5, panel IV). These results indicate that S100C can move from the cytoplasm into the nucleus of normal cells at confluence, but that this motility of the protein is lost in immortalized cells. In other words, cytoplasmic localization of S100C in immortalized cells does not depend on the nuclear exclusion capacity of S100C in the cells.

Interestingly, S100C was phosphorylated only in normal confluent cells (Fig. 5 b). This phosphorylation was markedly reduced by treatment of the cell extracts with alkaline phosphatase (an E. coli enzyme, 4 U) at 37°C for 1 h (Fig. 5 c). In addition, electrophoretic separation in the native condition followed by immunoblotting with S100C antibody revealed three (large, middle, and small) protein bands in normal semiconfluent cells as well as immortalized cells at semiconfluent and confluent stages (Fig. 5 d). However, the middle band was lost in normal confluent cells (Fig. 5 d). The middle band reappeared when normal confluent cell extracts were treated with alkaline phosphatase. When the normal confluent cell extracts were added to permeabilized immortalized cells, S100C moved...
into the nucleus, whereas the protein remained in the cytoplasm when alkaline phosphatase pretreated extracts were added (Fig. 5e). These results indicate that the S100C in normal cells is phosphorylated specifically at the confluent stage, forms a complex with unidentified protein(s) (Fig. 5d, large band), and moves into the nucleus.

**Physiological Significance of Phosphorylation of Threonine 10 in S100C**

We attempted to determine which amino acid(s) of S100C in normal fibroblasts were phosphorylated in response to high cell density. Furthermore, in order to determine whether endogenous and recombinant S100Cs were phosphorylated at the same or at distinct site(s), we performed 2-D separation of lysylic fragments of immunoprecipitated \(^{32}\)P-labeled endogenous S100C and \(^{32}\)P-labeled recombinant S100C. As shown in Fig. 6a, only one peptide derived from endogenous S100C was phosphorylated (Fig. 6a, left panel, NC1), and the same was true of recombinant S100C (Fig. 6a, right panel, NR1). Locations of phosphopeptide spots NC1 and NR1 were completely consistent, indicating that endogenous and recombinant S100Cs are phosphorylated at the same site. To identify the phosphopeptide, we performed NH\(_2\)-terminal sequence analysis of the peptide. As a result, both the sequences of phosphopeptides (NC1 and NR1) were ISSPTETERCIESLIAVFQK (data not shown). Phosphoamino acid analysis of \(^{32}\)P-labeled S100C...
Sakaguchi et al. S100C and Cell Growth showed that threonine was phosphorylated in endogenous S100C (Fig. 6 b, left). When recombinant S100C was incubated with confluent normal cell lysates, threonine residues were also phosphorylated (Fig. 6 b, right). These results indicate that S100C is phosphorylated on threonine residue(s) of the NH₂-terminal 20-amino acid fragment ISSPTETERCIESLIAVFQK (I4-K23 region) in vivo and in vitro.

phosphoserine (P-S) standards are indicated at the left vertical axis. Threonine was the amino acid phosphorylated in S100C. (c) Phosphorylation and nuclear accumulation of S100C. Various purified recombinant S100C homologues (wild-type S100C, 8-10 A/T S100C, 8 A/T S100C, and 10 A/T S100C) were labeled with a fluorescent probe as described in Materials and Methods. In vitro phosphorylation reactions of these labeled homologues were performed (upper panel). These 32P-labeled recombinant S100C homologues were subjected to SDS-PAGE and detected by autoradiography (upper panel, top) or CBB staining (upper panel, bottom). Wild-type S100C (lane 1) and 8 A/T S100C (lane 3) were strongly phosphorylated by coincubation with confluent normal cell homogenates, but 8-10 A/T S100C (lane 2) and 10 A/T S100C (lane 4) were not phosphorylated under the same conditions. Confluent HeLa cells permeabilized with digitonin (lower panel, 1–4) were incubated with various reaction mixtures (upper panel, lanes 1–4). Exogenously added fluorescent S100C homologues in the permeabilized cells were visualized under a fluorescent microscope (lower panel, 1–4). Nuclear transition of the wild-type S100C (lower panel, 1 and 1’) and the 8 A/T S100C (bottom panel, 3 and 3’) in the permeabilized cells, but the nonphosphorylation type 8-10 A/T (lower panel, 2 and 2’) and 10 A/T S100C (lower panel, 4 and 4’) were not imported into the nuclei. Bars, 20 µm.
Our findings raise the possibility that the phosphorylation site may be important for nuclear import of S100C. To test whether this phosphorylation regulates nuclear localization of S100C, we produced three recombinant S100C protein homologues lacking the phosphorylation sites of the I4-K23 region. The threonines 8 (T8; bold italics) and 10 (T10; bold italics) were changed to alanine (8-10 A/T S100C), and T8 alone (8 A/T S100C) or T10 alone (10 A/T S100C) was changed to alanine. As shown at the top of Fig 6 c, we found that wild-type S100C and mutant-type 8 A/T, but not 8-10 A/T S100C or 10 A/T S100C, were phosphorylated by incubation with confluent normal cell lysates. Thus, T10 was the primary site of phosphorylation in normal cells at high cell density.

We further investigated nuclear movement of exogenous recombinant S100C homologues that were added to the confluent permeabilized HeLa cells. Unlike the wild-type protein, the mutants (8-10 A/T S100C and 10 A/T S100C) showed almost entirely extranuclear localization (Fig 6 c, lower panel). The mutant 8 A/T S100C was localized in the nuclei (Fig. 6 c, lower panel). Thus, we found that the phosphorylation on a T10 is necessary to direct S100C to the nucleus.

To determine whether endogenous S100C can move from the cytoplasm into the nucleus under normal physiological conditions, we microinjected rabbit anti-S100C antibody or anti-albumin antibody (a non-cross-reactive IgG against S100C) directly into the cytoplasm of living normal cells at confluence. Consequently, rabbit anti-S100C antibody entered the nuclei of the injected cells at a frequency of 85% (Fig. 7, a-1 and a-2), whereas anti-albumin antibody injected into the cytoplasm did not (Fig. 7, c-1 and c-2). These results indicate that the nuclear envelope was intact and that the rabbit anti-S100C antibody bound to S100C moved into the nucleus from the cytoplasm. Contrarily, when the rabbit anti-S100C antibody was injected into the cytoplasm of immortalized cells at confluence, the antibody remained in the cytoplasm (Fig. 7, b-1 and b-2). It is well known that the antibody cannot go through nuclear pores due to its large size. Therefore, the present results
Suggest that S100C in living normal cells at confluence can move from the cytoplasm into the nucleus but that S100C in immortalized cells cannot.

Involvement of Nuclear S100C in the Cell Growth Arrest

A n-ti-S100C antibody was microinjected into the cytoplasm of normal quiescent cells at confluence to determine the biological significance of nuclear accumulation of S100C. Only when the injected anti-S100C antibody formed a complex with S100C protein and moved into nuclei (Fig. 7, d-1 and d-3, arrows) did the cells incorporate BrdU into their nuclei (Fig. 7, d-2 and d-3, arrows). On the other hand, cytoplasmic injection of anti-albumin antibody or IgG fraction prepared from preimmune serum showed no movement of the antibody into their nuclei and did not induce the incorporation of BrdU (data not shown). Since blocking the intranuclear S100C functions with anti-S100C antibody that entered the nucleus caused DNA synthesis in quiescent cells, nuclear accumulation of S100C may be closely related to inhibition of DNA synthesis in normal human fibroblasts at confluence.

To further evaluate the association of nuclear S100C with the cell growth arrest, we employed a Tet-on/off gene expression system. Since the endogenous S100C in Tet-off HeLa cells was localized only in the cytoplasm, the exogenous S100C may also be localized in the cytoplasm. A n NLS was linked to S100C by a PCR technique to compel exogenous S100C to move into the nucleus. Tet-off HeLa cells were transfected with an empty vector (a, panels I and II; b, panels III and IV), with pTRE S100C (a, panels III and IV; b, panels III and IV), and with pTRE S100C-NLS (a, panels V and VI; b, panels V and VI) were stained for S100C or BrdU under tetracycline-plus (a, panels I, III, and V, green; b, panels I, III, and V, left, red) and -minus (a, panels II, IV, and VI, green; b, panels II, IV, and VI, left, red) conditions. When tetracycline was removed from the medium, S100C was detected in the nuclei of Tet-off HeLa cells transfected with pTRE S100C-NLS (a, panel VI, green), and their BrdU incorporation was remarkably decreased (b, panel VI, red). Nuclei were simultaneously stained with Hoechst 33258 (b, panels I–VI, right, blue). Bars, 20 μm. (c) Tritiated thymidine incorporation by Tet-off HeLa cells transfected with pTRE S100C-NLS was assessed under tetracycline-plus and -minus conditions. After deprivation of tetracycline in the medium, DNA synthesis decreased in a time-dependent manner. (d) 6 h after deprivation of tetracycline from the culture medium, transfected cells were further incubated with [32P]orthophosphate for 6 h, and the cells were then immunoprecipitated with rabbit anti-S100C antibody. Phosphorylated S100C was detected by autoradiography (upper). Immunoprecipitated S100C was detected by Western blotting (lower). Phosphorylation of S100C in these cells was not observed. (e) Under the condition of deprivation of tetracycline in the culture medium, the expressions of three cyclin-dependent kinase inhibitors, p21Waf1, p27Kip1, and p16Ink4a, were analyzed in semi-confluent Tet-off HeLa cells transfected with the pTRE empty vector (left), and the pTRE S100C (middle) and pTRE S100C-NLS expression vectors (right) by Western blotting. (Lanes 1–4) 0, 3, 6, and 12 h after deprivation of tetracycline, respectively.
The overexpression of exogenous wild-type S100C with the formation of cell protrusions with densely orga-
nized cell density. This morphological change was associated with actin filaments in the cytoplasm in
normal and immortalized cells. Furthermore, we observed that high expression of exogenous S100C was
directly associated with actin filaments in the cytoplasm in immortalized cells at low cell density as com-
pared with their normal counterparts, and that S100C was regulated in immortalized cells at low cell density as com-
pared with their normal counterparts, and that S100C was

In this study, we found that S100C was remarkably down-
regulated in immortalized cells at low cell density as com-
pared with their normal counterparts, and that S100C was
directly associated with actin filaments in the cytoplasm in
normal and immortalized cells. Furthermore, we observed that high expression of exogenous S100C caused drastic changes in the morphology of immortalized cells at low cell density. This morphological change was associated with the formation of cell protrusions with densely organized actin filaments. Thus, it is likely that cytoplasmic S100C is implicated in the regulation of actin organization and actin filament dynamics. Intracytoplasmic injection of anti-S100C antibody caused multinucleation in most of the injected normal fibroblasts at low cell density (data not shown). In addition, multinucleated cells were often observed in cultures of immortalized cells at low cell density. Thus, formation of the S100C immunocomplex may lead to the abnormal formation of actin contractile ring in cyto-
kinesis (Haraguchi et al., 1997).

Nuclear Accumulation of S100C and Cell Density–dependent Growth Arrest

Normal human fibroblasts go into the stage of growth arrest at confluence. However, little is known about the molecular mechanism underlying this phenomenon. A clue to resolve this matter, it is important to understand how the information of growth arrest is transported from the cell–cell contact sites into the nucleus, where the on/off switch of several gene expression systems related to growth arrest are present. In other words, sites of cell–cell contact regions may represent signaling hotspots on the cell surface.

S100C was phosphorylated in normal human fibroblasts at high cell density. Interestingly, S100C was released from actin filaments when S100C was specifically phosphorylated on threonine 10. In other words, the binding ability of S100C to actin filaments was extremely diminished by the phosphorylation even in the presence of a high concentration of Ca²⁺ (data not shown). Phosphorylated S100C was accumulated in the nuclei of normal human fibroblasts. This result may be reasonable for the nuclear import mechanism of S100C because it may be impossible for S100C to move into the nucleus if the protein remains to be linked to actin filaments in the cytoplasm. Thus, dissociation of S100C from actin filaments may be one factor involved in the nuclear import mechanism of the protein.

In immortalized cells, S100C was neither phosphorylated nor imported to the nucleus. Thus, phosphorylation of S100C on threonine 10 may be essential to import into the nucleus through interaction with putative S100C-binding protein(s) containing an NLS (Dingwall and Laskey, 1991) and to contribution to the cell density–dependent growth arrest. In fact, when the phosphorylated S100C in normal cell lysates from confluent culture was dephosphorylated by treatment of the lysates with alkaline phosphatase, the nuclear import of S100C was markedly diminished. Furthermore, recombinant S100C protein homologues lacking the phosphorylation site never localized in the nucleus. Thus, we emphasize that the phosphorylation on threonine 10 is necessary for the cytoplasmic S100C to move to the nucleus. Since we did not find the NLS sequence in S100C by examining the amino acid sequence of this protein, we suppose that phosphorylated S100C could be associated with an unknown NLS-bearing protein and then their complex could move into the nucleus through interaction with nuclear transporters, such as importin-α (Gorlich et al., 1994; Moroianu et al., 1995; Weis et al., 1995) and importin-β (Chi et al., 1995; Radu et al., 1995; Cicogna et al., 1999).

Nuclear accumulation of S100C seems to be closely related to cell density–dependent growth arrest in cultures of normal human fibroblasts. The neoplastic cells such as

Discussion

Association of Cytoplasmic S100C with the Regulation of Actin Organization and Its Dynamics

In this study, we found that S100C was remarkably down-
regulated in immortalized cells at low cell density as com-
pared with their normal counterparts, and that S100C was
directly associated with actin filaments in the cytoplasm in
normal and immortalized cells. Furthermore, we observed that high expression of exogenous S100C caused drastic changes in the morphology of immortalized cells at low cell density. This morphological change was associated with the formation of cell protrusions with densely organized actin filaments. Thus, it is likely that cytoplasmic S100C is implicated in the regulation of actin organization

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HELa, K M S T-6/R as, and Saos-2 cells show no contact inhibition of growth. Therefore, we hypothesized that nuclear import of S100C could not occur in neoplastic cells. In fact, we found that S100C was localized only in the cytoplasm of neoplastic HELa, K M S T-6/R as, and Saos-2 cells, and that the phosphorylation of S100C in these cells did not occur even after confluence (data not shown). Thus, disorder of the nuclear import mechanisms of S100C may impair cell density-dependent growth arrest in immortalized and neoplastic cells at confluence.

To clarify the relationship between nuclear accumulation of S100C and cell growth arrest, we transfected Tet-off HELa cells with a plasmid pTRE S100C-NLS. Under deprivation of tetracycline in the culture medium, the transfected cells stably expressed significant amount of S100C-NLS fusion protein which was not phosphorylated but accumulated in the nuclei of the transfected Tet-off HELa cells. By this approach, it became clear that accumulation of S100C-NLS in the nuclei of HELa cells significantly inhibited DNA synthesis of the cells. Interestingly, expression of both p21WAF1 and p16INKA, the well known inhibitors of cyclin-dependent kinases (Hunte, 1993; Serrano et al., 1993), was increased in parallel with the nuclear accumulation of S100C. These results indicate that p21WAF1 and p16INKA may mediate dephosphorylation of S100C. Thus, whenever cytoplasmic S100C is artificially compelled to move into the nucleus, S100C can act as a mediator of the cell-cycle arrest independently of its phosphorylation or nonphosphorylation conditions. However, naturally, when the phosphorylation of S100C does not occur in the cytoplasm, S100C can neither move into the nucleus nor act as a cell-cycle downregulator. Consequently, we conclude that the phosphorylation of S100C is necessary for the nuclear import and the following suppression of DNA synthesis in cells.

It is clear that S100C shuttles between the cytoplasm and the nucleus of normal human fibroblasts in a cell density-dependent fashion. Recent studies also have demonstrated that the same proteins reside both at adherent junctions and in the nucleus. For example, the tight junction protein ZO-1 accumulates in the nuclei of a cell density-dependent fashion (Gottardi et al., 1996), and the focal contact protein Zyxin shuttles between the nucleus and the sites of cell adhesion in fibroblasts (Nix and Beckerle, 1997).

β-Catenin, a protein present at cell–cell adherent junctions, has been shown to work as a DNA-binding transcriptional regulator when β-catenin-Lef-1 transcription factor complex accumulates in the nucleus (Gumbiner, 1995; Brehens et al., 1996; Huber et al., 1996; Orsulic and Peifer, 1996). Recently, Carrion et al. (1999) have reported that DREAM (downstream regulatory element [DRE]-antagonist modulator), an EF-hand type Ca2+-binding protein, binds to the DRE sequence and acts as a location-dependent gene silencer of the human proaryphenin gene. Thus, the structure of the EF-hand helix-loop-helix motif domain may be compatible with a nucleic acid–binding function. In fact, we found that both cellular S100C and recombinant S100C protein bound to double-stranded DNA coupled with a cellulose column (data not shown). Like DREAM, the EF-hand type Ca2+-binding protein S100C may also work as a DNA-binding transcriptional regulator for cell density-dependent growth arrest.

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