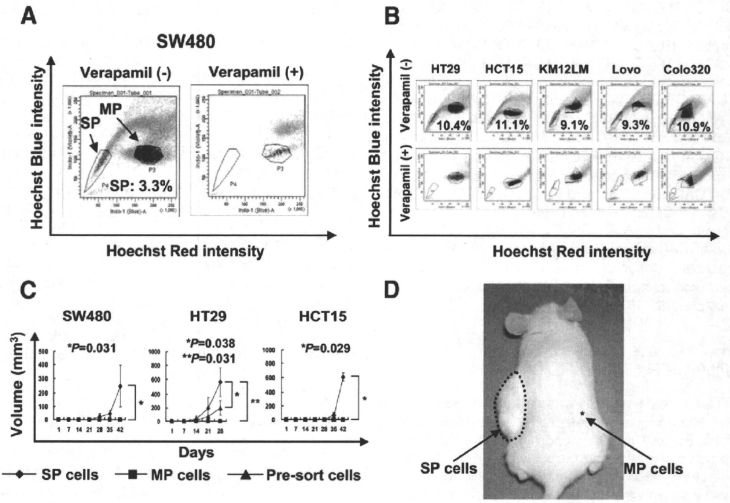

Figure 1. Isolation of colon CSCs/TICs from colon cancer cell lines and tumor growth of the SP cells. **A:** Colon cancer cell line SW480 was stained with Hoechst 33342 dye as described under *Materials and Methods*, with or without verapamil. Stained cells were analyzed using a BD FACSAria II fluorescence-activated cell sorting system. Frequency of SP cells was 3.3%. **B:** Colon cancer cell lines (HT29, HCT15, KM12LM, Lovo, and Colo320) were stained with Hoechst 33342 dye with or without verapamil. Stained cells were analyzed using a BD FACSAria II system. Frequencies of SP cells ranged from 9.1% for KM12LM cells to 11.1% for HCT15 cells. **C:** SP cells, MP cells, and presorted cells of colon cancer cell lines SW480, HT29, and HCT15 were inoculated subcutaneously into the backs of NOD/SCID mice (1×10^5 cells injected). Data are reported as means ± SD. *P* values indicate differences between cell types according to a Mann-Whitney *U*-test. **D:** Representative tumor growth in NOD/SCID mice at the SP cell injection site (1×10^5 cells injected). SP cells and MP cells were inoculated subcutaneously into the left and right side of the back, respectively.

described under *Materials and Methods*. Side population cells could be detected in all six colon cancer cell lines analyzed (ie, SW480, HT29, HCT15, Colo320, Lovo, and KM12LM) (Figure 1, A and B). The frequency of SP cells ranged from 3.3% for SW480 to 11.1% for HCT15 cells. All these SP cells were specifically inhibited by verapamil, as has been shown previously,[14] suggesting that these SP cells were specific for ABC transporter expression. Because previous studies showed that some colon cancer SP cells were not enriched with a CSC/TIC population,[15] it was essential to confirm the presence of CSCs/TICs in SP cells for further analysis. We inoculated these SP cells subcutaneously into the back of immunodeficient NOD/SCID mice using serial dilution. The SP cells derived from SW480, HCT15, and HT29 showed higher tumor initiating ability, compared with MP cells (Table 1). Furthermore, SW480, HT29, and HCT15 SP cells showed faster tumor growth, compared with MP cells (Figure 1, C and D), suggesting the presence of CSCs/TICs in these SP cells. In contrast, the SP cells derived from Colo320, Lovo, and KM12LM did not show any difference in tumorigenicity or tumor growth, compared with MP cells. We therefore restricted further analysis to the SW480, HT29, and HCT15 SP cells as colon cancer CSCs/TICs.

RT-PCR Analysis of Colon Cancer SP Cells

To examine the molecular properties of SP cells, we performed RT-PCR analysis. SOX2 and POU5F1 are representative markers for embryonal stem cells and CSCs/TICs.[16] The SP cells derived from SW480, HT29, and HCT15 showed higher expression of both SOX2 and POU5F1, compared with MP cells (Figure 2A). ALDH1A1, a colon CSC/TIC marker,[6] was expressed at a higher level in SP cells of HCT15 than in MP cells, but SP cells of SW480 and HT29 did not show any difference in comparison with MP cells. SW480 and HT29 SP cells also showed higher expression of LGR5, which is known as a normal colon stem cell marker.[17] To confirm the expression of stem cell markers, we also performed real-time PCR. The SW480 SP cells expressed 90 times higher SOX2, 7 times higher POU5F1, 153 times higher LGR5, and 6.1 times higher ALDH1A1, compared with MP cells (Figure 2B). These findings indicate that these SP cells had molecular properties similar to those of embryonal stem cells.

Resistance to Chemotherapeutic Reagents

Although SP cells derived from liver cancer cell line HuH7 have showed resistance to chemotherapy,[13] we know of no conclusive previous studies of such resistance in co-

Table 1. Tumor Initiating Ability of Colon Cancer SP Cells

Cell line (% SP cells)	Tumor initiating ability*		
	$1 \times 10^{4\dagger}$	$1 \times 10^{3\dagger}$	$1 \times 10^{2\dagger}$
SW480 (3.3)			
SP cells	4/4	4/6	4/4
MP cells	2/4	3/5	0/4
HT29 (10.4)			
SP cells	3/3	2/3	3/3
MP cells	3/3	0/3	0/3
HCT15 (11.1)			
SP cells	3/3	3/4	3/3
MP cells	1/3	1/4	0/3
Colo320 (10.9)			
SP cells	2/2	1/2	1/2
MP cells	2/2	2/2	1/2
Lovo (9.3)			
SP cells	0/1	1/1	0/1
MP cells	1/1	0/1	0/1
KM12LM (9.1)			
SP cells	1/2	2/2	1/1
MP cells	1/2	2/2	1/1

MP, main population; SP, side population.

*Tumor initiating ability is expressed as the ratio of tumor-initiation to injection.

†The tumor initiation abilities were evaluated at day 42 after injection of the indicated number of cells.

lon SP cells. We performed a cell survival study of colon cancer SP cells using the chemotherapeutic agents irinotecan and etoposide. The SW480 and HCT15 SP cells were more resistant to both irinotecan and etoposide than were MP cells (Figure 3, A and B). This finding is consistent with findings for CSCs/TICs derived from other organs.[22,24]

Expression of HLA and Tumor-Associated Antigens in SP Cells

Because CTLs recognize tumor-associated antigen (TAA)-derived antigenic peptides presented by HLA class I molecules, expression of HLA class I molecules is essential for activation of CTLs. Several types of malignancies have been reported to lose the expression of HLA class I molecules through various mechanisms and so escape CTL attack.[18] We therefore evaluated the expression of HLA class I molecules and TAA. We assessed the differences of HLA class I and HLA-A24 expression between SP cells and MP cells by flow cytometry. Because ELISA study has revealed that HCT15 cells lack B2M because of gene mutations of *B2M*,[19] we transduced wild-type B2M cDNA into HCT15 cells and so established HCT15-B2M cells. The SW480, HT29, and HCT15-B2M SP cells showed HLA class I and HLA-A24 expression at the same level as MP cells (Figure 4, A and B). Furthermore, we assessed the expression of one of the colon cancer TAAs, CEP55, by both RT-PCR and real-time PCR (Figure 2, A and B). Both SP cells and MP cells derived from SW480, HT29, and HCT15-B2M expressed CEP55 mRNA at the same level. These data raised the possibility that SP cells are also sensitive to CTLs specific for the CEP55-derived antigenic peptide. Because both SP cells and MP cells expressed CEP55 mRNA at the same level, this appeared to be an ideal target for comparing the susceptibilities of SP cells and MP cells to CTLs.

Susceptibility of CSCs/TICs to CTLs, in Vitro *and* in Vivo

We had previously established CTL clone 41, which is specific for the cancer-related, antigen-derived, HLA-A24-restricted peptide Cep55/c10orf3_193(10).[10] CTL clone 41 recognized CEP55-positive and HLA-A24-positive cancer cells, as described previously.[10,11] In the present study, we used a ^{51}Cr release assay to examine whether CTL clone 41 can recognize SP cells. All SP cells derived from SW480, HT29, and HCT15-B2M showed susceptibility to CTL clone 41 at the same level as the MP cells and the presorted bulk cell lines (Figure 4C). This indicates that the colon CSCs/TICs were sensitive to CTLs.

To analyze the cytotoxic activity of the CTL clone *in vivo*, we performed a Winn assay. SW480 SP cells with or without CTL clone 41 were injected into the backs of NOD/SCID mice subcutaneously. CTL clone 41 significantly inhibited the tumorigenicity of SW480 SP cells (Figure 4D). Because CTLs were injected at the same time and place as the SP cells in the Winn assay, we could not rule out the possibility that SP cells were killed *in vitro*. We

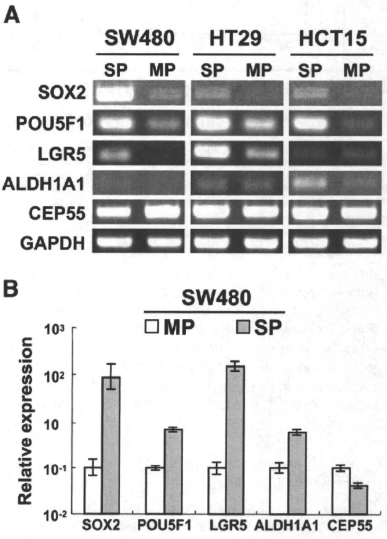

Figure 2. Expression of stem cell markers in SP and MP cells. **A:** mRNAs purified from SW480, HT29, and HCT15 SP and MP cells were analyzed by RT-PCR. **B:** mRNA purified from SW480 SP cells and MP cells were analyzed with real-time PCR. mRNA expression level is relative to MP cells. Data are reported as means ± SD.

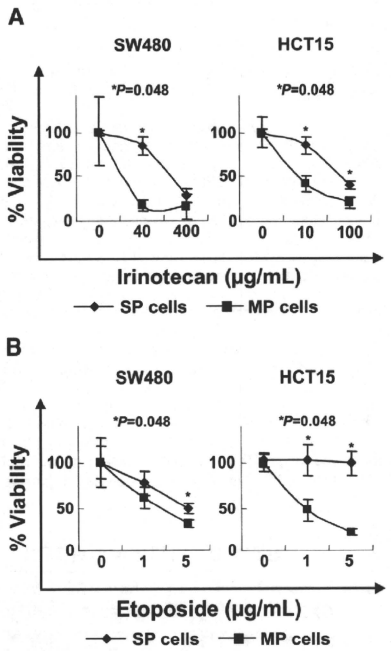

Figure 3. Sensitivity to chemotherapeutic agents. SP cells and MP cells derived from SW480 and HCT15 were incubated in the presence of irinotecan (CPT-11) (**A**) or etoposide (VP-16) (**B**) for 3 days. After incubation, the cell viabilities were measured by WST-1 assay. Data are reported as means ± SD. Differences between SP cells and MP cells were examined for statistical significance using the Mann-Whitney *U*-test.

therefore used an adoptive transfer model, as described under *Materials and Methods*. SW480 SP cells were inoculated into the back of NOD/SCID mice subcutaneously. Three weeks later, after confirmation of palpable tumors, CTLs were injected intravenously. Tumors of CTL-injected mice were significantly inhibited in growth, compared with tumors of control mice (Figure 4E). These data indicate that CTLs could recognize CSCs/TICs both *in vitro* and *in vivo*.

Discussion

In the present study, we successfully isolated colon cancer CSCs/TICs as SP cells, using Hoechst 33342 staining. Side population cells were first described by Goodell et al,[12] and CSCs/TICs of several types of malignancies were successfully isolated as SP cells in subsequent studies.[14,20–24] Haraguchi et al[13] isolated SP cells from gastrointestinal cancer cell lines; they reported the gene expression profiles and resistance to chemotherapeutic agents of SP cells derived from liver cancer cell line Huh7, but did not determine their tumorigenicity. Burkert et al[15] found that SP cells derived from gastrointestinal cancers cell lines HT29, HGT101, Caco2, and HRA19a1.1 were not enriched with a CSC/TIC population. In the present study, we were able to isolate SP cells from all six colon cancer cell lines studied (SW480, HT29, HCT15, KM12LM, Lovo, and Colo320). However, in only three of the six cell lines did the SP cells show higher tumorigenicity than MP cells, suggesting that these SP cells were enriched with CSC/TIC populations. Thus, SP cells might not be the definitive phenotype of CSCs/TICs, and confirmation of tumorigenicity in immunodeficient mice is essential for validation of SP cells as a source of CSCs/TICs. In the present study, the SP cells derived from SW480, HCT15, and HT29 cells were confirmed to be enriched with CSCs/TICs. Furthermore, these SP cells expressed stem cell markers, including SOX2, POU5F1 and LGR5, at higher levels than MP cells, suggesting correspondence with CSCs/TICs. Thus, these SP cells would be a useful tool for analysis of colon CSCs/TICs.

In the present study, we evaluated the immunogenicity of colon CSCs/TICs. Colon cancer CSCs/TICs expressed HLA class I molecules, and also CEP55, which is one of the TAAs. Furthermore, colon CSCs/TICs expressed several other TAA-encoding genes (data not shown), including BIRC5 (encoding apoptosis inhibitor survivin), BIRC7 (encoding livin), WT1, CTAG1B (alias *NY-ESO-1*), and MAGEA4. As a novel finding, colon cancer CSCs/TICs were sensitive to CTLs both *in vitro* and *in vivo*. Recently, Todaro et al[25] showed that colon CSCs/TICs were sensitive to γδT cells. Because both CTLs and γδT cells kill target cells through secretion of perforin (encoded by the *PRF1* gene) and granzyme B (encoded by *GZMB*), these observations strongly suggest that CSCs/TICs are sensitive to PRF1- and GZMB-dependent apoptosis. Todaro et al[26] had earlier reported that PROM1-positive ($CD133^+$) colon cancer CSCs/TICs secrete IL-4 in an autocrine manner and upregulate the antiapoptotic proteins CFLAR (c-FLIP), BCL2L1 (Bcl-xL), and PEA15 (PED), thereby gaining resistance to chemotherapeutic agents. Saigusa et al[27] reported that distant recurrence of rectal cancer after chemotherapy was related to the expression of CSC/TIC markers such as PROM1 (CD133), POU5F1 (Oct3/4), and SOX2. These reports support the idea that colon CSCs/TICs are resistant to apoptotic cell death. The fact that immunocytes induce apoptosis in their target cells raises the question of whether colon CSCs/TICs are also sensitive to immunotherapy.

In the present study, and in that of Todaro et al,[25] colon CSCs/TICs were sensitive to perforin- and granzyme B-dependent apoptosis. Thus, both CTLs and γδT cells can be useful tools for colon CSC/TIC targeting therapy. However, because γδT cells do not recognize target cells in an antigen-specific manner, immunotherapy using γδT cells should also recognize the non-CSC/TIC population. Because the number of γδT cells is restricted *in vivo*, it may be in doubt whether γδT cell can recognize colon

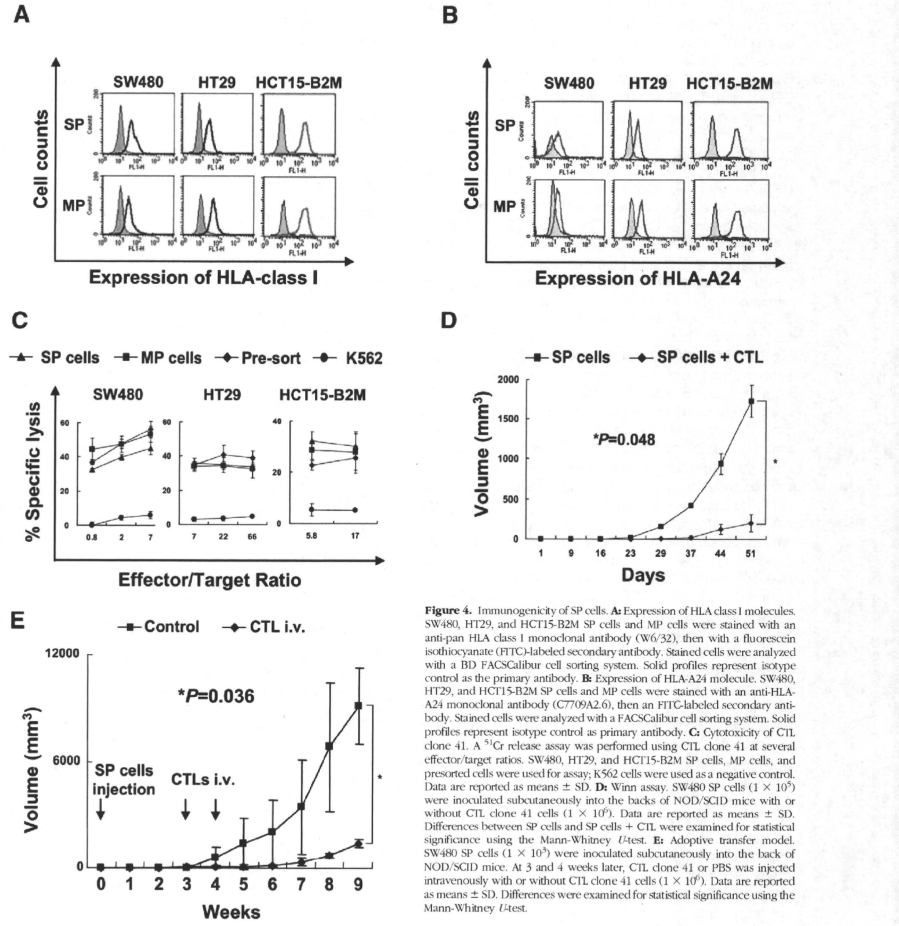

Figure 4. Immunogenicity of SP cells. **A:** Expression of HLA class I molecules. SW480, HT29, and HCT15-B2M SP cells and MP cells were stained with an anti-pan HLA class I monoclonal antibody (W6/32), then with a fluorescein isothiocyanate (FITC)-labeled secondary antibody. Stained cells were analyzed with a BD FACSCalibur cell sorting system. Solid profiles represent isotype control as the primary antibody. **B:** Expression of HLA-A24 molecule. SW480, HT29, and HCT15-B2M SP cells and MP cells were stained with an anti-HLA-A24 monoclonal antibody (C7709A2.6), then an FITC-labeled secondary antibody. Stained cells were analyzed with a FACSCalibur cell sorting system. Solid profiles represent isotype control as primary antibody. **C:** Cytotoxicity of CTL clone 41. A ^{51}Cr release assay was performed using CTL clone 41 at several effector/target ratios. SW480, HT29, and HCT15-B2M SP cells, MP cells, and presorted cells were used for assay; K562 cells were used as a negative control. Data are reported as means ± SD. **D:** Winn assay. SW480 SP cells (1×10^5) were inoculated subcutaneously into the backs of NOD/SCID mice with or without CTL clone 41 cells (1×10^6). Data are reported as means ± SD. Differences between SP cells and SP cells + CTL were examined for statistical significance using the Mann-Whitney *U*-test. **E:** Adoptive transfer model. SW480 SP cells (1×10^5) were inoculated subcutaneously into the back of NOD/SCID mice. At 3 and 4 weeks later, CTL clone 41 or PBS was injected intravenously with or without CTL clone 41 cells (1×10^6). Data are reported as means ± SD. Differences were examined for statistical significance using the Mann-Whitney *U*-test.

cancer CSCs/TICs *in vivo* efficiently. Recently, based on a large cohort study, Ogino et al[28] reported that lymphocytic reaction to tumor was associated with longer survival of colorectal cancer patients. They did not analyze the subtypes of infiltrating lymphocytes; however, the findings from this large-scale study strongly support the notion that immune reaction to tumor cells is important for control of the disease.

Wei et al[29] reported recently that glioma-derived CSCs/TICs suppressed T-cell proliferation and activation, and induced T-cell apoptosis through expression of co-stimulatory inhibitory molecule CD274 (B7-H1) and soluble LGALS3 (galectin-3); glioma CSCs/TICs enhance the induction of regulatory T cells. We also observed that SW480 SP cells express higher mRNA of the immunosuppressive cytokine IL-10 than MP cells (data not

shown). Thus, colon CSCs/TICs may have immunosuppressive potential and so inhibit CTL induction. However, colon CSCs/TICs are efficiently killed by CTLs, and colon CSCs/TICs have no influence on the effector phase of CTLs. Thus, adoptive cell transfer of CSC/TIC-specific CTL clones, T-cell-receptor–induced T cells, or peptide vaccination accompanied by an anti-IL-10 monoclonal antibody might be an effective approach for eliminating colon CSCs/TICs.

In the present study, we observed that both colon CSCs/TICs and non-CSCs/TICs were sensitive to CEP55-specific CTLs at the same level. This finding seems reasonable, given that CSCs/TICs express CEP55 mRNA at the same level. Huge numbers of TAAs have already been reported,[30,31] and the next challenge is to identify which TAAs would be the most suitable targets for cancer immunotherapy. According to the manner of expression in CSCs/TICs and non-CSCs/TICs, TAAs can be classified into three categories: i) CSC/TIC-specific antigens, such as SOX2 and ALDH1A1; ii) non-CSC/TIC-specific antigens; and iii) shared antigens, such as CEP55.[32] The frequencies of colon CSCs/TICs are 1% to 10%, and in the present study these cells had 10- to 100-fold higher tumorigenicity than non-CSCs/TICs. It is likely, therefore, that 1% to 10% of colon CSC/TIC populations have almost the same tumorigenic potential as 90% to 99% of the non-CSC/TIC population. To achieve a complete cure of the disease, shared antigens seem to a be reasonable candidate strategy. *In vivo*, however, CTL numbers are limited. Given that 1 L of peripheral blood contains approximately 5×10^9 lymphocytes, there are approximately 5×10^8 CD8 T cells in 1 L of peripheral blood and approximately 3×10^9 CD8 cells in the total volume of peripheral blood in a human adult. If the CTL precursor frequency reaches 0.1% of CD8 T cells in a patient receiving peptide vaccination therapy, then the total peptide-specific CTLs can be calculated as 3×10^6 cells in whole blood. This is not an inconsiderable number. Visible tumors as large as 1 cm diameter contain 1×10^9 tumor cells, and the estimated effector/target ratio (E/T) *in vivo* is 0.003. This ratio may be too low to expect an anti-tumor effect *in vivo*. However, if we focus only on CSCs/TICs, then the effector/target ratio will be improved. For targeting CSCs/TICs with 1% frequency, the effector/target ratio is correspondingly improved (E/T = 0.3). Thus, focusing only on the CSC/TIC population with CSC/TIC-specific antigens seems to be a better approach for advanced cancer cases. For prevention of disease recurrence after treatment, the target cells are likely to be limited, so shared antigens might be a reasonable choice for cancer immunotherapy.

Recently, some research groups have reported that monoclonal antibodies for insulin-like growth factor-1 receptor (IGF-1R), δ-like 4 ligand (DLL4), and CD47 efficiently eliminate colon cancer and leukemia CSCs/TICs.[33–36] These approaches are also fascinating, and a reasonable option for elimination of CSCs/TICs. An antibody is a relatively stable protein, but the half-life in peripheral blood is approximately 2 to 3 weeks, and therefore serial administration is needed to maintain the effects of the antibody. On the other hand, antigenic peptide vaccination can induce specific CTLs as memory cells *in vivo*, such that the specific immunity will last for several years. Thus, peptide vaccination therapy may also be useful for prevention of post-treatment cancer recurrence.

In conclusion, we report here the novel finding that colon cancer CSCs/TICs are as sensitive to CTLs as are non-CSCs/TICs, and that CEP55, a tumor-associated antigen, is a suitable antigen for targeting colon cancer CSCs/TICs.

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STEM CELLS
CANCER STEM CELLS

Combination of a Ptgs2 Inhibitor and an Epidermal Growth Factor Receptor-Signaling Inhibitor Prevents Tumorigenesis of Oligodendrocyte Lineage-Derived Glioma-Initiating Cells

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Key Words. Neural stem cells • p53 • Glioma • Microarray • Oligodendrocyte precursor cells • HRas • Glioma-initiating cells

ABSTRACT

Recent findings have demonstrated that malignant tumors, including glioblastoma multiforme (GBM), contain cancer-initiating cells (CICs; also known as cancer stem cells), which self-renew and are malignant. However, it remains controversial whether such CICs arise from tissue-specific stem cells, committed precursor cells, or differentiated cells. Here, we sought to examine the origin of the CICs in GBM. We first showed that the overexpression of oncogenic *HRas*^{I61} transformed *p53*-deficient oligodendrocyte precursor cells (OPCs) and neural stem cells (NSCs) into glioma-initiating cell (GIC)-like cells in mice. When as few as 10 of these GIC-like cells were transplanted in vivo, they formed a transplantable GBM with features of human GBM, suggesting that these GIC-like cells were enriched in CICs. DNA microarray analysis showed that widespread genetic reprogramming occurred during the OPCs' transformation: they largely lost their OPC characteristics and acquired NSC ones, including the expression of *prominin1*, *hmga2*, *ptgs2*, and *epiregulin*. In addition, the combination of a Ptgs2 inhibitor and an epidermal growth factor receptor (EGFR)-signaling inhibitor prevented the tumorigenesis of transformed OPCs and human GICs (hGICs) obtained from anaplastic oligodendroglioma, but not of transformed NSCs or hGICs obtained from GBM. Together, these findings suggest that GBM can arise from either OPCs or NSCs and that the therapeutic targets for GBM might be different, depending on each GIC's cell-of-origin. STEM CELLS *2011;29:590–599*

Disclosure of potential conflicts of interest is found at the end of this article.

INTRODUCTION

Cancer-initiating cells (CICs; also referred to as cancer stem cells) self-renew indefinitely and continuously generate the amplifying cancer cells that form the majority of cells in a tumor [1, 2]. It is believed that CICs can arise from normal tissue-specific stem cells, precursor cells, or differentiated cells that have acquired stem cell characteristics as a result of oncogenic mutation. In fact, the overexpression of oncogenes can induce hematopoietic stem/progenitor cells to transform into leukemic stem cell-like cells, which form leukemia when a small number of them are transplanted in vivo [2, 3], suggesting that such induced cancer models can be used to investigate the cell-of-origin for CICs. A number of mutations in oncogenes and tumor-suppressor genes are known to be involved in tumorigenesis; however, except for leukemia, the relationship between the cell-of-origin for CIC and such genetic alterations has not been determined [2, 3].

We and others have shown that specified oligodendrocyte precursor cells (OPCs) and astrocytes can revert to neural stem-like cells that, when cultured under appropriate conditions, can form floating aggregates, express neural stem cell (NSC) markers, and differentiate into neurons as well as glial cells [4–7], suggesting that OPCs and astrocytes, as well as NSCs, can serve as the cell-of-origin for brain CICs.

Among a number of mutations associated with gliomagenesis, p53 is the most frequently mutated tumor-suppressor gene in human glioblastoma multiforme (GBM) [8–11], and increased activation of the Ras-signaling pathway is also found in human gliomas, including about 90% of GBM cases [10–12]. Moreover, the deletion of both p53 and NF1, which negatively regulates the Ras-signaling pathway, causes malignant gliomas in mice [13, 14]. Together, these findings led us to examine whether the combination of p53 deletion and Ras activation can induce cultured NSCs, OPCs, and astrocytes to transform into glioma-initiating cell (GIC)-like cells.

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Materials and Methods

Animals and Chemicals

Mice were obtained from the Laboratory for Animal Resources and Genetic Engineering at the RIKEN Center for Developmental Biology (CDB) and from Charles River Japan, Inc. All mouse experiments were performed following protocols approved by the RIKEN CDB Animal Care and Use Committee. Genotyping of *p53*-knockout mice was done by polymerase chain reaction (PCR) as described previously [15]. Chemicals and growth factors were purchased from Sigma-Aldrich (St. Louis, MO, www.sigmaaldrich.com) and Peprotech (Rocky Hill, NJ, www.peprotechec.com), respectively, except where indicated.

Cell Culture

NSCs were prepared from embryonic day 13.5 *p53*-deficient mouse telencephalon and expanded as described previously [16]. For immunostaining, neurospheres were cultured on poly-D-lysine (15 μg/ml)-coated and fibronectin (1 μg/ml, Invitrogen, Carlsbad, CA, www.invitrogen.com)-coated eight-well chamber slides (Nalge Nunc, Rochester, NY, www.nalgenunc.com) in the presence of basic fibroblast growth factor (bFGF; 10 ng/ml) and epidermal growth factor (EGF; 10 ng/ml) for up to 1 day. Astrocyte differentiation was induced in NSC cultures by changing the medium to Dulbecco's modified Eagle's medium (DMEM; Nacalai Tesque, Kyoto, Japan, www.nacalai.co.jp/global) with 10% fetal calf serum (FCS) for three weeks. OPC differentiation was induced by culturing NSCs in DMEM containing platelet-derived growth factor AA (10 ng/ml), bFGF (2 ng/ml), and 0.25% FCS (OPC medium) and purified by sequential immunopanning, as described previously [17]. The human oligodendroglioma cell line Hs683 and GBM line U251, both of which were purchased from ATCC (Manassas, VA, www.atcc.org), were cultured in DMEM supplemented with 10% FCS, 100 units/ml penicillin G, and 100 μg/ml streptomycin (Nacalai Tesque, Japan).

Transfection

Transfection of NSCs, astrocytes, OPCs, and human GICs (hGICs) was performed using the Nucleofector procedure, according to the supplier's instructions (Lonza, Cologne, Germany, www.lonzabio.com). In brief, 2×10^6 cells were suspended in the mouse NSC nucleofector solution (100 μl) with 10 μg vectors, and then were transfected using the nucleofector device. Transfected cells were cultured in their optimized medium.

Immunostaining

Immunostaining was carried out as described previously [17]. The following antibodies were used to detect antigens: mouse anti-glial fibrillary acidic protein (GFAP; 1:500; Millipore, Billerica, MA, www.millipore.com, 1:400; Sigma for human cells), rat anti-Nestin (1:1,000; BD Pharmingen, Franklin Lakes, NJ, 1:200; Millipore for human cells), mouse anti-MAP2(a+b) (1:200; Abcam, Cambridge, MA, www.abcam.com), mouse anti-beta tubulin isotype III (1:400; Sigma for human cells), mouse A2B5 (1:2; hybridoma supernatant; ATCC), mouse anti-galactocerebroside (GC; 1:2; hybridoma supernatant; ATCC), rat anti–green fluorescence protein (anti-GFP; 1:1,000; Nacalai Tesque), rabbit anti-prominin1 (1:100; Abcam), and rabbit anti-human CD133 (1:50; Abcam). The antibodies were detected with goat anti-rat IgG-A488 (1:400; Invitrogen), goat anti-mouse IgG-Cy3 (1:400; Jackson ImmunoResearch, West Grove, PA, www.jacksonimmuno.com), goat anti-rabbit IgG-Cy3 (1:400; Jackson ImmunoResearch), goat anti-mouse IgG-A488 (1:400; Invitrogen), and goat anti-mouse IgM-Texas Red (1:400; Jackson ImmunoResearch). To visualize nuclei, the cells were counterstained with 4′,6-diamidino-2-phenylindole (1 μg/ml).

Paraffin-embedded tumors were sectioned at 6-μm thickness. Antigens were retrieved by HistoVT One according to the supplier's instructions (Nacalai Tesque). Endogenous peroxidase activity was inactivated by applying 0.3% H_2O_2 for 15 minutes at room temperature (RT). The sections were then pretreated with blocking solution (2% skim milk, 0.3% Triton X-100, phosphate-buffered saline [PBS]) for 30 minutes at RT, and incubated with mouse anti-epidermal growth factor receptor vIII (EGFRvIII) antibody clone DH8.3 (1:20, Novocastra) for 30 minutes at RT. The antibodies were visualized with the Vectastain ABC kit (Vector Laboratories, Burlingame, CA, www.vectorlabs.com) and diaminobenzidine (Vector Laboratories).

Proliferation Assay

Two thousand cells were cultured in 100 μl of culture medium in each well of 96-well plates. To examine cell proliferation, the 3-(4,5-di-methylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay was performed as follows. Ten microliters of MTT (5 mg/ml, Nacalai Tesque) was added to each well on days 0, 2 or 3, and 4 in vitro. The cells were incubated for 4 hours, the medium was replaced with 100 μl of DMSO, the cells were dissociated, and cell proliferation was quantified on a Benchmark microplate reader (Bio-Rad, Hercules, CA, www.bio-rad.com) with the absorption spectrum at 570 nm.

Soft Agar Assay

A soft agar assay was performed to examine whether the transfected cells could proliferate anchorage independently. The transfected cells were suspended in 0.3% top agar made with the optimized medium and layered onto 0.6% bottom agar made with the same medium. After the top agar had polymerized, culture medium was added, and the cells were cultured for 20 days with medium changes every three days.

Reverse Transcription Polymerase Chain Reaction (RT-PCR)

RT-PCR was carried out as described [4]. Dimethylsulfoxide (DMSO) or Betaine was added to the reaction mixture for *olig1* (5% DMSO), *olig2* (5% DMSO), *contactin1* (5% DMSO), *sox2* (10% DMSO), *nestin* (5% DMSO), and *egfr variant III* (*egfrvIII*) (0.5 M Betaine). Cycle parameters were 20 seconds at 94°C, 40 seconds at 58°C, and 45 second at 72°C for 35 cycles. For *gapdh*, they were 15 seconds at 94°C, 30 seconds at 53°C, and 90 seconds at 72°C for 22 cycles.

The following oligonucleotide DNA primers were synthesized. For exogenous *hras*, the 5′ primer was 5′-ATGACA GAATACAAGCTTGTGGTG-3′, and the 3′ primer was 5′-ATTAACCCTCACTAAAGGGAAG-3′. For *amphiregulin* (*areg*), the 5′ primer was 5′-ATTCAGTCAGAGTTGAA CAGGT-3′, and the 3′ primer was 5′-ACTTTTCTCCA CACCGTTCACC-3′. For *nephroblastoma overexpressed gene* (*nov*), the 5′ primer was 5′-GCATTAACTGCATTGAGCA GAC-3′, and the 3′ primer was 5′-TCTTGGAGGAAGGCCT CATTG-3′. For *prominin1* (*prom1*), the 5′ primer was 5′-AGGCTACTTTGAACATTATCTGCA-3′, and the 3′ primer was 5′-GGCTTGTCATAACAGGATTGT-3′. For *twist homolog 2* (*twist2*), the 5′ primer was 5′-ATGGAGGAGGGCTC CAGCTC-3′, and the 3′ primer was 5′-CTAGTGGGAGGCG GACATGG-3′. For *Kruppel-like factor 4* (*klf4*), the 5′ primer was 5′-CACATGAAGCGACTTCCCCC-3′, and the 3′ primer

was 5′-TTGATGTCCGCCAGGTTGAAG-3′. For *muscleblind-like 3* (*mbnl3*), the 5′ primer was 5′-CTGTGACAA TCTGCATGGATTAC-3′, and the 3′ primer was 5′-TTG CCTGTAGTTGTTGGAACGTA-3′. For *S100 calcium binding protein A6* (*s100a6*), the 5′ primer was 5′-ATGG CATGCCCTCTGGATCAG-3′, and the 3′ primer was 5′-TTATTTCAGAGCTTCATTGTAGATC-3′. For *paired related homeobox 1* (*prrx1*), the 5′ primer was 5′-CAGGCCTTG GAGCGTGTCTT-3′, and the 3′ primer was 5′-TCAGTT GACTGTTGGCACCTG-3′. For *high mobility group AT-hook 2* (*hmga2*), the 5′ primer was 5′-ATGAGCGCAC GCGGTGAGGG-3′, and the 3′ primer was 5′-CTAATC CTCCTCTGCGGACTC-3′. For *prostaglandin-endoperoxide synthase 2* (*ptgs2*), the 5′ primer was 5′-CATTCTTTGCC CAGCACTTCA-3′, and the 3′ primer was 5′-GTGGCATA CATCATCAGACCA-3′. For *contactin1*, the 5′ primer was 5′-GTCACCAGCCAGGAGTACTC-3′, and the 3′ primer was 5′-CAGGAGCAAGCTGAGGAGAC-3′. For *NK2 homeobox 2* (*nkx2.2*), the 5′ primer was 5′-ATGTCGCT-GACCAACA CAAAGA-3′, and the 3′ primer was 5′-TCAC-CAAGTC CACTGCTGGGCCTG-3′. For *myelin basic protein* (*mbp*), the 5′ primer was 5′-ATGGCATCACAGAAGA-GACCCT-3′, and the 3′ primer was 5′-CTGTCTCTTCCTCCCAGCTTAAA-3′. For *proteolipid protein* (*plp*), the 5′ primer was 5′-GACAAGTTTGTGGGCAT-CACC-3′, and the 3′ primer was 5′-TCGGCCCATGAGTT-TAAGGAC-3′. For *lipoma HMGIC fusion partner-like 3* (*lhfpl3*), the 5′ primer was 5′-GCTCTTCCACTACTG-CATCGG-3′, and the 3′ primer was 5′-ATTCCGATGA-TAGCCAGGATGT-3′. For *breast carcinoma amplified sequence 1* (*bcas1*), the 5′ primer was 5′-GAAAGACTC-CAGCTGCCAAAC-3′, and the 3′ primer was 5′-ATCCGCTTTGGTCCCAGGCC-3′. For *G0/G1switch 2* (*g0s2*), the 5′ primer was 5′-CCTGGCCAAGGAGAT-GATGGC-3′, and the 3′ primer was 5′-CTAGGAG-GCGTGCTGCCGG-3′. For *protein phosphatase 2* (formerly 2A), *regulatory subunit B, beta* (*ppp2r2b*), the 5′ primer was 5′-TTCAGCCACAGTGGGAGGTA-3′, and the 3′ primer was 5′-TTTGCTAAAGTCCAGACTGTC-3′. For *nucleosome assembly protein 1-like 5* (*nap115*), the mouse 5′ primer was 5′-ATGGCCGACCCCGAGAAGCAG-3′, the human 5′ primer was 5′- ATGGCCGACTCGGAAAACCA-3′, and the 3′ primer was 5′-GAGCTCTTGGATCTTGGCGAG-3′. For *heparin-binding EGF-like growth factor* (*hbegf*), the mouse 5′ primer was 5′- CTTTCTCCTCCAAGCCACAAG-3′, and the 3′ primer was 5′- CCATGCCCAACTTCACTTTCTC-3′. For *epiregulin* (*ereg*), the mouse 5′ primer was 5′- CATCTAC CTGGTGGACATGAG-3′, and the 3′ primer was 5′- CTG AGGTCACTCTCTCATATTC-3′. For *egfr*, the mouse 5′ primer was 5′- GATGAAAGAATGCATTTGCCAAG-3′, and the 3′ primer was 5′- GGGGCTGATTGTGATAGACAGG-3′. For *egfrvIII*, the mouse 5′ primer was 5′-ATGCGACCCT CCGGGACGG-3′, and the 3′ primer was 5′-ATTCCGTTA CACACTTTGCGGC-3′. The primers for *nestin, musashi1, sox2, olig1, olig2, mash1*, and *gapdh* were described previously [16].

Microarray Hybridization and Data Processing

Five micrograms of total RNA were labeled with biotin by in vitro transcription using the One-Cycle Target Labeling procedure (Affymetrix, Santa Clara, CA, www.affymetrix.com). The cRNA was subsequently fragmented and hybridized to the GeneChip Mouse Genome 430 2.0 array (Affymetrix), according to the manufacturer's instructions. The microarray image data were processed with the GeneChip Scanner 3000 (Affymetrix) to generate cell library (CEL) data. The CEL data were then subjected to analysis with the dChip software [18], which can normalize and process multiple datasets simultaneously. Data were normalized within the respective groups, according to the program's default setting. Statistical significance was determined by the eBayes method [19] and by ANOVA for two- and three-sample comparisons, respectively. The q value, which is an extension of a quantity called the "false discovery rate (FDR)," was examined to evaluate the genome-wide tests of significance [20, 21]. FDR < 0.1.

Human Brain Tumors

Eleven GBMs, five anaplastic astrocytomas, five anaplastic oligodendrogliomas (AOs), three anaplastic oligoastrocytomas, and two hGICs, hGIC1 and hGIC2, were used following the research guidelines of the RIKEN Center for Developmental Biology and Kumamoto University Graduate School of Medical Science. The detailed characterization of the hGICs will be reported elsewhere (T.T and T.K., unpublished data). Poly(A)+ RNA was prepared from glioma spheres using a QuickPrep mRNA Purification Kit (GE Healthcare, Little Chalfont, U.K., www.gehealthcare.com). Human control brain total RNA was purchased from Invitrogen. The cDNAs were synthesized using a Transcription First Strand cDNA Synthesis Kit (Roche, Basel, Switzerland, http://www.roche.com).

Flow Cytometry

Cells transfected with vectors or immunolabeled for Prom1 (1:200; Abcam) were analyzed in a JSAN cell sorter (Bay Bioscience, Kobe, Japan, www.baybio.co.jp) using dual-wavelength analysis (488 nm solid-state laser and 638-nm-semiconductor laser). Propidium iodide-positive (i.e., dead) cells were excluded from the analysis.

Vector Construction

Full-length mouse *HRas* was amplified from mouse NSC cDNA using RT-PCR and Phusion polymerase (Finnzymes, Espoo, Finland), according to the manufacturer's instructions, and was cloned into a pDrive vector (Qiagen, Venlo, Netherlands, www.qiagen.com). $HRas^{L61}$ was made by replacing the glycine at codon 61 with leucine, by PCR. The nucleotide sequences were verified using the BigDye Terminator Kit version 3.1 (Applied Biosystems, Foster City, CA, www.appliedbiosystems.com) and ABI sequencer model 3130xl (Applied Biosystems). $HRas^{L61}$ cDNA was inserted into the pCMS-EGFP vector, resulting in pCMS-EGFP-HRasL61.

The following oligonucleotide DNAs were synthesized. For the full-length mouse *HRas*, the 5′ primer was 5′-TGAATTCGCCACCATGACAGAATACAAGCTTGTGGTG-3′ and the 3′ primer was 5′-ACTCGAGTCAGGACAGCACA-CATTTGCAG-3′. For $HRas^{L61}$, the 5′ primer was 5′-ACAG-CAGGTCTAGAAGAGTATA-3′ and the 3′ primer was 5′-TATACTCTTCTAGACCTGCTGT-3′.

Intracranial Cell Transplantation into the Brain of Nude Mice

Control cells and transfected cells were suspended in 5 μl of culture medium and injected into the brain of 5- to 8-week-old female nude mice that had been anesthetized with 10% pentobarbital. The stereotactic coordinates of the injection site were 2-mm forward from lambda, 2-mm lateral from the sagittal suture, and 5-mm deep.

Brain Fixation and Histopathology

The dissected mouse brains were fixed in 4% paraformaldehyde at 4°C overnight. After fixation, the brains were cryoprotected with 12%–18% sucrose in PBS and embedded in Tissue-Tek OCT compound (Miles, Elkhart, IN). Coronal

sections (10-μm thick) were prepared from the cerebral cortex and stained with H&E using a standard technique.

Oral Administration of Drugs to Mice That Had Been Injected with Transformed Cells

The EGFR-signaling inhibitor, Gefitinib (200 mg/kg/day; AstraZeneca, London, U.K., www.astrazeneca.com), and Ptgs2 inhibitor, celecoxib (60 mg/kg/day; Astellas, Tokyo, Japan, www.astellas.com), were orally administered every day after the operation, using a disposable flexible-type animal-feeding needle (Fuchigami, Kyoto, Japan).

Statistical Analysis

The survival data were analyzed for significance by Kaplan-Meier methods using GraphPad Prism version 4 software (p values were calculated with the log-rank test, GraphPad Software, La Jolla, CA, www.graphpad.com).

RESULTS

The Combination of Ras Activation and p53 Deletion Transforms NSCs and OPCs, but Not astrocytes, into GIC-like Cells

We prepared NSCs, astrocytes, and OPCs as described previously [22–24]. Over 95% of the NSCs, 98% of the astrocytes, and 95% of the OPCs were positive for their respective specific markers, Nestin, GFAP, and A2B5 (Fig. 1A, 1B). We transfected these cell populations with either a control vector or a $HRas^{L61}$ expression vector [25], and established cell lines (NSC-C, AST-C, OPC-C, NSC-L61, AST-L61, and OPC-L61), which maintained their original marker immunoreactivities, although the transfected astrocytes lost their GFAP immunoreactivity during culture, as described previously [9] (Fig. 1C, 1D). We first examined whether Ras activation could induce the transformation of NSCs, astrocytes, or OPCs. Both NSC-L61 and OPC-L61 formed colonies in soft agar, whereas AST-L61 did not, although Ras activation significantly accelerated the proliferation of all the transfected lines, determined by the MTT assay (Fig. 1E–1J). These data suggest that the combination of Ras activation and p53 deletion transforms NSCs and OPCs but not astrocytes.

To investigate the tumor-forming ability of the transfected cells, we injected 1,000 cells of each type into the brain of nude mice. Mice that received either NSC-L61 (n = 10 of 10) or OPC-L61 (n = 9 of 9) developed brain tumors and died within 30 days, whereas none that were given injections of 10^3 AST-L61 (n = 10), or 10^5 control NSC-C (n = 3), AST-C (n = 3), or OPC-C (n = 3) showed evidence of brain tumorigenesis (Fig. 2A–2C). Although tumors that had characteristics of human astrocytoma, including hypercellularity and pleomorphism, formed in three of eight mice injected with 10^4 AST-L61 cells (Fig. 3), the secondary transplantation of 10^4 GFP+ cells did not result in brain tumors, suggesting that AST-L61 does not contain bona fide GIC-like cells or that AST-L61 cells need an additional mutation(s) to transform into GICs.

We further examined the tumorigenic ability of NSC-L61 and OPC-L61. Five of seven mice injected with 100 NSC-L61 cells and three of six mice injected with 10 NSC-L61 cells formed brain tumors (Fig. 2A). In the case of OPC-L61, all of the mice (5/5) injected with 100 cells and three of four mice injected with 10 cells developed brain tumors and died (Fig. 2B). These results suggest that both NSC-L61 and OPC-L61 were highly enriched in GIC-like cells.

NSC-L61 and OPC-L61 Cells Form Transplantable GBM with Features of Human GBM

We next examined the histopathology of the brain tumors formed from NSC-L61 and OPC-L61 (Fig. 2D–2K), to determine their type. The tumors were composed of GFP^+ cells, many of which were invading the adjacent brain tissue (Fig. 2D, 2H). H&E staining revealed that the tumors had characteristics of human GBM, including hypercellularity, pleomorphism, multinuclear giant cells, mitosis, and necrosis [26] (Fig. 2E–2G, 2I–2K). To characterize the tumors further, we acutely immunolabeled the dissociated tumor cells for both GFP and neural markers, and found that the tumor-forming cells maintained their original immunoreactivity (Supporting Information Fig. 1).

We then performed serial transplantation experiments using cells from the tumors that had formed in mice injected with either 100 NSC-L61 or 100 OPC-L61 cells. Within four weeks, all of the mice (n = 10 each for NSC-L61- and OPC-L61-derived tumors) that received secondary transplantation developed brain tumors that recapitulated the phenocopy of the primary transplantation (Fig. 2L–2O), indicating that NSC-L61 and OPC-L61 had a high capacity for self-renewal. Moreover, we found that 76% of the NSC-L61 and 44% of the OPC-L61 cells were positive for Prominin1 (Prom1), a putative marker for brain CICs [27, 28] and NSCs [29], whereas only 3% of the control NSCs and 4% of the OPCs were positive for Prom1 (Supporting Information Fig. 2). These data collectively suggest that a significant proportion of both NSC-L61 and OPC-L61 cells are transformed into GIC-like cells.

OPC-L61 Acquired the Expression of NSC-Specific Genes and Extensively Lost the Expression of OPC-Specific Genes

We used gene expression profiling to characterize the changes in gene expression that occurred during the transformation of NSCs and OPCs. We found that the gene expression profile of OPC-L61 was similar to that of control NSC-C and NSC-L61 but different from that of OPC-C (Fig. 4A–4C). A group of genes that were highly expressed in OPC-C showed decreased expression in OPC-L61 and vice versa, suggesting that the OPCs underwent global reprogramming of their gene expression during their transformation to OPC-L61.We then used RT-PCR to assess whether OPC-L61 acquired the expression of NSC-specific genes and lost that of OPC-specific genes (Fig. 4D, 4E). Tissue-specific stem cell markers, including *prom1*, *hmga2*, and *nov*, were expressed in OPC-L61 but not OPC-C, whereas the expression of several OPC-specific genes, *contactin1*, *olig1*, *olig2*, *mbp*, and *plp*, significantly decreased in OPC-L61. Moreover, a number of genes, including *twist2*, *klf4*, *mbnl3*, *s100a6*, *prrx1*, *ptgs2*, and *ereg*, were predominantly expressed in OPC-L61, NSC-C, and NSC-L61, whereas *lhfpl3*, *bcas1*, *g0s2*, *ppp2r2b*, and *nap1l5*, all of which were expressed in OPC-C, decreased in OPC-L61. Together, these data suggest that during transformation, the gene expression profile of OPCs changes markedly, and becomes similar to that of NSCs.

The Combination of a Ptgs2 Inhibitor and an EGFR-Signaling Inhibitor Prevents the Tumorigenicity of OPC-Derived GIC-Like Cells and Oligodendroglioma-Derived GICs

The finding that OPCs acquired characteristics of NSCs when transformed into GIC-like cells led us to examine whether the upregulated genes in the GIC-like cells include therapeutic targets. Among the candidate genes, we focused on Ptgs2 and

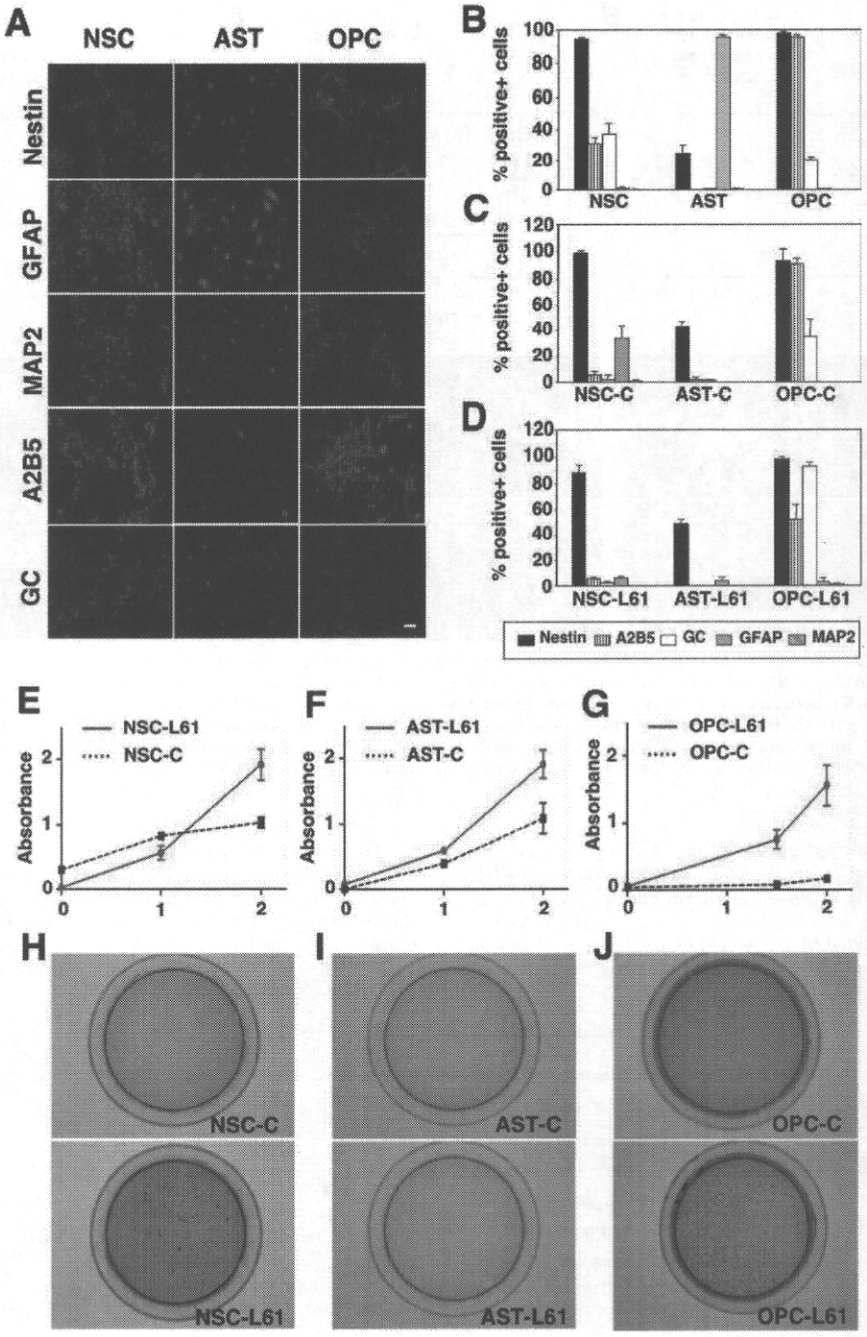

Figure 1. Characterization of $HRas^{L61}$-transfected *p53*-deficient NSCs, ASTs, and OPCs. **(A):** *p53*-deficient NSCs, ASTs, and OPCs immunolabeled for neural lineage markers (red) and 4′,6-diamidino-2-phenylindole (blue). Scale bar = 15 μm. **(B–D):** Proportion of neural lineage marker-positive cells in untransfected cells, NSCs, ASTs, and OPCs **(B)**, control vector-transfected cells NSC-C, AST-C, and OPC-C **(C)**, and $HRas^{L61}$ vector-transfected cells NSC-L61, AST-L61, and OPC-L61 **(D)**, are shown as the mean ± SD of three cultures. **(E–G):** Proliferation of untransfected (dotted black line) and $HRas^{L61}$ vector-transfected (red line) cells, determined using the 3-(4,5-di-methylthiazol-2-yl)-2,5-diphenyltetrazolium bromide assay. Results shown are the mean ± SD of three cultures. **(H–J):** NSC-L61 **(H)** and OPC-L61 **(I)**, but not AST-L61 **(J)**, formed colonies in soft agar. Abbreviations: AST, astrocyte; GC, galactocerebroside; GFAP, glial fibrillary acidic protein; MAP2, microtubule associated protein 2; NSC, neural stem cell; OPC, oligodendrocyte precursor cell.

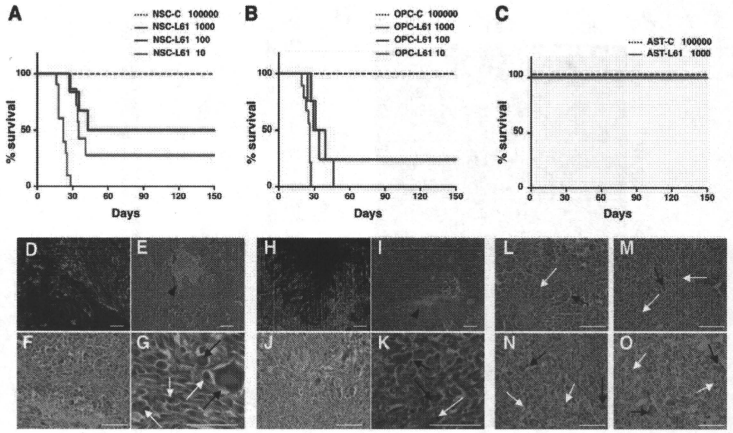

Figure 2. NSC-L61 and OPC-L61, but not AST-L61, are enriched in glioma-initiating cell-like cells. **(A–C):** Survival curves for mice injected with a limiting dilution of NSC-L61 **(A)**, OPC-L61 **(B)**, and AST-L61 **(C)**. **(D–O):** Brain sections with tumors derived from NSC-L61 **(D–G)** and OPC-L61s **(H–K)**. Both types of transformed cells invaded the brain parenchyma (green in **[D, H]**). H&E staining of the tumors showed necrosis (arrowhead in **[E, I]**), hypercellularity and hypervascularity, multinuclear giant cells (black arrow), and mitotic cells (white arrow) **(G, K)**; these pathological features are similar to human glioblastoma multiforme. H&E staining of secondary tumors **(M, O)** showed they were phenocopies of the primary tumors **(L, N)**. Scale bar = 100 μm. Abbreviations: AST, astrocyte; NSC, neural stem cell; OPC, oligodendrocyte precursor cell.

factors in the epidermal growth factor (EGF)-signaling pathway, because *ptgs2*, *egf receptor* (*egfr*), and various types of EGFR ligands, are highly expressed in human gliomas and other cancers and are involved in tumor progression [30, 31]. Indeed, we found that the OPC-L61 and NSC-L61 cells expressed *egfr* and EGFR ligands *areg*, *hbegf*, *ptgs2*, and *ereg* (Fig. 5A).

To evaluate the expression of *ptgs2*, EGFR ligands, and *egfr* in GICs, we established two hGIC lines, hGIC1 and hGIC2, from primary AO and GBM tissues, respectively, as shown previously [26, 27, 32]. Both of the hGIC lines formed transplantable malignant gliomas in the brains of nude mice when as few as 10 cells were transplanted, suggesting that

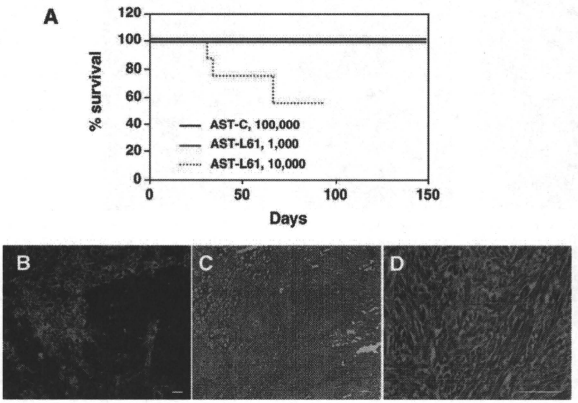

Figure 3. Pathological features of tumors formed by AST-L61. **(A):** Survival curves for mice injected with control astrocytes (AST-C) or AST-L61. **(B):** AST-L61 cells invaded the brain parenchyma (green). **(C, D):** H&E staining of the tumors showed a monotonous fibrous morphology with neither necrosis nor multinucleic giant cells. Scale bar = 100 μm. Abbreviation: AST, astrocyte.

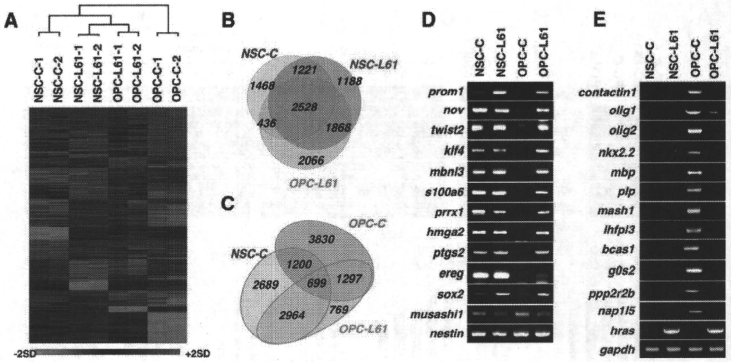

Figure 4. Evidence of global changes in gene expression in OPC transformation. **(A):** Hierarchical clustering using the Affymetrix murine 430A 2.0 microarray demonstrated that OPC-L61 exhibited a gene expression profile most similar to NSC-L61. **(B, C):** Diagram of the number of genes that were expressed specifically or commonly in NSC-C, OPC-C, NSC-L61, and OPC-L61. **(D, E):** Expression analysis of NSC-specific genes **(D)** and OPC-specific genes **(E)** in NSC-C, NSC-L61, OPC-C, and OPC-L61 by reverse transcription polymerase chain reaction. *gapdh* expression was an internal control. Abbreviations: NSC, neural stem cell; OPC, oligodendrocyte precursor cell.

these lines were also enriched in CICs (T.T. and T.K., unpublished observation). We confirmed that the hGICs expressed *ptgs2* and EGFR ligands, whose expression was undetectable in normal brain samples (Fig. 5B). We also found that hGIC1 expressed *egfr* version III (*egfrvIII*), a constitutively active form of EGFR that is expressed in malignant glioma, and *egfr*, whereas hGIC2 expressed *egfr* only. Moreover, we confirmed the expression of *egfrvIII* in the human AO and GBM sections and in paraffin-embedded hGIC xenografts by immunohistochemical analysis, as shown previously (Supporting Information Fig. 3) [33]. We further found that *ptgs2* and EGFR ligands were predominantly expressed in malignant human gliomas and that 5 of 11 GBM, 2 of 5 AO, and an oligodendroglioma cell line Hs683 expressed *egfrvIII* (Fig. 5C; Supporting Information Fig. 4). Together, these data suggest that both *Ptgs2* and EGFR-signaling pathways are involved in GIC functions.

Inhibitors for Ptgs2 and the EGFR-signaling pathways are used separately as chemotherapeutic reagents for lung cancer, intestinal neoplasm, non-small cell lung carcinoma, and glioma in human. As their use in combination has been shown to block tumorigenesis in both $APC^{Min/+}$ mice [34] and head-and-neck carcinoma xenografted mice [35], but has not been examined for GBM, we tested the efficacy of their combination in NSC-L61, OPC-L61, hGIC1, and hGIC2. Gefitinib, an EGFR inhibitor, and Celecoxib, a Ptgs2 inhibitor, prevented the proliferation of NSC-L61, OPC-L61, and hGIC cells in a dose-dependent manner, and the combination had additive effects, although control NSCs and OPCs were also affected (Fig. 5D–5G).

We next addressed whether this drug combination blocks the tumorigenesis of NSC-L61, OPC-L61, or hGICs in vivo, as neither Gefitinib nor Celecoxib alone showed any effect on the survival time of NSC-L61- (data not shown), OPC-L61-, or hGIC1-injected mice (Supporting Information Fig. 5). The mean survival time of mice injected with OPC-L61 was significantly longer in the drug-treated group (34.1 ± 9.5 days, $p = .005$), compared with control (23.0 ± 1.9 days), whereas the combination had little effect on mice injected with NSC-L61 (21.0 ± 2.9 days in drug-treated vs. 19.7 ± 6.9 days in control; Fig. 5H, 5I). In addition, the mean survival time of mice injected with hGIC1 was longer in the drug-treated group (56.2 ± 8.2 days, $p = .0027$), compared with control mice (44.5 ± 3.4 days), whereas the combination did not increase the mean survival time of mice injected with hGIC2 (37.6 ± 1.1 days in drug-treated vs. 34.6 ± 2.6 days in control; Fig. 5J, 5K). We confirmed that the drug combination could block the tumorigenesis of an oligodendroglioma cell line, Hs683, but not of a GBM line, U251 (Supporting Information Fig. 4). In addition, we found that the knockdown of both *egfr* and *ptgs2* inhibited the proliferation of OPCL61 and hGIC1 cells but not of NSCL61 and hGIC2 cells (data not shown). Together, these results suggest that both EGFR and Ptgs2 are crucial for the proliferation of oligodendrocyte lineage-derived malignant glioma, and that a drug combination targeting both pathways specifically prevents its tumorigenesis.

Discussion

Here, we demonstrated that a combination of oncogenic $HRas^{L61}$ overexpression and *p53* deletion, both of whose pathways are frequently mutated in human GBM [8–12], transformed NSCs and OPCs into GIC-like cells. The injection of only 10 of these GIC-like cells formed transplantable GBM with characteristics of human GBM in the brain of nude mice, suggesting that these cells are enriched in CICs and that both NSCs and OPCs are likely cells-of-origin for GBM. In contrast, we found that the same combination could not transform astrocytes; AST-L61 cells did not form either colonies in soft agar or tumors in vivo when 10^3 of them were transplanted. Interestingly, when 10^4 AST-L61 cells were

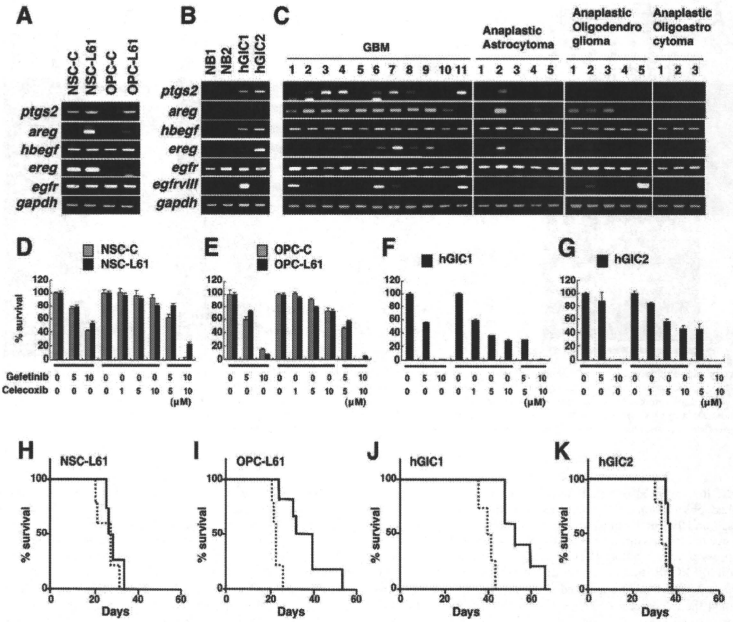

Figure 5. Combination of a Ptgs2 inhibitor and an epidermal growth factor receptor (EGFR)-signaling inhibitor delays the tumorigenesis of oligodendrocyte lineage-derived GICs. **(A–C):** Expression analysis of *ptgs2*, EGFR ligands (*areg*, *hbegf*, and *ereg*), *egfr*, and *egfrvIII* in GIC-like cells, hGICs, and human glioma samples (GBM, anaplastic astrocytoma, anaplastic oligodendroglioma, and anaplastic oligoastrocytoma), by reverse transcription polymerase chain reaction. *gapdh* expression was an internal control. **(D–G):** Cytotoxic effects of Gefitinib and Celecoxib on induced glioma cells (black column in **[D, E]**), their parental cells (gray column in **[D, E]**), hGIC1 **(F)**, and hGIC2 **(G)**. **(H–K):** Survival curve of NSC-L61- **(H)**, OPC-L61- **(I)**, hGIC1- **(J)**, or hGIC2-injected mice **(K)**, treated with the drug combination (C+G, solid line). Control mice were given water only (dotted line). Abbreviations: GBM, glioblastoma multiforme; GIC, glioma-initiating cell; hGIC, human GIC; NSC, neural stem cell; OPC, oligodendrocyte precursor cell.

transplanted into the brain of nude mice, they formed invasive astrocytoma. Theoretically, because tumors are likely to arise from one or a few CICs, AST-L61 cells are not GIC-like cells but might be premalignant cells that need additional mutation(s) to transform into GIC-like cells, or they might need a specific niche to induce tumorigenesis [36]. It will be interesting to examine which oncogenic mutations can transform astrocytes into GICs.

It has been thought that precursor cells and differentiated cells acquire characteristics of tissue-specific stem cells when they are transformed. Indeed, here we found that when OPCs were transformed into GIC-like cells, they lost their original features and acquired characteristics of NSCs. Although the detailed mechanism of the dedifferentiation caused by transformation remains to be elucidated, it is likely that epigenetic modification plays an important role, as we previously showed that epigenetic modification is involved in OPC reversion [16, 37] and that activation of the Ras-signaling pathway induces alterations in epigenetic modification, chromatin structure, and gene expression [38–42]. As OPCs can be purified and cultured in serum-free medium with defined chemicals and mitogens, OPC transformation might be a good model for investigating the molecular mechanisms of dedifferentiation in tumorigenesis.

Using GIC-like cell models, we demonstrated that oligodendrocyte lineage-derived GBMs (hGIC1) are sensitive to treatment with a Ptgs2 inhibitor and an EGFR-signaling inhibitor in combination, whereas those derived from GBM tissues (hGIC2) were not. As there is much evidence showing that chromosome 1p and 19q loss is a marker for increased sensitivity to standard therapies (chemotherapy and radiation therapy), we examined the 1p and 19q status in the two hGIC lines using the fluorescence in situ hybridization and found that hGIC2 had lost both 1p and 19q, whereas hGIC1 only lost 1p (data not shown), suggesting that the increased sensitivity to the Gefitinib/Celecoxib combination in hGIC1 was not related to the 1p/19q deletions.

There are several possible explanations for why the drug combination appeared more effective in the oligodendrocyte lineage-derived tumors than in GBM tissues. First, EGFR signaling is known to be involved in OPC proliferation and tumorigenesis [43, 44]. Second, the accumulation of Cox2-expressing astrocytes is more often observed in high-grade oligodendroglioma than in GBM [45, 46]. Third, hGIC1 and Hs683 strongly expressed egfrvIII, which was shown by Mellinghoff et al. to cause "pathway addiction" of the tumor cells [47]. Fourth, the National Cancer Institute's Repository for Molecular Brain Neoplasia Data (REMBRANDT) database [48] revealed that the downregulation of either *ptgs2* or *egfr* mRNA is correlated with a significant increase in the survival of oligodendroglioma, but not of GBM patients (Supporting Information Fig. 6). Thus, these data suggest that the combination of these inhibitors with irradiation/chemotherapy may be effective in patients suffering from oligodendrocyte lineage-derived GBMs and point to potential new clinical approaches combining current and GIC-specific therapies.

Conclusion

In this study, we have shown that induced GBM models are useful for investigating the cells-of-origin of GBM, their characteristics, and therapeutic targets, when combined with studies using hGICs and human glioma samples. Our results also suggest that the therapeutic targets for GBM are different according to the cell-of-origin of the GICs. In future studies, it will be important to find specific markers for classifying GBM according to its cell-of-origin.

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Disclosure of Potential Conflicts of Interest

The authors indicate no potential conflicts of interest.

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