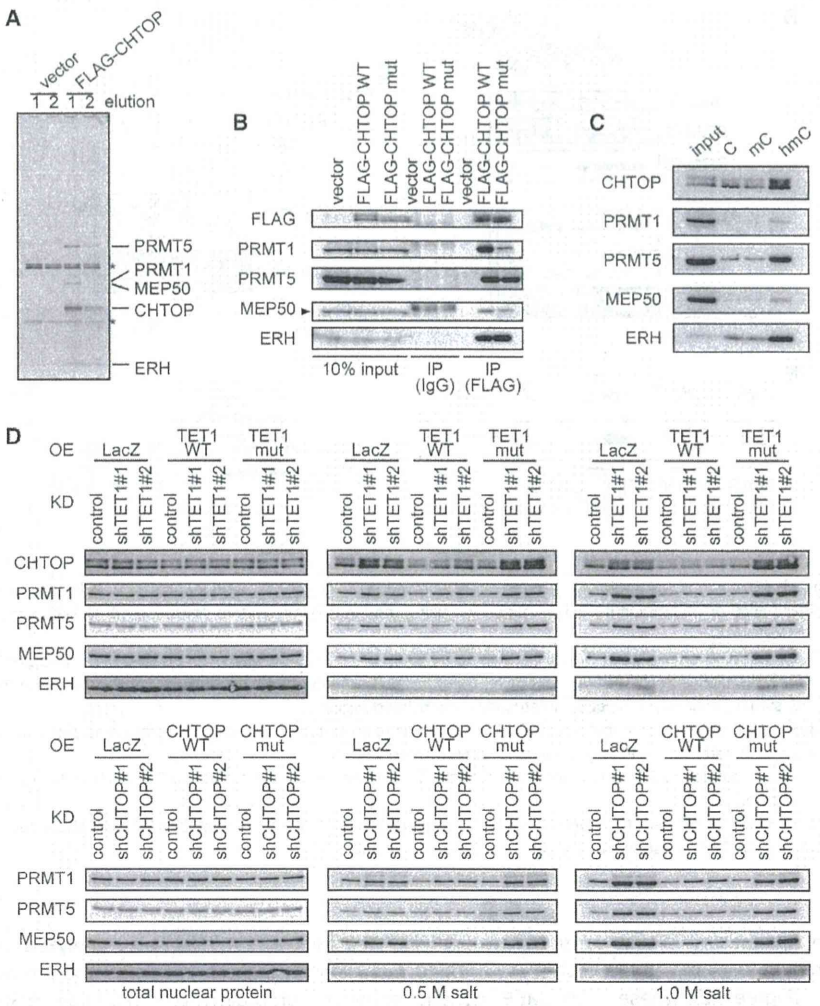

Figure 5. CHTOP Associated with the Methylosome Binds to 5hmC

(A) CHTOP is associated with the methylosome. Lysates from HEK293FT cells transfected with FLAG-CHTOP were subjected to immunoprecipitation with anti-FLAG antibody followed by SDS-PAGE and silver staining, and coprecipitated proteins were identified by mass spectrometry. Asterisks indicate immunoglobulin chains.

(B) CHTOP is associated with the methylosome in GB2 cells. The immunoprecipitates prepared as in (A) were subjected to immunoblotting analysis with the indicated antibodies.

(C) CHTOP and the methylosome preferentially bind to 5hmC in GB2 cells.

(D) Immunoblotting analysis of methylosome components extracted with salt buffer from the chromatin fractions prepared from GB2 cells infected with a lentivirus expressing the indicated shRNAs and/or a lentivirus expressing wild-type or mutant TET1 (upper panels) or CHTOP (lower panels). KD, knockdown.

See also Figure S4 and Table S3.

regulation of gene expression and RNA processing. Of particular note, it has been reported that PRMT1-mediated dimethylation of H4R3 is important for subsequent histone modifications such as acetylation and thereby is involved in modulating transcriptional activation (Huang et al., 2005; Wang et al., 2001).

To examine whether CHTOP is required for the association of the methylosome with chromatin, chromatin samples prepared from GB2 cells were incubated with NaCl and extracted proteins were analyzed by immunoblotting analysis (Meshorer et al., 2006). We found that knockdown of CHTOP resulted in increased amounts of PRMT1, PRMT5, MEP50, and ERH extracted from the chromatin fraction (Figures 5D, S4A, and S4B). We also found that knockdown of TET1 led to the increased extraction of these proteins, as well as increased extraction of CHTOP. In addition, the increased extraction of these proteins caused by knockdown of TET1 or CHTOP could be suppressed by overexpression of wild-type TET1 or CHTOP, but not of mutant TET1 or CHTOP. These results suggest that CHTOP associated with 5hmC functions as a recruiter of the methylosome.

H4R3 Is Methylated by PRMTs in a CHTOP- and/or TET1-Dependent Manner

We next investigated whether H4R3 is methylated by PRMTs in a CHTOP- and/or TET1-dependent manner. Immunoblotting analysis revealed that knockdown of either TET1 or CHTOP resulted in a reduction in the amounts of both H4R3me2a and H4R3me2s (Figure 6A). We also performed chromatin immunoprecipitation (ChIP) assays with antibodies against PRMT1, PRMT5, H4R3me2a, and H4R3me2s. We found that these are associated with the *EGFR*, *AKT3*, *CDK6*, *CCND2*, and *BRAF* genes, but not the *HPRT1* gene (Figure 6B). Knockdown of either CHTOP or TET1 reduced the association of PRMT1 and PRMT5 with these genes (Figure 6B). Furthermore, we found that knockdown of either CHTOP or TET1 resulted in decreases in both the asymmetrical and symmetrical dimethylation of H4R3 (Figure 6B), whereas knockdown of PRMT1 or PRMT5 led to a decrease in the asymmetrical or symmetrical dimethylation of H4R3, respectively (Figure S5A). We also found that knockdown of either TET1 or CHTOP led to an increase in the trimethylation of H3K27, whereas the trimethylation of H3K36 and the acetylation of H4 were not affected (Figure S5B). Consistent with these results, knockdown of either CHTOP or PRMT1 suppressed the expression of these genes (Figures 6C and 6D), whereas knockdown of PRMT5 barely changed their expression, except for *CCND2*.

Consistent with the above findings, RNA sequencing (RNA-seq) analyses revealed that knockdown of TET1,

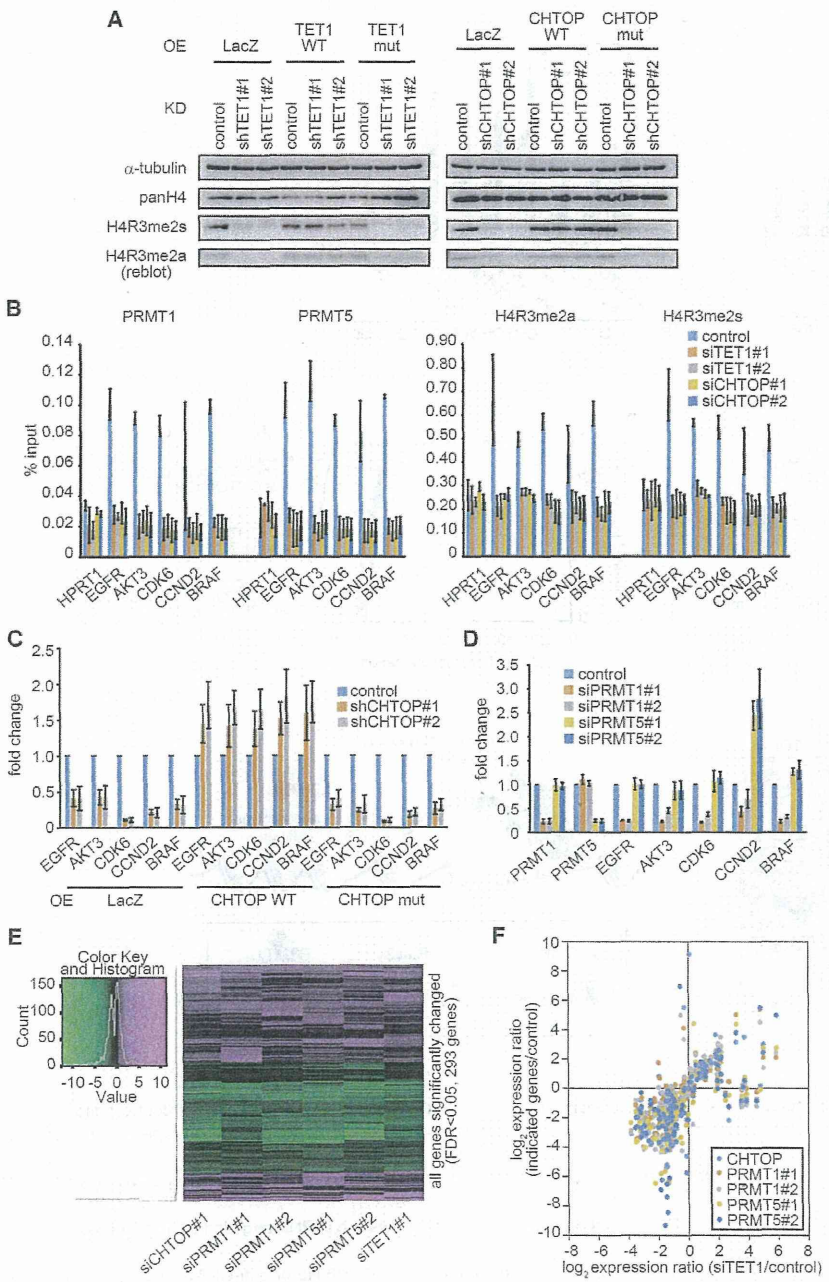

Figure 6. The CHTOP-Methylosome Complex Associated with 5hmC Methylates H4R3 and Transactivates Cancer-Related Genes

(A) Immunoblotting analysis of H4R3me2a and H4R3me2s in GB2 cells infected with a lentivirus expressing the indicated shRNAs and/or a lentivirus expressing wild-type or mutant TET1 (left panels) or CHTOP (right panels).

(B) PRMTs and H4R3me2 are associated with 5hmC-enriched loci in a TET1- and CHTOP-dependent manner. ChIP assays were performed with GB2 cells transfected with the indicated siRNAs. Data show the means ± SD of three independent experiments.

(C) qRT-PCR analyses of the indicated genes were performed using GB2 cells infected with a lentivirus expressing shRNA targeting CHTOP and/or a lentivirus expressing wild-type or mutant CHTOP. Data show the means ± SD of three independent experiments.

(D) qRT-PCR analyses of the indicated genes were performed using GB2 cells transfected with siRNA targeting PRMT1 or PRMT5. Data show the means ± SD of three independent experiments.

(E) RNA-seq analysis of GB2 cells transfected with the indicated siRNAs.

(F) Scatterplot comparing transcriptome between TET1 knockdown cells and CHTOP, PRMT1, or PRMT5 knockdown cells. Genes whose expression was significantly changed are shown.

See also Figure S5.

CHTOP Is Required for Maintaining 5hmC Levels

We next examined the expression levels of CHTOP in glioblastoma cells and hNPCs. We found that GB2~GB5, GB11, and GB13 cells, but not GB1 cells, express somewhat higher levels of CHTOP than hNPCs (Figure S6A). Furthermore, we found that knockdown of CHTOP results in a reduction in global 5hmC levels in GB2 cells (Figure S6B). We have also found that overexpression of wild-type, but not of GAR mutant, CHTOP restores 5hmC levels. These results suggest that CHTOP is required for maintaining 5hmC levels and that upregulation of CHTOP as well as TET1 is responsible for the elevated levels of 5hmC in glioblastoma cells. This may be one of the reasons why 5hmC levels are not elevated in hNPCs, in which only TET1, but not CHTOP, are upregulated.

CHTOP, PRMT1, or PRMT5 resulted in similar changes in gene-expression patterns in GB2 cells (Figures 6E and S5C) and that the gene-expression profile of TET1 knockdown cells strongly correlated with the profiles of cells in which the other genes were knocked down (Figure 6F). In addition, we found that 5hmC was overrepresented in the promoters and intragenic regions of approximately 30% of genes whose expression was significantly changed (false discovery rate < 0.05).

CHTOP Is Required for the Tumorigenicity of Glioblastoma Cells

Finally, we investigated the importance of CHTOP in the proliferation and tumorigenicity of glioblastoma cells. We found that knockdown of CHTOP led to decreases in sphere formation of

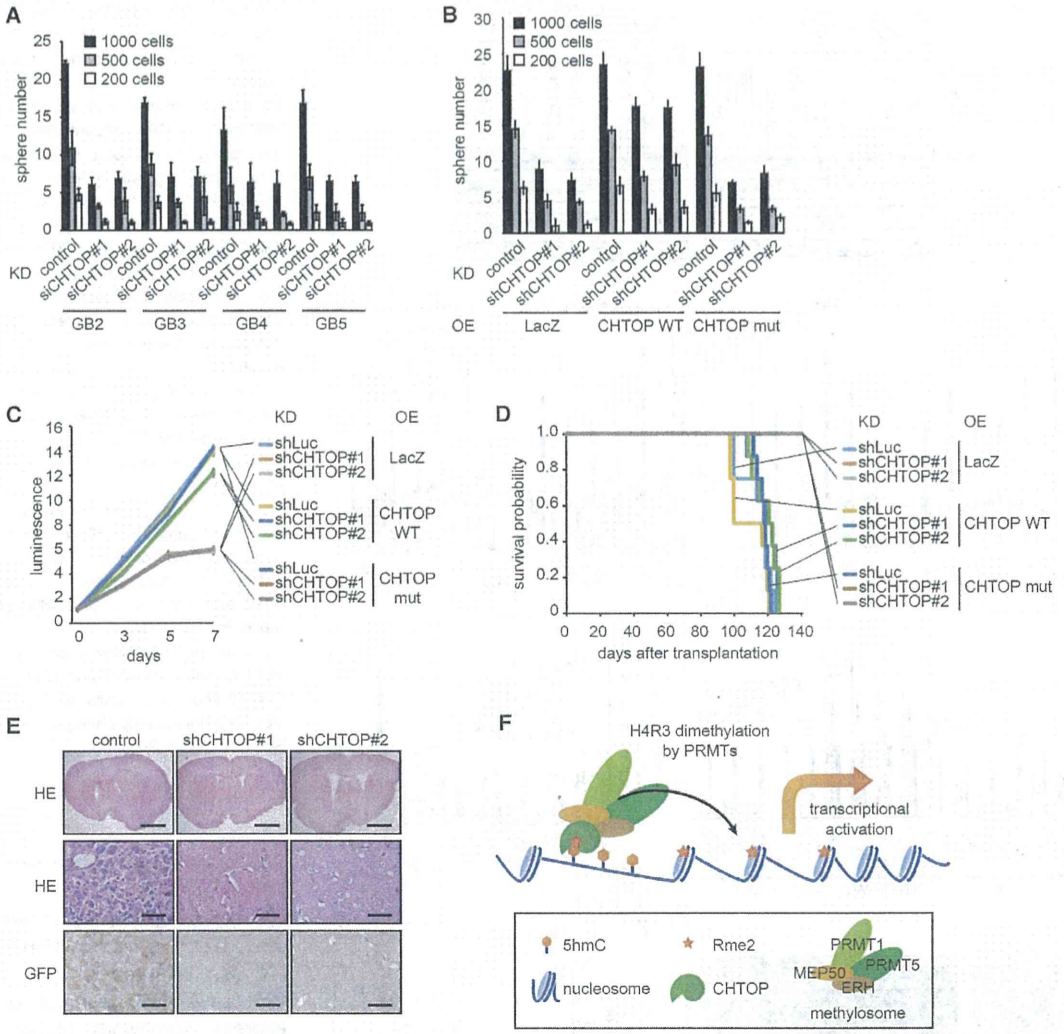

Figure 7. CHTOP Is Required for the Tumorigenicity of Glioblastoma Cells

(A) The number of spheres of glioblastoma cells transfected with siRNA targeting CHTOP. Data show the means ± SD of three independent experiments.

(B) The number of spheres of GB2 cells infected with a lentivirus expressing shRNA targeting CHTOP and/or a lentivirus expressing wild-type or mutant CHTOP. Data show the means ± SD of three independent experiments.

(C) Growth curves of GB2 cells infected with a lentivirus expressing shRNA targeting CHTOP and/or a lentivirus expressing wild-type or mutant CHTOP. Data show the means ± SD of three independent experiments.

(D) Kaplan-Meier survival curves of mice transplanted with 1.0×10^4 GB2 cells infected with a lentivirus expressing shRNA targeting CHTOP and/or a lentivirus expressing wild-type or mutant CHTOP.

(E) Histological examination of tumors developed in the mice in (D). At day 100, tissue sections were stained with HE or anti-GFP antibody. The scale bars represent 2 mm (upper panels) and 50 μm (lower panels).

(F) Schematic representation of 5hmC-mediated transcriptional activation. For details, see text.

See also Figure S6.

GB2~GB5 cells (Figures 7A and 7B) and GB2 cell proliferation (Figure 7C). These phenotypes were rescued by overexpression of wild-type CHTOP, but not by GAR mutant CHTOP. Mice receiving shCHTOP-expressing GB2 cells survived significantly longer than control mice (Figures 7D and 7E). Furthermore, we found that overexpression of CHTOP restored the tumorigenicity of shCHTOP-expressing GB2 cells (Figure 7D). These results suggest that 5hmC serves as a recruitment signal for the CHTOP-methylosome complex, which in turn methylates H4R3 and thereby activates the transcription of genes required for glioblastomagenesis (Figure 7F).

DISCUSSION

It is well known that glioblastomas contain genetic alterations in the p53, RB, and RTK pathways (Chen et al., 2012; Parsons

et al., 2008; Cancer Genome Atlas Research Network, 2008), as well as other genes, including the neurofibromatosis type 1 gene (Cancer Genome Atlas Research Network, 2008), the NF-κB inhibitor α gene (Bredel et al., 2011), and/or the IDH1 gene (Parsons et al., 2008). In the present study, we have shown that epigenetic alterations are also critical for the tumorigenicity of glioblastoma cells. We showed that proneural glioblastoma contains elevated levels of 5hmC and TET1 and that TET1-mediated production of 5hmC is required for glioblastomagenesis. We found that knockdown of TET1 in glioblastoma cells resulted in decreases in their proliferation, sphere formation, and tumorigenicity. Furthermore, we demonstrated that ectopic overexpression of wild-type, but not of a catalytically inactive mutant, TET1 restored the growth, sphere formation, and tumorigenicity, as well as 5hmC levels in glioblastoma cells in which TET1 had been knocked down.

Our results are in striking contrast to previous studies showing that 5hmC levels are markedly reduced in many tumor cells (Haffner et al., 2011; Kraus et al., 2012; Müller et al., 2012; Orr et al., 2012). This may be due to the differences in the culture conditions used and/or tumor subtypes. We cultured primary glioblastoma cells in serum-free conditions to retain their stem-cell-like properties and tumorigenicity. Indeed, our results showed that HeLa and U87MG cells cultured in the presence of serum contain extremely low levels of 5hmC.

Although most of previous studies did not consider subtypes of glioblastoma, Noushmehr et al. (2010) have reported that the IDH1 mutation is highly enriched in recurrent and secondary proneural glioblastoma and is strongly linked to the glioma-CpG island methylator phenotype (G-CIMP). Thus, secondary proneural glioblastomas are expected to have lower 5hmC levels. However, they have also reported that only a minor population of primary glioblastoma patients (<10%) display G-CIMP and IDH1 mutations. In this study, we focused on primary glioblastomas that can be cultured in serum-free media and found that most of the glioblastoma cell lines we established belong to the proneural subtype. Furthermore, we performed dot blot analysis of 5hmC using glioblastoma specimens of all subtypes and found that primary proneural glioblastomas that do not have an IDH1 mutation have markedly higher levels of 5hmC compared to other subtypes. We speculate that 5hmC may function differently at the molecular level in primary proneural glioblastoma compared to other subtypes of glioblastoma and other tumor cell types, and accordingly, 5hmC may recruit different molecules and elicit different downstream signals in proneural glioblastoma cells than it does in other tumor cells.

We have shown that 5hmC is not simply a demethylation intermediate but rather functions itself as an epigenetic mark modulating gene expression. Our results are consistent with previous findings showing that 5hmC is stably present in the genomes of ESCs and neuronal cells (Ficz et al., 2011; Guo et al., 2011; Hahn et al., 2013; Wu et al., 2011) and that enrichment of 5hmC is not necessarily associated with DNA demethylation (Hahn et al., 2013). Furthermore, Mbd3/NURD and MeCP2 have been reported to bind to both 5hmC and 5mC (Mellén et al., 2012; Yildirim et al., 2011). A systematic analysis of 5hmC-binding proteins using quantitative mass-spectrometry-based proteomics has identified a number of specific 5hmC-binding proteins (Spruijt et al., 2013). These reported results suggested that 5hmC, 5fC, and 5caC may recruit transcription regulators in certain cell types, as well as DNA repair proteins, which may also be involved in DNA demethylation. CHTOP was not identified in this latter study, presumably because this laboratory used mouse ESCs, mNPCs, and adult mouse brain tissue.

We found that TET1-mediated enrichment of 5hmC is critical for the expression of a number of cancer-related genes such as *EGFR*, *AKT3*, *CDK6*, *CCND2*, and *BRAF*. Furthermore, we found that CHTOP associated with 5hmC recruits the methylosome and that a component of the methylosome complex, PRMT1, methylates H4R3 and transactivates these genes. We investigated these genes because their products are key components of the RTK/RAS/PI(3)K- or the RB-signaling pathways and have been reported to be frequently altered in glioblastoma and play critical roles in glioblastomagenesis (Chen et al., 2012; Parsons et al., 2008; Cancer Genome Atlas Research Network, 2008). We would like to investigate whether hydroxymethylation of these five genes is necessary for the tumorigenicity of glioblastoma cells in future studies.

We found that TET1 knockdown in GB2 cells alters expression of many genes that do not have 5hmC peaks. It is possible that alterations in the expression of the genes that have 5hmC may affect that of other genes that do not have 5hmC. In addition, previous studies have shown that the TET family of proteins can interact with O-linked N-acetylglucosamine transferase (OGT) and function as a recruiter of OGT to chromatin (Chen et al., 2013; Deplus et al., 2013; Vella et al., 2013). We therefore speculate that TET1 has an important role that is independent of its catalytic activity.

Interestingly, we found that knockdown of CHTOP results in a reduction in global 5hmC levels in glioblastoma cells, whereas overexpression of CHTOP restores 5hmC levels. Thus, CHTOP may be required for maintaining 5hmC levels. For example, CHTOP may protect 5hmC from demethylation. Our results suggest that upregulation of CHTOP as well as TET1 may be responsible for the elevated levels of 5hmC observed in glioblastoma cells. We would like to investigate this issue in more detail in future studies. In addition, we found that hNPCs express somewhat lower levels of CHTOP than glioblastoma cells. It is therefore possible that reduced expression of CHTOP in hNPCs contributes, at least in part, to the poor expression of 5hmC, despite high TET1 expression in these cells.

Glioblastoma stem cells are subsets of glioblastoma cells that possess the capability of self-renewal and exhibit extensive tumorigenicity (Gilbertson and Rich, 2007; Lathia et al., 2011; Singh et al., 2004). Glioblastoma stem cells have been reported to be resistant to both chemotherapy and radiotherapy and thus are responsible for the poor prognosis of glioblastoma (Bao et al., 2006; Chen et al., 2012). In this study, we utilized glioblastoma cells cultured in serum-free medium, which enriches for glioblastoma stem cells (Lee et al., 2006). Thus, it is possible that 5hmC is critical for the tumorigenicity of glioblastoma stem cells. To test this possibility, we need to analyze the CD15- and/or CD133-positive stem cell population (Singh et al., 2004; Son et al., 2009). It also remains to be examined whether 5hmC is required specifically for glioblastoma stem cells or required for both glioblastoma stem and nonstem cells.

In conclusion, we found that 5hmC recruits the CHTOP-methylosome complex, which methylates H4R3 and transactivates cancer-related genes. Of particular interest is the fact that knockdown of TET1 as well as CHTOP results in the strong suppression of glioblastoma cell tumorigenicity. We therefore speculate that TET1 could be a promising molecular target for glioblastoma therapy. Because TET1-deficient mice are viable and fertile (Dawlaty et al., 2011, 2013), compounds targeting TET1 would be expected to have few serious side effects.

EXPERIMENTAL PROCEDURES

Antibodies

Antibodies used in immunoblot, ChIP, and (h)MeDIP assays are listed in Table S4.

Cell Culture

Following informed consent, tumor samples classified as primary glioblastoma were obtained from patients undergoing surgical treatment at the University of Tokyo Hospital, as approved by the Institutional Review Board. Mouse experiments were also approved by the Institutional Review Board. Tumors were washed and mechanically and enzymatically dissociated into single cells. Tumor cells were cultured in Dulbecco's modified Eagle's medium (DMEM)/F12 (Life Technologies) containing B27 supplement minus vitamin A (Life Technologies), epidermal growth factor, and fibroblast growth factor 2 (20 ng/ml each; Wako Pure Chemicals Industries). Fetal and ESC-derived hNPCs were purchased from Lonza and Millipore, respectively, and cultured under the same conditions. HEK293FT, HeLa, and human glioblastoma U87MG cells were cultured in DMEM (Nissui) containing 10% fetal bovine serum. GB2 cells transfected with siRNA targeting TET1 or control were seeded into a 96-well plate at the indicated cell number. The number of spheres was counted after 7 days. Cell viability was measured by CellTiter-Glo (Promega) according to the manufacturer's instructions.

RNAi

For lentivirus production, the lentiviral vector CS-Rfa-CG harboring an shRNA driven by the H1 promoter was transfected with the packaging vectors pCAG-HIV-gp and pCMV-VSV-G-RSV-Rev into HEK293FT cells using Lipofectamine 2000 Transfection Reagent (Life Technologies). All plasmids were kindly provided by H. Miyoshi (RIKEN BioResource Center). Virus supernatants were purified by ultracentrifugation at 25,000 rpm at 4°C for 90 min (SW28 rotor; Beckman Coulter Genomics). The target sequences for shRNAs are as follows: shTET1 no.1: 5′-GCATATTCCTTTGAAATAA-3′; shTET1 no. 2: 5′-GAACTAAACAAGATTAAGT-3′; shCHTOP no. 1: 5′-CTAAATGAGCGCTTTACTA-3′; shCHTOP no. 2: 5′-CCAAGATGTCTCTAAATGA-3′. The infection efficiency of the lentiviruses was more than 95%, as judged by GFP or Venus fluorescence. Transfection of Stealth siRNA duplexes targeting human TET1 (Life Technologies; catalog no. 10620318 and 10620319) or Silencer Select Pre-Designed siRNA targeting human CHTOP (Life Technologies; catalog no. s25092 and s25093) were performed using Lipofectamine RNAiMAX (Life Technologies) according to the manufacturer's instructions.

RNA Isolation and qRT-PCR

Total RNA was prepared by the NucleoSpin RNA Clean-up kit (Macherey-Nagel) and reverse transcribed with PrimeScript Reverse Transcriptase (TaKaRa). qPCR reactions were performed with Sybr Green I using a LightCycler480 (Roche Applied Science). The results were normalized with the detected values for TATA box-binding protein mRNA. Absolute mRNA levels of the TET family of genes were determined according to the standard curves generated by serial dilutions of plasmids containing TET1~TET3. Primers used in qRT-PCR are shown in Table S5.

(h)MeDIP

Cells were digested with proteinase K and RNase A, and genomic DNA was purified by phenol/chloroform extraction. Purified genomic DNA was sonicated to 200–500 bp with a Handy Sonic (TOMY). (h)MeDIP was performed as described previously (Weber et al., 2005) with minor modifications. Briefly, 4 μg of fragmented genomic DNA was immunoprecipitated with 4 μl of polyclonal antibody against 5hmC (Active Motif) or 4 μg of monoclonal antibody against 5mC (Eurogentec) at 4°C overnight in a 500 μl of IP buffer (10 mM sodium phosphate [pH 7.0], 140 mM NaCl, and 0.05% Triton X-100). The mixture was incubated with 30 μl of Dynabeads Protein G at 4°C for 2 hr and washed three times with 1 ml of IP buffer. The beads were suspended in 20 μg of proteinase K and incubated at 55°C for at least 3 hr. Immunoprecipitated DNA was purified by phenol/chloroform extraction followed by isopropanol precipitation.

ACCESSION NUMBERS

Profiling and (h)MeDIP-seq data from this study are available from the Sequence Read Archive database (http://www.ncbi.nlm.nih.gov/sra) under the accession number SRP045590.

SUPPLEMENTAL INFORMATION

Supplemental Information includes Supplemental Experimental Procedures, six figures and five tables and can be found with this article online at http://dx.doi.org/10.1016/j.celrep.2014.08.071.

AUTHOR CONTRIBUTIONS

H.T. designed and performed most of the experiments. T. Sato performed dot blot analysis. R.K.-N. and Y.N.-N. established glioblastoma cell lines and discussed the results. K.M., Y.K., and K.S. performed sequence analysis and analyzed the bioinformatic data. H.O. and C.T. supervised the production of recombinant CHTOP. Y.M. performed immunohistochemical analysis of glioblastoma specimens. Y.S., Takeo Suzuki, Tsutomu Suzuki, H.K.-H., and M.O. performed mass spectrometric analysis. T.T., Y.I., A.M., and N.S. prepared glioblastoma specimens. H.T. and T.A. wrote the paper.

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LABORATORY INVESTIGATION

Strong therapeutic potential of γ-secretase inhibitor MRK003 for CD44-high and CD133-low glioblastoma initiating cells

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Abstract The Notch signal regulates both cell viability and apoptosis, and maintains stemness of various cancers including glioblastoma (GBM). Although Notch signal inhibition may be an effective strategy in treating GBM initiating cells (GICs), its applicability to the different subtypes of GBM remains unclear. Here, we analyzed the effectiveness of MRK003, a preclinical γ-secretase inhibitor, on GICs. Nine patient-derived GICs were treated by MRK003, and its efficacy on cell viability, apoptosis, sphere forming ability and Akt expression level which might be related to Notch downstream and be greatly important signals in GBM was evaluated. MRK003 suppressed viability and sphere-formation ability, and induced apoptosis in all GICs in varying doses of MRK003. Based on their sensitivities to MRK003, the nine GICs were divided into "relatively sensitive" and "relatively resistant" GICs. Sensitivity to MRK003 was associated with its inhibitory effect on Akt pathway. Transgenic expression of the myristoylated Akt vector in relatively sensitive GICs partially rescued the effect of MRK003, suggesting that the effect of MRK003 was, at least in part, mediated through inhibition of the Akt pathway. These GICs were differentiated by the expression of CD44 and CD133 with flow cytometric analysis. The relatively sensitive GICs are CD44-high and CD133-low. The IC_{50} of MRK003 in a set of GICs exhibited a negative correlation with CD44 and positive correlation with CD133. Collectively, MRK003 is partially mediated by the Akt pathway and has strong therapeutic potential for CD44-high and CD133-low GICs.

Keywords Glioma · MRK003 · GBM initiating cells · CD44 · CD133

Introduction

Glioblastoma (GBM) is the most malignant primary brain tumor in humans. Despite the momentous progress in surgical and neuro-radiological techniques, the median overall survival period of GBM patients is from 14.6 to 16.0 months post diagnosis without major improvement for decades [1–4]. GBM is characterized by a heterogeneous population of tumor cells, exhibiting high invasive ability and chemo- and radio-resistance [2]. Accumulated evidence has suggested that tumor initiation is caused by a small fraction of tumor cell termed GBM initiating cells (GICs) [5, 6]. The significance of targeting GICs may be important for successful treatment of GBM [7, 8].

The Notch signals play a variety of roles in cancer initiation and propagation, and are critical for maintenance of stemness [9]. This pathway is mediated by cell–cell contact, thereby initiating the binding of a ligand to a Notch

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receptor with subsequent activation of the intracellular signaling events. Upon binding of ligand, Notch intracellular domain (NICD) is released by γ-secretase, which then translocates to the nucleus, interacts with the specific transcriptional factors, and subsequently activates downstream target genes [9, 10]. The activation of Notch signaling was identified in a variety of cancers, including GBM [10–15]. Notch displays intense crosstalk with other oncogenic pathways, including phosphoinositide 3-kinase (PI3K)/Akt pathway that is a major pathway in GBM [16], Janus-activated kinase (JAK)/STAT pathway, Sonic hedgehog pathway and Wnt pathway [10, 17–21]. Hence, suppression of the Notch signal inhibition may offer an ideal strategy for the treatment of multiple types of cancers.

MRK003 is expected as a novel Notch inhibitor, and is known to be the most effective small molecule inhibitors amongst several other Notch inhibitors [22]. Data obtained with pre-clinical studies for pancreatic carcinoma, breast cancer, and T cell lymphoblastic leukemia demonstrated that MRK003 significantly suppressed cell proliferation and induced apoptosis in vivo [23–27]. Recent studies including ours have suggested that MRK003 suppresses both proliferation and invasion of GBM cell lines [19–21, 28]. In addition, MRK003 suppressed tumor growth and tumor initiation capacity in two GBM neurosphere lines [29]. Saito et al. revealed that Notch inhibition demonstrated good response at rate of 43.9 % for proneural subtype of GBM [30]. However, study with patient-derived GICs treated by MRK003 has never been reported.

In this study, we performed a set of in vitro assays including cell viability assay, apoptosis assay and sphere formation assay to analyze the effect of MRK003 on nine patient-derived GICs. Results of these assays demonstrated that MRK003 suppresses GICs viability and sphere formation, and promotes their apoptosis. Nine GICs was classified into relatively sensitive GICs and relatively resistant GICs. Forced expression of the active form of Akt in MRK003-treated relatively sensitive GICs partially rescued the phenotype caused by MRK003, indicating that the mechanism of action is partially mediated through the Akt pathway. Relatively sensitive GICs expressed high-CD44 and low-CD133. In summary, these data indicate that MRK003 may exhibit significant therapeutic potential for GBM harboring GICs with CD44-high and CD133-low expression.

Materials and methods

GBM patient-derived cell culture and transfection

GBM cells used in this study were GICs derived from GBM surgical specimens. Diagnosis was based on the World Health Organization classification [3]. Seven GICs (30R, 1123M, Me83, MD13, 528P, 157NS, and 146NS) were established from freshly resected GBM sample of consenting patients in the Department of Neurological Surgery at The Ohio State University [31–34]. TGS01 and TGS04 GIC were isolated from surgically removed GBM tissues at the University of Tokyo (by TT and YI) [35]. All GBM cells already have been confirmed as tumor-initiating cells since cultured GBM cells have the ability to self-renewal in vitro and mimic the original tumor after intracranial transplantation into immunocompromised mice [31–34]. All patient materials and protocols in this study were approved by the ethics committees of Kanazawa University, the Ohio State University and the University of Tokyo. These GBM-derived neurospheres were cultured as described previously [6, 36, 37].

Vector

Recombinant pcDNA vectors carrying the constitutive, active myristoylated allele of Akt were used for transfection into 30R and 1123M by Nucleofector Kit (Lonza, Basel, Switzerland) by following the company's protocol.

Compounds

The stock solutions of MRK003 (Merck & Co., Inc.; Whitehouse Station, NJ) were dissolved in DMSO at a concentration of 10 mM. The specificity of MRK003 as a γ-secretase inhibitor has been confirmed by us and other investigators [22–25, 27].

Viability assay

Cell viability assay was performed with Cell counting kit-8 (DOJINDO, Kumamoto, Japan) by following the company's protocol. Briefly, all the GBM spheres were dissociated into single cell suspensions by StemPro Accutase (Gibco/Life Technologies). These dissociated GICs were seeded at a density of 1×10^3 cells/100 μl per well into a 96-well Coaster ultra-low attachment plate (Corning, NY) with either MRK003 or DMSO control for 72 h. IC_{50} for MRK003 of each was calculated from non-linear curve fit graph using Graph pad prism 5 (Graph Pad Software, Inc., San Diego).

Apoptosis assay

Apoptosis assay was performed using the Annexin V-FITC detection kit as per the manufacturer's protocol (BD Pharmingen, San Diego, CA). GICs were seeded at a density of 1×10^5 cells/2 ml/well in a 6-well plate in neurosphere medium with MRK003 or DMSO control.

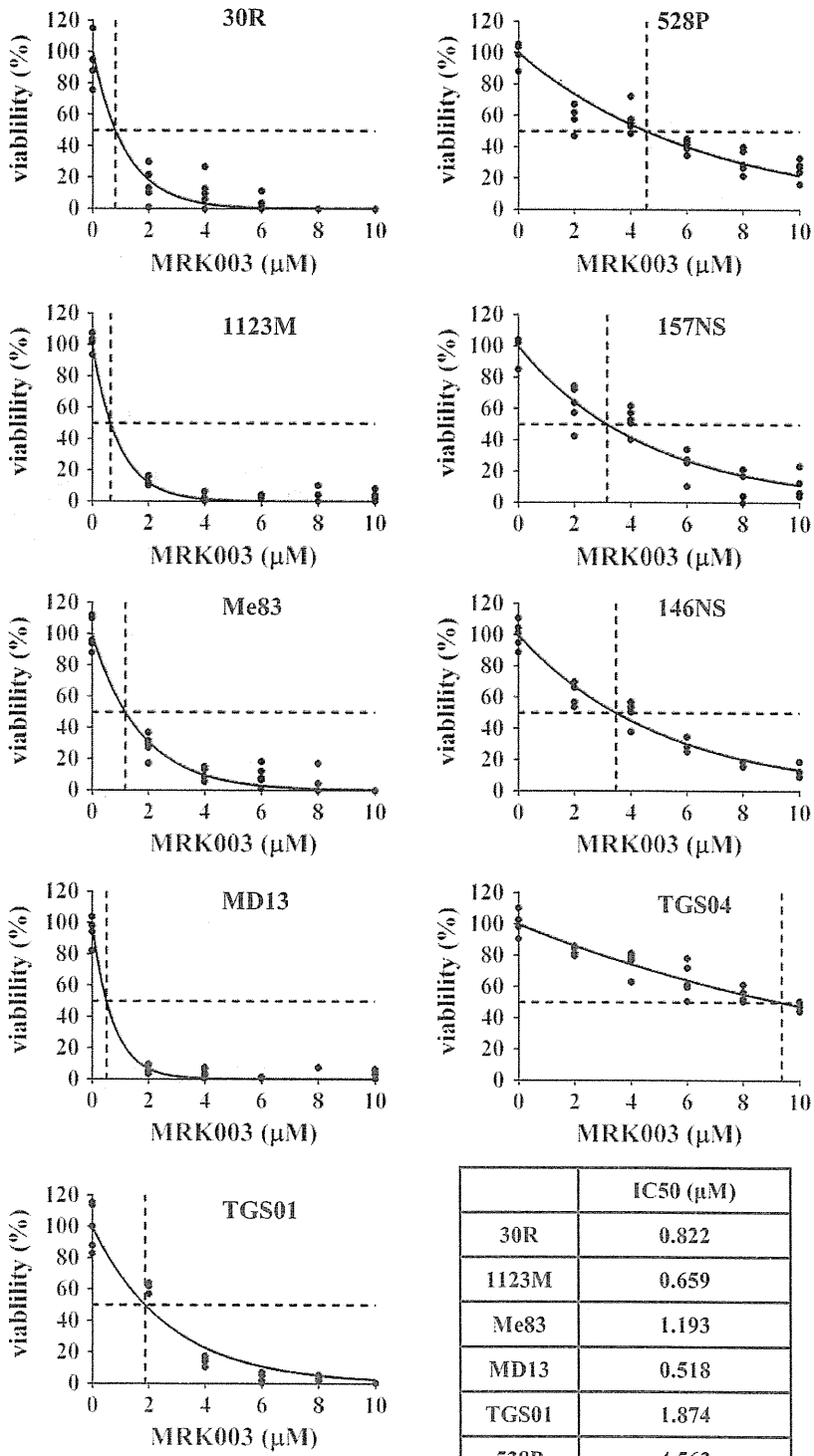

Fig. 1 MRK003 inhibited viability of nine GICs derived from patients in a dose-dependent manner. 30R, 1123M, MD13, Me83 and TGS01 were relatively sensitive for MRK003. 528P, 157NS, 146NS and TGS04 were relatively resistant for MRK003. Experiments were performed three times. Each data shown were representative. IC_{50} was X-value of intersection of non-linear fitting *graph line* with 50 % viability dotted line

	IC50 (μM)
30R	0.822
1123M	0.659
Me83	1.193
MD13	0.518
TGS01	1.874
528P	4.563
157NS	3.17
146NS	3.48
TGS04	9.371