An Epigenetic Genome-Wide Screen Identifies SPINT2 as a Novel Tumor Suppressor Gene in Pediatric Medulloblastoma

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Abstract

Medulloblastoma (MB) is a malignant cerebellar tumor that occurs primarily in children. The hepatocyte growth factor (HGF)/MET pathway has an established role in both normal cerebellar development as well as the development and progression of human brain tumors, including MB. To identify novel tumor suppressor genes involved in MB pathogenesis, we performed an epigenome-wide screen in MB cell lines, using 5-aza-2′-deoxycytidine to identify genes aberrantly silenced by promoter hypermethylation. Using this technique, we identified an inhibitor of HGF/MET signaling, serine protease inhibitor kunitz-type 2 (SPINT2/HAI-2), as a putative tumor suppressor silenced by promoter methylation in MB. In addition, based on single nucleotide polymorphism array analysis in primary MB samples, we identified hemizygous deletions targeting the SPINT2 locus in addition to gains on chromosome 7 encompassing the HGF and MET loci. SPINT2 gene expression was down-regulated and growth, cell motility in vitro, and increased overall survival times in vivo in a xenograft model (P < 0.0001). Taken together, these data support the role of SPINT2 as a putative tumor suppressor gene in MB, and further implicate dysregulation of the HGF/MET signaling pathway in the pathogenesis of MB. [Cancer Res 2008;68(23):9945–53]

Introduction

Central nervous system tumors are the most common form of pediatric solid malignancy, with medulloblastoma (MB) accounting for 25% of cases (1, 2). This cerebellar tumor affects young children, with a peak incidence at the age of 7 years and 5-year survival of ~60% (3). Treatment includes a combination of surgery, radiation, and chemotherapy—therapies with significant neurocognitive, endocrinologic, hematologic, and oncologic side effects (4–7).

Although MB typically arise sporadically, some cases occur in family cancer syndromes such as nevoid basal cell carcinoma syndrome or Turcot syndrome—with mutations in the Hedgehog transmembrane receptor Patched (PTCH) or the Wnt signaling member APC, respectively (8, 9). PTCH mutations are found in ~10% of sporadic MB cases (10). Other Hedgehog pathway members (HESF1, SMO, and PTCH2) are implicated in fewer cases (11–13). APC mutations occur infrequently in sporadic MB, although activating mutations of β-catenin are seen in up to 5% of cases (14). MYC family amplifications occur in <10% of cases (15). Known genetic abnormalities explain tumorigenesis for only a subset of sporadic MB cases. The identification of novel genes and pathways involved in MB pathogenesis may help to explain the etiology of tumors in the remainder of cases, as well as to provide novel targets for therapy.

The role of the HGF/MET signal transduction pathway in the formation and progression of brain tumors including malignant gliomas is well-established (16). It also plays a critical role in cerebellar development (17). Furthermore, the HGF/MET pathway has recently been implicated in MB pathogenesis (15, 18, 19).

To identify novel genes involved in MB pathogenesis that have escaped detection by conventional genetic analysis, we used a genome-wide epigenetic screen to discover putative tumor suppressor genes (TSG) silenced by promoter-region methylation. This approach involved up-regulating epigenetically silenced genes using 5-aza-2′-deoxycytidine (5-aza-dC) treatment, followed by expression microarray analysis (20–22). As aberrant promoter methylation may function alone or in concert with genetic events such as loss of heterozygosity (LOH) to induce TSG silencing, we cross-referenced our microarray data with data from a high resolution Affymetrix SNP-array platform to identify genes targeted by methylation and/or LOH events (23). Using this approach, we identified methylation-mediated gene silencing and hemizygous deletion of SPINT2 in MB. SPINT2 normally functions to inhibit the HGF/MET signaling pathway. We hypothesized that up-regulated HGF/MET signaling resulting from loss of normal pathway inhibition due to SPINT2 silencing contributes to MB pathogenesis. Functional analysis in vitro and in vivo support the role of SPINT2 as a putative novel TSG in MB.

Materials and Methods

Cell lines, cell culture, and normal cerebellar samples. The ONS76 cell line was obtained from the Institute for Fermentation. The UW228 and UW426 cell lines were obtained from Dr. J. Silber (University of Washington, Seattle, WA). The D425 and D458 cell lines were obtained from Dr. D. Bigner (Duke University, Durham, NC). The MHH-MED-1 and MED8A cell lines were obtained from Dr. R. Gilbertson (St. Jude Children’s Research Hospital, Memphis, TN). The RES262 cell line was obtained from Dr. M.S. Bobola (University of Washington, Seattle, WA). All other cell lines were purchased from the American Type Culture Collection. Daoy, D283, ONS76, UW228, and UW426 cell lines were cultured in DMEM with 10% fetal bovine serum (FBS). The D425 and D458 cell lines were cultured in IMEM with 20% FBS.
5 cc of 1 mol/L HEPES, and 15 CC of 7.5% sodium bicarbonate. MHH-MED-1 was cultured in DMEM with 10% FBS, and MDE8A in DMEM with 20% FBS. The RES262 MB cell line was cultured in DMEM/F12 medium supplemented with 2% FBS. RKO (colorectal cancer) and PFSK (supratentorial PNET) cell lines were cultured in DMEM with 10% FBS. The G401 cell line (rhomboid tumor) was cultured in DMEM/F12 with 10% FBS. Lymphoblasts were cultured in RPMI 1640 with 15% FBS. Medium and reagents for cell culture were purchased from Wisent, Inc. Normal human fetal and adult cerebellar genomic DNA and RNA samples were purchased from Biochain.

5-aza-dC treatment protocol, reverse transcription-PCR/quantitative real-time PCR, and affymetrix HG U133 plus 2.0 expression arrays. Cell lines were plated at 20% to 30% confluence. Twenty-four hours later, fetal and adult cerebellar genomic DNA and RNA samples were purchased (Qiagen, Inc.). Reverse transcription-PCR (RT-PCR) was performed using Platinum Taq DNA Polymerase (Invitrogen) in an MJ Research PTC-200 thermal cycler (Bio-Rad). Quantitative real-time RT-PCR (qRT-PCR) was performed using Platinum SYBR Green Supermix (Invitrogen), in an MJ Research PTC-200 thermal cycler fitted with a Chromol detector (Bio-Rad). Primer sequences for RT-PCR and qRT-PCR were as follows: SPINT2-F, 5′-aacagcattatcagcagc-3′; SPINT2-R, 5′-agagtagcagagagc-3′; MET-F, 5′-cactgcttaagtagtactcctg-3′; MET-R, 5′-ggaggtagtatgattaagcgc-3′; HGF-F, 5′-ctatgcagagggacaaagga-3′; and HGF-R, 5′-cactgcttaagtagtactcctg-3′. Expression levels for the ACTB gene were used for normalization of relative gene expression levels.

Cell lines were subjected to expression profiling after 5-aza-dC or vehicle treatment using the Affymetrix HG U133 plus 2.0 platform (Affymetrix). As described above, total RNA was extracted using TRIzol, and RNA was quality checked by Bioanalyzer. Array hybridization was performed by our local genomics facility (The Center for Applied Genomics, TCAG, The Hospital for Sick Children, Toronto, Canada). Data analysis was done using the Affymetrix GeneChip Operating Software (GCOS) software for normalization and pairwise comparison between individual 5-aza-dC-treated and untreated cell lines, and filtered to identify genes of interest for further study using the Inforse sorteD K de program.

DNA isolation from tumor samples and single nucleotide polymorphism GeneChip mapping array analysis. Fresh-frozen MB specimens were stored at −80°C before extraction of nucleic acid. Samples were pulverized under liquid nitrogen. For genomic DNA isolation, −25 to 50 mg of crushed tissue was subjected to SDS/Proteinase K digestion (Roche) for 3 h at 50°C. Homogenates were extracted thrice with saturated-saline-filtered (Invitrogen) before precipitation of DNA with 2 volumes of anhydrous ethanol and 10% (vol/vol) 10 mol/L ammonium acetate. Precipitated DNA was washed thrice with 70% ethanol and resuspended in reduced EDTA-TE [10 mmol/L Tris, 0.1 mmol/L EDTA (pH 8.0)]. Samples were quantitated by NanoDrop ND-1000, and DNA integrity was assessed by agarose gel electrophoresis before submission for SNP array analysis.

Single nucleotide polymorphism (SNP) array genotyping was performed using the Affymetrix 50 K Hind 240 and 50 K Xba 240, or the 250 K Nsp and 250 K Sty GeneChip Mapping arrays as directed by the manufacturer (Affymetrix). Briefly, 250 ng of DNA was digested with HindIII, XbaI, NspI, or StyI (New England Biolabs), adapter-ligated, and PCR amplified using a single primer with AmpliTaq Gold (Applied Biosystems). Amplified PCR products were pooled, concentrated, and fragmented with DNAase I. Products were then labeled and hybridized overnight to the respective arrays. Arrays were washed using an Affymetrix GeneChip Fluidics Station 450 and scanned using the GeneChip Scanner 3000 7G. CEL files were generated using the Affymetrix GCOS 3.0.

Bisulfite genomic sequencing. The technique of bisulfite genomic sequencing has been previously described (24). Briefly, genomic DNA was subjected to bisulfite conversion using the MethylEasy DNA Bisulfite Modification kit (Human Genetic Signatures). After bisulfite conversion, the SPINT2 promoter region was amplified using bisulfite-PCR methods. Primer sequences for SPINT2 bisulfite-PCR were as follows: Fwd 5′-TTTATTAGGTGCGT-3′, Rev 5′-AAACCTCTCAACCCTCGC-3′. PCR products were gel-purified, TA were cloned into pCR2.1 vector (Topo TA Cloning kit; Invitrogen), transformed into TOP10 chemically competent cells, and plated under antibiotic selection. Plasmid DNA from isolated colonies was extracted by miniprep (Qiagen) and sequenced to determine SPINT2 methylation status. Multiple clones were sequenced, providing a consensus of the promoter-region methylation status. Bisulfite sequencing data were analyzed using BiQ Analyzer software (25).

Methylation-specific PCR. Methylation-specific PCR (MSP) was performed as previously described (26). Published MSP primer pairs designed to specifically amplify either unmethylated or methylated SPINT2 promoter-region DNA after bisulfite conversion were used (27). Genomic DNA from a panel of 70 primary MB samples was isolated using a standard SDS-proteinase K technique, and subjected to bisulfite conversion. MSP was performed on this panel of tumor samples, in addition to the MB cell line D283 (positive control for SPINT2-MSP primers) and three normal human cerebellar samples (positive controls for SPINT2-USP primers). Template-negative samples and samples containing genomic DNA not subjected to bisulfite conversion were used as negative controls for both SPINT2-MSP and SPINT2-USP primer sets.

SPINT2 expression construct and stable cell line generation. A plasmid containing full-length human SPINT2 cDNA was obtained from the Mammalian Gene Collection (SPINT2-IRAU5-A9 in pOTB7). After the PCR-mediated addition of a COOH-terminal FLAG tag sequence, this cDNA was subcloned into the pcDNA3.1+ expression vector (Invitrogen), and sequence verified. Empty pcDNA3.1+ and an enhanced green fluorescent protein (EGFP)-pcDNA3.1+ expression construct were used as negative controls. To produce stable transfectants, expression vectors were linearized, transfected into the D283 and ON576 MB cell lines using FuGene6 (Roche), and kept under G418 antibiotic selection. Transfected cells were subsequently plated into 96-well plates at 1 cell per well, and expanded to obtain stably transfected clones. Two stable D283 clones reexpressing SPINT2 (D283-SPINT2-FLAG-High and D283-SPINT2-FLAG-Low) and one ON576 clone (ON576-SPINT2-FLAG) were selected for further study, with SPINT2 expression levels verified at both the transcript and protein levels by qRT-PCR and Western blotting (Supplementary Figs. S1 and S2).

Western blotting. Monoclonal anti-FLAG M2 antibody (Sigma-Aldrich F3165) was used for SDS-PAGE. An immunoblot for the transferrin receptor was performed as a loading control (Invitrogen/Zymed 13-6800).

Cell proliferation assay. The Promega CellTiter 96 AQueous One Solution Cell Proliferation Assay was used, as per the manufacturer’s instructions (Promega). Cells were seeded into 96-well plates (1,000 cells per well) in triplicate. Absorbance at 490 nm was measured 2 h after the addition of 20 μL of MTS reagent per well, every 24 h over a 96-h period.

Colonies formation in soft agar. A base layer of 1.5% agar/2× DMEM/FBS was prepared in 35-mm plates. Upper layer agar was made using 1.5% agar, 2× DMEM, FBS, and sterile water, and kept in liquid phase in a 42°C water bath. Cells were resuspended in 0.75% agar/DMEM/FBS and overlaid on the base layer with 3,000 cells per 35-mm plate and subsequently kept in a humidified chamber at 37°C for 2 wk. Plates were stained with crystal violet, digitally imaged (Zeiss Axiover 200 M inverted light microscope), and colony counts performed in an automated fashion using Volocity software particle recognition analysis. Each cell line was plated in triplicate, and the data presented are representative of three separate experiments.

Artificial wound-healing assay. An artificial wound-healing assay was performed to assess cell migratory ability. Cell lines were grown to 80% confluence in medium containing 10% FBS. A uniform scratch defect was performed to assess cell migratory ability. Cell lines were grown to

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Crystal violet focus formation assay. Equal numbers (n = 10,000) of ONS76-Empty Vector and ONS76-SPINT2-FLAG cells were plated separately in 10-cm tissue culture plates and grown for a period of 5 d. Plates were then washed twice with ice-cold 1 × PBS, fixed for 10 min with ice-cold methanol, and stained with 0.5% crystal violet (made in 25% methanol) for 10 min at room temperature. Plates were then rinsed in ddH2O, allowed to dry, and imaged.

Orthotopic intracranial xenografts. D283 cells stably transfected with empty vector or the D283-SPINT2-FLAG-High expression construct were used for xenograft experiments. Cells were released from the culture plates using Accutase (Sigma-Aldrich), washed twice in 1 × PBS, resuspended in a small volume of serum-free 1 × DMEM, at a final concentration of 50,000 cells/ml, and kept on ice until the time of injection. Mice were anesthetized using i.p. ketamine/xylazine. Intracranial injection of 100,000 cells (2 × 10^6 cells/volume of serum-free 1 × PBS, fixed for 10 min with ice-cold methanol, and stained with 0.5% crystal violet (made in 25% methanol)) was performed in the midline cerebellum of male Nu/Foxn1/Nu mice (ages 5–6 wk; Charles River), using a murine stereotactic head frame and Hamilton syringe. Tissues were harvested twice with ice-cold 1 × PBS, fixed for 10 min with ice-cold methanol, and stained with 0.5% crystal violet (made in 25% methanol) for 10 min at room temperature. Plates were then rinsed in ddH2O, allowed to dry, and imaged.

Results

5-aza-dC microarray and SNP array analysis. The 5-aza-dC expression microarray screen identified increased transcript levels for genes known to be methylated in MB, including CASP8, CASK2, DNAS1, GSTPI, HIC1, RASSF1, S100A6, S100A10, SNGE1, TIMP3, and ZIC2 (28–31). To identify novel gene candidates from this microarray screen, we focused on genes demonstrating >2-fold up-regulation in expression after 5-aza-dC treatment, in 2 or more MB cell lines, with predicted promoter-region CpG islands, and which were also identified as targets for deletion or LOH based on SNP array analysis. In addition, we focused on genes known to be TSGs in other tumor types or involved in signaling pathways implicated in cerebellar development or MB pathogenesis. One gene candidate was an inhibitor of HGF/MET signaling, SPINT2. It showed between 5.28- and 21.11-fold (log2 ratios, 2.4–5.4) increase in transcript levels in 6 of 9 MB cell lines (Daoy, D283, ONS76, UW228, UW426, and D425) after 5-aza-dC treatment (Fig. 1A). This increased expression after treatment was confirmed by qRT-PCR (Fig. 1B). These findings suggested that SPINT2 was silenced by promoter-region methylation in these MB cell lines. In addition to being a target of aberrant promoter methylation, 1 MB cell line (MED8A) and 6 primary MB samples (MB 7, 9, 22, 23, 29, and 76) showed hemizygous loss of SPINT2 (region between black dashed lines below chromosome). D, qRT-PCR data for SPINT2 in pooled normal fetal cerebellum (red) and primary MB samples (blue). Forty-one of 56 tumors showed SPINT2 expression levels of <50% compared with normal fetal cerebellum.
based on SNP array analysis. Large-scale gains (involving either all of chromosome 7 or the 7q arm) encompassing numerous genes including the HGF and MET loci (7q21.1 and 7q31, respectively) were seen in 62/201 (30.8%) primary tumors examined on the SNP array platforms.®

Quantitative RT-PCR for SPINT2, MET, and HGF. For a subset of primary tumors, mRNA was available for qRT-PCR analysis of SPINT2 gene expression. In total, 41 of 56 (73.2%) primary MBs showed >50% reduction in SPINT2 expression compared with a sample of 5 pooled normal fetal cerebella (Fig. 1D). Of 6 primary tumors with hemizygous deletion targeting the SPINT2 locus, cDNA was available to correlate SPINT2 expression status in 3 samples (MB 7, 9, and 29). All 3 samples showed reduced SPINT2 expression compared with normal fetal cerebellum, with 2 of 3 demonstrating expression levels below 50% that of normal cerebellum (MB 7 and 9). Sufficient material was available for 44 primary MBs to assess the expression levels of additional HGF/MET signaling members by qRT-PCR. In this subset of MBs, MET receptor expression was up-regulated by 2-fold in 20 of 44 (45.5%) of samples demonstrating expression levels below 50% that of normal cerebellum (MB 7 and 9). Sufficient material was available for 44 primary MB samples assessed, 24 of 70 (34.3%) yielded MSP results as assessed by an MTS assay and a Crystal Violet Focus Formation Assay (Supplementary Fig. S5; Fig. 4B). As expected, the D283 cell line yielded an MSP product only with primers specific for methylated template. In contrast, three normal cerebellar samples produced MSP product only with primers specific for unmethylated template. Among the primary MB specimens assessed, 24 of 70 (34.3%) yielded MSP product using primers specific for methylated template, qRT-PCR expression data for SPINT2 was available for 11 of the primary MB specimens that were positive for methylation by MSP. In 10 of 11 (90.9%) tumors, SPINT2 levels were reduced by over 50%, with 8 of 11 expressing SPINT2 at levels <10% that of normal fetal cerebellum (Fig. 3B).

Effect of SPINT2 on MB cell proliferation, anchorage-independent growth, and motility. To determine the effect of stable SPINT2 reexpression on cell proliferation, an MTS assay was performed using D283 and ONS76 cells transfected with empty vector, EGFP, or SPINT2 expression constructs. As seen in Fig. 4A, stable reexpression of SPINT2 in D283 cells reduced proliferation compared with empty vector and EGFP-expressing controls. In addition, the level of SPINT2 reexpression correlated inversely with proliferation, with the D283-SPINT2-FLAG-Low clone proliferating somewhat more rapidly than the D283-SPINT2-FLAG-High clone. Similarly, stable reexpression of SPINT2 in the ONS76 cell line reduced proliferation compared with empty vector or EGFP-expressing controls as assessed by an MTS assay and a Crystal Violet Focus Formation Assay (Supplementary Fig. S5; Fig. 4A).

**Figure 2.** Bisulfite sequencing data for SPINT2. The promoter-region, first exon and transcription start site (arrow). Vertical black tick marks, CG dinucleotides within the promoter-region CpG island. Horizontal black bar, the region sequenced, which is expanded below. Each circle represents a single CG dinucleotide site; open circles, unmethylated; filled circles, methylated. Each row represents replicate data for the respective sample. The D283 MB cell line shows extensive methylation compared with normal adult and fetal cerebellum (Cb).

**Figure 3A.** Bisulfite sequencing data for SPINT2 in D283 and three normal human cerebellar samples (Fig. 3A). As expected, the D283 cell line yielded an MSP product only with primers specific for methylated template. In contrast, three normal cerebellar samples produced MSP product only with primers specific for unmethylated template. Among the primary MB specimens assessed, 24 of 70 (34.3%) yielded MSP product using primers specific for methylated template, qRT-PCR expression data for SPINT2 was available for 11 of the primary MB specimens that were positive for methylation by MSP. In 10 of 11 (90.9%) tumors, SPINT2 levels were reduced by over 50%, with 8 of 11 expressing SPINT2 at levels <10% that of normal fetal cerebellum (Fig. 3B).
To assess the effect of stable SPINT2 reexpression on the ability of the MB cells to grow in anchorage-independent conditions, we tested colony formation in soft agar using the stably transfected D283 cell lines. Empty vector controls produced a mean number of 669.3 ± 50.1 colonies. In contrast, the D283-SPINT2-FLAG-High and D283-SPINT2-FLAG-Low clones produced mean colony counts of 89.7 ± 18.5 and 274.0 ± 30.8, respectively. There were fewer colonies produced by the high-expressing SPINT2 clone compared with the low-expressing SPINT2 clone (Fig. 4B–C).

An artificial wound-healing assay was performed to assess the effect of SPINT2 reexpression on MB cell motility (Fig. 5). Twenty-four hours after the creation of an initial defect in the cell monolayer, the empty vector control displayed over 50% closure of the defect (Fig. 5A–B). In contrast, the D283-SPINT2-FLAG-High expressing clone showed minimal closure of the initial defect (Fig. 5C–D).

Orthotopic intracranial xenografting of stably transfected D283 cell lines. Mice harboring intracerebellar xenografts derived from D283 MB cells stably transfected with empty vector exhibited a mean overall survival (OS) after initial tumor engrafting of 29.3 d (Fig. 6A). Mice with xenografts derived from the D283-SPINT2-FLAG-High clone showed a mean OS of 64.0 d. The difference in mean OS was statistically significant ($P < 0.0001$). Microscopically, empty vector control xenografts resembled the human anaplastic MB subtype (Fig. 6B). Interestingly, SPINT2 reexpression resulted in regions of intratumoral necrosis not seen in empty vector control–derived tumors (Fig. 6B). In addition, SPINT2-reexpressing tumors exhibited increased apoptotic activity compared with controls, as shown by increased immunopositivity for cleaved Caspase-3 (Fig. 6B). Finally, Ki-67 labeling was reduced from 29.3% ± 3.01% in control tumors to 20.51% ± 1.58% ($P = 0.0012$) in the SPINT2 transfecant tumors (Fig. 6B).

**Discussion**

To uncover novel TSGs involved in MB pathogenesis, we used a genome-wide approach using 5-aza-dC treatment to interrogate the MB epigenome in 9 MB cell lines. We identified for the first time the inhibitor of HGF/MET signaling, SPINT2, as a novel candidate TSG in MB. The first genome-wide approach to the MB...
epigenome performed by Fruhwald and colleagues (32) identified aberrant methylation affecting ~6% and 1% of genes in MB cell lines and primary tumors respectively. Three additional genome-wide studies have been published (29, 30, 33). Waha and colleagues (30) performed a differential methylation hybridization technique, from which they identified secretory granule neuroendocrine protein 1 (SGNE1/7B2) as a putative TSG that is methylated in MB. Using a technique called array-based profiling of reference-independent methylation status, Pfister (29) identified zinc-finger protein of the cerebellum family member 2 (ZIC2) as being methylated in a subset of 20 MB specimens. A genome-wide approach examining 3 MB cell lines recently published by Anderton (33) identified tumor-specific methylation of the COL1A2, S100A10, S100A6, HTATIP2, CDH1, and LXN genes. Furthermore, they identified a clinicopathologic correlation for COL1A2 methylation, which, although common in nondesmoplastic/nodular MBs of all ages and desmoplastic/nodular MBs of childhood, is a rare occurrence among desmoplastic/nodular MBs of infancy (33). Our epigenome-wide study examining 9 MB cell lines and 201 primary tumors adds to the list of epigenetically silenced genes, identifying SPINT2 as a putative TSG targeted frequently for promoter-region methylation-mediated silencing, and further implicates the HGF/MET signaling pathway in this disease.

HGF/MET signaling plays a role in cerebellar development, contributing to cerebellar granule cell precursor (GCP) proliferation and survival (17, 34–36). HGF and MET are expressed in the developing and adult cerebellum (34, 35). Murine cerebellar GCPs proliferate in vitro in response to exogenous Hgf (17). In vitro stimulation of Hgf/Met signaling also prevents apoptosis of GCPs induced by serum starvation (36). In contrast, the reduced Hgf/Met signaling seen in a murine hypomorphic Met
mutant produces a small cerebellum with foliation defects in the central and posterior cerebellar vermis (17). Furthermore, the reduced Hgf/Met signaling in this model results in GCP proliferation that is 25% lower than wild-type GCPs (17).

Aberrant HGF/MET signaling has been implicated in brain tumor pathogenesis through its influence on cell cycle progression, tumor cell migration and invasion, angiogenesis, and protection from apoptotic stimuli (16). This pathway, however, has only recently been implicated in MB pathogenesis (15, 18, 19). Using CGH and array-CGH methods, Tong and colleagues (15) identified single copy gains encompassing the MET locus on chromosome 7q in 38.5% of samples in a cohort of 13 human MBs. By lower resolution CGH alone, they identified gain of the entire 7q chromosome arm in 4 samples and gain of the 7q31-35 region in 1 tumor (15). We similarly identified large-scale gains affecting either all of chromosome 7 or the 7q arm based on SNP array analysis in 62 of 201 (30.8%) primary MBs. We did not however observe any high-level amplifications targeting the MET or HGF loci. Interestingly, in our study, increased HGF or MET gene expression did not correlate with copy number gain, suggesting that HGF and MET expression are not copy number driven, and that these genes are not driving clonal selection in tumors with gains on chromosome 7.

Li and colleagues (19) identified MET receptor and HGF expression in MB cell lines and primary tumors. They showed that up-regulation of HGF/MET signaling increased cell proliferation, anchorage-independent growth, cell-cycle progression, and resistance to chemotherpay-induced apoptosis in MB cell lines (19). In addition, after HGF treatment, the Daoy MB cell line exhibited a more aggressive, anaplastic phenotype (19). Furthermore, high MET expression in primary tumors correlated with reduced OS (19). More recently, Li and colleagues (18) identified a link between HGF/MET signaling and MYCC in MB. Despite these initial studies, the extent to which aberrant HGF/MET signaling contributes to MB, as well as the diverse mechanisms by which this pathway may be dysregulated, remain to be determined.

Based on the results of our screen, SPINT2 was chosen for further study for multiple reasons. SPINT2 was up-regulated after 5-aza-dC in 6 of 9 MB cell lines and was a recurrent target of hemizygous deletion based on SNP array analysis. In addition, by qRT-PCR analysis, SPINT2 expression was reduced by >50% in 41 of 56 (73.2%) primary MBs compared with normal fetal cerebellum. Furthermore, SPINT2 functions as a TSG and is silenced by promoter-region methylation in hepatocellular carcinoma, renal cell carcinoma, and gliomas (27, 37, 38). In addition, low SPINT2 expression has been associated with more advanced stage malignancy and poor prognosis in breast cancer (39). The HGF/MET pathway has an established role in normal cerebellar development (17). Finally, although the HGF/MET oncogenic signaling pathway has recently been implicated in MB pathogenesis (18, 19), the role of SPINT2 in MB has not yet been examined.

The SPINT2 protein is one of two known inhibitors of HGF activator (HGFA; refs. 40, 41). HGFA is a protease that converts the inactive, single-chain precursor form of HGF to its active heterodimeric form, which can then bind to the MET receptor (16, 42). By inhibiting the activation of HGF by HGFA, SPINT2 limits signaling via the HGF/MET pathway. Epigenetic silencing of SPINT2 may allow HGF/MET signaling to continue without inhibition, contributing to the malignant phenotype.

Similar to SPINT2, an additional HGFA inhibitor (SPINT1) also showed >2-fold increase in expression by 5-aza-dC microarray analysis (3 of 9 cell lines; Supplementary Fig. S6). Bisulfite sequencing confirmed promoter methylation in the UW228 MB cell line (Supplementary Fig. S6). Despite this, MSP on primary MBs failed to identify SPINT1 promoter methylation, raising the question of whether SPINT1 methylation in MB cell lines was biologically significant or an artifact of cell culture (data not shown). Furthermore, qRT-PCR analysis of SPINT1 and SPINT2 expression...
in normal fetal cerebellum showed SPINT2 expression to be \( \sim 4.5 \)-fold higher than SPINT1 (Supplementary Fig. S7). Therefore, one might infer that SPINT2 serves as the primary biologically relevant inhibitor of HGF/MET signaling in the cerebellum.

After identifying increased SPINT2 expression with 5-aza-dC treatment in 6 of 9 MB cell lines, SPINT2 promoter methylation was confirmed by bisulfite sequencing in the D283 MB cell line, in comparison with normal human fetal and adult cerebellar samples that are unmethylated. MSP showed SPINT2 methylation in 34.3% (24 of 70) of primary MBs.

In vitro analysis supported a role of SPINT2 as a TSG in MB, as stable reexpression in the D283 MB cell line reduced proliferative capacity, anchorage-independent growth, and cell motility in vitro. Stable reexpression of SPINT2 in the ONS76 MB cell line similarly reduced its proliferative capacity in vitro. Furthermore, mice harboring intracerebellar xenografts derived from SPINT2-reexpressing D283 cells showed survival times more than double that of mice engrafted with empty vector–transfected cells. Immunohistochemical analysis of xenograft samples provided some explanation for the prolonged survival of mice harboring SPINT2-reexpressing xenografts. Intratumoral necrosis was widespread in xenograft specimens from SPINT2 transfectants. Furthermore, SPINT2-reexpressing xenografts showed increased apoptotic activity as evidenced by increased immunopositivity for cleaved Caspase-3 compared with controls. Given that HGF treatment confers resistance to chemotherapy-induced apoptosis in Daoy cells and resistance to apoptosis in serum-starved GCPs, one explanation for this finding may be sensitization to apoptotic stimuli in the SPINT2 transfectants (19, 36). Finally, SPINT2 xenografts showed reduced Ki-67 staining compared with empty-vector controls—a marker of reduced proliferation in vivo.

We identify SPINT2 as a putative TSG involved in MB pathogenesis, and show promoter-region methylation-mediated epigenetic silencing of this gene in MB. In addition, this work contributes to the body of evidence implicating the HGF/MET oncogenic signaling pathway in MB pathogenesis. We have uncovered another mechanism for uncontrolled HGF/MET signaling in this tumor. In fact, reduced SPINT2 expression seems to be a more frequent event in primary MB than either HGF or MET overexpression. Our study shows that dysregulation of HGF/MET signaling due to loss of normal pathway inhibition is a frequent event in MB, providing some rationale for targeting this signaling axis in MB with current and future therapeutic interventions (43–47).

**Disclosure of Potential Conflicts of Interest**

No potential conflicts of interest were disclosed.
Acknowledgments

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