The Notch Target Hes1 Directly Modulates Gli1 Expression and Hedgehog Signaling: A Potential Mechanism of Therapeutic Resistance

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Abstract

Purpose: Multiple developmental pathways including Notch, Hedgehog, and Wnt are active in malignant brain tumors such as medulloblastoma and glioblastoma (GBM). This raises the possibility that tumors might compensate for therapy directed against one pathway by upregulating a different one. We investigated whether brain tumors show resistance to therapies against Notch, and whether targeting multiple pathways simultaneously would kill brain tumor cells more effectively than monotherapy.

Experimental Design: We used GBM neurosphere lines to investigate the effects of a gamma-secretase inhibitor (MRK-003) on tumor growth, and chromatin immunoprecipitation to study the regulation of other genes by Notch targets. We also evaluated the effect of combined therapy with a Hedgehog inhibitor (cyclopamine) in GBM and medulloblastoma lines, and in primary human GBM cultures.

Results: GBM cells are at least partially resistant to long-term MRK-003 treatment, despite ongoing Notch pathway suppression, and show concomitant upregulation of Wnt and Hedgehog activity. The Notch target Hes1, a repressive transcription factor, bound the Gli1 first intron, and may inhibit its expression. Similar results were observed in a melanoma-derived cell line. Targeting Notch and Hedgehog simultaneously induced apoptosis, decreased cell growth, and inhibited colony-forming ability more dramatically than monotherapy. Low-passage neurospheres isolated from freshly resected human GBMs were also highly susceptible to coinhibition of the two pathways, indicating that targeting multiple developmental pathways can be more effective than monotherapy at eliminating GBM-derived cells.

Conclusions: Notch may directly suppress Hedgehog via Hes1 mediated inhibition of Gli1 transcription, and targeting both pathways simultaneously may be more effective at eliminating GBM-derived cells. Clin Cancer Res; 16(24); 6060–70. ©2010 AACR.

Glioblastoma (GBM) is the most common malignant primary central nervous system tumor in adults and is characterized by resistance to chemo- and radiotherapy (1). Prognosis remains very poor, with most patients surviving less than 2 years (2) despite recent advances in surgery and chemotherapy. It has become clear that GBMs are a diverse group of tumors, with different subtypes activating distinct sets of oncogenes and signaling pathways (3). Because of this, no single therapy is likely to be effective against all GBMs, and a number of pharmacologic agents with activity against specific targets such as epidermal growth factor receptor (EGFR), Akt, Hedgehog, mammalian target of rapamycin (mTOR), phosphoinositide 3-kinase, platelet-derived growth factor receptor (PDGFR), Raf, and transforming growth factor β (TGF-β), are being developed (4). However, even the use of targeted therapies can be limited by the emergence of resistant tumor cells, and resistance to EGFR inhibitors (5) and Hedgehog inhibitors (6) has already been documented.

An important developmental pathway required in at least a subset of GBMs is Notch. Aberrant Notch signaling was implicated in the initiation of T-cell lymphoblastic leukemia in the early 1990s (7), and has since been demonstrated in many different hematopoietic and epithelial tumors (8–10). Upregulation of Notch pathway components has been demonstrated in GBM (11–13) and the malignant embryonal tumor medulloblastoma (14, 15), and Notch pathway inhibition has emerged as a potential therapy for malignant brain tumors. The 4 Notch receptors (Notch 1–4) bind ligands (Jagged and Delta) expressed on adjacent cells, permitting cleavage of Notch via ADAM...
Translational Relevance

The emergence of therapeutic resistance is a significant concern when targeting many signaling pathways and tumor types. We found that in vitro Notch pathway blockade in glioblastoma (GBM) cells using a gamma-secretase inhibitor (GSI) led to increased activity in two other pathways important for neural development—Wnt and Hedgehog. The Notch target Hes1, a transcriptional repressor, can directly bind the first Gli1 intron, suggesting a mechanism by which Notch can inhibit Hedgehog activity. Inhibition of both Notch and Hedgehog in vitro dramatically decreased the growth of GBM cell lines and low-passage neurospheres derived from primary human tumors. These findings demonstrate that Notch-targeted therapeutics can lead to alterations in other developmental signaling cascades that promote tumor survival, and suggest that combined treatment with Hedgehog pathway inhibitors may be able to increase the efficacy of GSIs in some cancer patients.

Materials and Methods

Cell culture

DAOY, PFSK, U87, 22RV1, H157, KMS12, L428, Mel10, Reh, TOV-112D, and U937 were maintained in the recommended media with 10% fetal bovine serum (FBS) unless otherwise specified. HSR-GBM1 and HSR-GBM2 were maintained as neurosphere cultures in serum-free neurosphere media (25). Cell line identity was verified using SNP analysis. For all assays, cells were counted using GIJAVA Viacount reagent according to the manufacturer’s instructions (Millipore) and equal numbers of viable cells were used for all experiments.

For drug treatment assays, adherent cell lines were plated in 6- or 96-well plates (BD Falcon; BD Biosciences) with media containing 10% FBS. The next day media was changed to low serum (0.5% FBS) and MRK-003 (26), cyclopamine (Infinity Pharmaceuticals), or vehicle (DMSO or ethanol, respectively) was added to each well as specified. Media was changed to every 2 to 3 days as necessary. For neurosphere lines, cells were treated immediately on plating with drugs as specified. Cell biomass was measured using CellTiter96 (Promega) at regular intervals after treatment. Anchorage-independent growth assays measuring colony-forming ability were performed as previously described (19). Colonies were stained and counted 21 to 28 days after plating.

Neurosphere nucleofection assays were performed using the AMAXA Mouse NSC Nucleofector Kit (Lonza) according to the manufacturer’s instructions, using program A-033 with 2 × 10⁵ cells per condition. Cells were nucleofected with Hes1 (27) or a control plasmid and allowed to recover for 24 hours in normal media before treatment with MRK-003 or vehicle. Transfection efficiency was quantified by cotransfection with CAG-green fluorescent protein (GFP) and microscopic quantification of the percentage of GFP-expressing cells. Cells were harvested after 48 hours for analysis.

Notch2 overexpression was achieved by incubating 4 × 10⁵ dissociated cells in a 12-well plate with neurosphere media and 8 μg/ml Polybrene (Sigma-Aldrich). Concentrated retrovirus designed to express Notch2 ICD with a truncated PEST domain (aa1703-2146) was added to the cells and the dish was rotated every 20 minutes for 2 hours, and 2 ml media was added to the cells. Cells were harvested 48 hours later. In some assays, infected cells were treated with MRK-003 24 hours after infection and were harvested 48 hours later.

shRNAs

Lentivirus was produced as previously described (28) from shRNA constructs against human Notch1 (TRCN0000003359 and TRCN0000003360) and Notch2 (TRCN0000004895 and TRCN0000004896). Neurosphere lines were infected as described earlier in the text. Cells were harvested 72 hours after infection, RNA was isolated, and target levels were assayed by quantitative PCR (qPCR).

Primary tumor-derived cell culture

JHH-GBM4, JHH-GBM10, JHH-GBM11, JHH-GBM14, JHH-GBM17, JHH-GBM18, JHH-GBM20, and JHH-GBM23 were generated from primary GBM surgical
specimens at Johns Hopkins Hospital (Baltimore, MD) as previously described (25, 28). JHH-GBM4, JHH-GBM17, JHH-GBM18, JHH-GBM20, and JHH-GBM23 were used as primary or very low-passage cultures (passage 0–2), whereas JHH-GBM10 and JHH-GBM11 were analyzed at passage 12–20. JHH-GBM14 was used both as a primary culture and at later passages (10–15) as indicated in the text.

Quantitative PCR

RNA was extracted using an RNeasy kit (Qiagen) with on-column DNase (Qiagen) according to the manufacturer's instructions. Reverse transcription was performed, and qPCR was done using SYBR Green PCR Master Mix (Applied Biosystems) on an i-Cycler IQ Real-Time detection system (Bio-Rad) according to the manufacturer's instructions. The following primers were obtained from published literature: hGli1, hPtc1B, and β-actin (29). hHes1, hHes5, hHey1, and hHey2 primers were designed using Primer3 (30) hHes1: forward (F) 5'-AGTGAGCACCTCCGGAAAC-3', reverse (R) 5'-TCACCTCTGAGATCGCT-3'; hHes5: forward (F) 5'-CCGGTGGGAGAAGATG-3', reverse (R) 5'-TAGTCCTGGTGACGGCTCT-3'. hAxin2 primers were a generous gift from Brian Simons (Johns Hopkins University, Department of Pathology): forward (F) 5'-CTGGTGCTGCTGCTGGAGAC-3', reverse (R) 5'-CGACTGTGACCCACACGAA-3'. The standard curve technique was used to determine expression levels and values were normalized to β-actin.

Protein analysis

Protein was extracted from cell pellets using RIPA buffer (R0278, Sigma-Aldrich) and 30 μg of this was run on each lane of a NuPage 4% to 12% Bis-Tris gel (Invitrogen) according to the manufacturer's instructions. The antibodies used were as follows: rabbit anti-Hes1 (1:1,000, AVIVA Systems Biology, 1:1,000, Toray Industries) rabbit monoclonal anti-Cleaved Notch1 (Cell Signaling), and mouse monoclonal anti-GAPDH (1:50,000, Research Diagnostics Inc.).

Chromatin immunoprecipitation

Chromatin Immunoprecipitation (ChIP) was performed using 2 different techniques and antibodies. For the Magna ChIP kit (Millipore), cells were grown in the appropriate media, harvested during log-phase growth, cross-linked using 1% formaldehyde, and processed according to the manufacturer’s instructions. The positive control was anti-Acetyl Histone H3, negative control was rabbit IgG, and Rabbit anti-Hes1 was used for pulldown (AVIVA Systems Biology). Nonquantitative PCR was performed using the primers in Supplementary Table S1. GAPDH and Hes1 primer sets were used as negative and positive controls, respectively, as Hes1 has previously been shown to bind its own promoter (31, 32). Some samples were run using qPCR as well.

The other technique used for ChIP has been previously described (33). Briefly, cells were grown in the appropriate media, harvested during log-phase growth, and cross-linked with formaldehyde. Hes1 antibody (5 μg; Millipore) or 5 μg control (rabbit IgG) was added to the sample and incubated for 12 hours at 4°C. After washing, cross-linking was reversed and qPCR was performed as described earlier in the text using the primers in Table 1. p63 and p27Kip primer sets were used as negative and positive controls, respectively (34). Linear amplification of each primer set used for qPCR was verified by a standard curve. qPCR calculations were done as previously described (35). Briefly, the average of the cycle threshold values (CT) was calculated for each input, sample, and control. The input CT was subtracted from the corresponding sample and control CTs. The following formula was then applied: power [1.9, negative ln (subtracted value)]. This value was used for further calculations. Each sample and control was normalized by dividing both numbers by the highest value so that each ChIP experiment was scaled from 0 to 1 and outliers were removed. For sample minus control values, a negative number was replaced with a zero.

Gene expression analysis

Gene expression was measured using Agilent’s 44K whole human genome microarrays at the Johns Hopkins Oncology Microarray Core, with labeling, hybridization, and detection performed according to the manufacturer’s instructions (Agilent Technologies). Differential gene expression, gene set enrichment analyses, and Analysis of Functional Annotation were performed as previously described (36, 37), using statistical packages from the R/Bioconductor project (38, 39). Gene annotation for the microarray used in this study was obtained from the corresponding R/Bioconductor metadata packages. Raw expression data along with MIAME (Minimal Information about a Microarray Experiment) required information are located in the GEO database (40).

Table 1. Top differentially expressed genes in microarray

<table>
<thead>
<tr>
<th>Pathway</th>
<th>Up</th>
<th>Down</th>
</tr>
</thead>
<tbody>
<tr>
<td>Notch pathway</td>
<td>CCND1, CREBBP, DLL1, DLL3, ELAVL4, IGF1R, KLF4, TFCR</td>
<td>EFEMP1, HES1, HES5, HEY1, HEY2, HOXA5, HOXA7, HOXA9, Wnt pathway</td>
</tr>
<tr>
<td>Wnt pathway</td>
<td>ACAP1, CREBBP, NRFA1, SFRP1, WNT5B, WNT7A</td>
<td>ERBB2, FRZB, FZD8, TCF7L1</td>
</tr>
<tr>
<td>Hedgehog pathway</td>
<td>MYCN, GLI2, NR4A1</td>
<td>GLI1, GLI3, SUFU</td>
</tr>
<tr>
<td>Other pathways</td>
<td>ABCA1, VEGFA</td>
<td>HOXA4, HOXC9, PDPN, PDGFRB, RB1, S100B, TGFBI</td>
</tr>
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NOTE: Genes annotated in "Top 100" gene list are given in bold.
Results

GBM neurosphere cultures survive long-term Notch inhibition

To confirm previous reports (24, 41) and examine Notch suppression in the newly derived GBM neurosphere lines JHH-GBM10 and JHH-GBM14, we treated dissociated neurospheres with MRK-003 and evaluated expression of the Notch pathway targets Hes1 and Hes5. We also looked at an adherent, serum-cultured GBM-derived line, U87. We observed that MRK-003 treatment significantly decreased expression of Hes1 in all lines, with inhibition ranging from 32% (JHH-GBM10) to 57% (JHH-GBM14; Fig. 1A). Significant reductions in the expression of Hes5 ranging from 87% (HSR-GBM1) to 95% (JHH-GBM14; Fig. 1A) were also noted in 3 GBM neurosphere lines. Interestingly, U87 and HSR-GBM2 did not express Hes5 at sufficient levels for quantitation, indicating some heterogeneity in Notch target levels between tumors. MRK-003 treatment also inhibited Hes1 expression by 40% in the medulloblastoma cell line DAOY (Supplementary Fig. S1A). In addition to down-regulation of Hes1 transcripts, Hes1 protein levels were suppressed by MRK-003 treatment in HSR-GBM1 (Fig. 1B) and DAOY (Supplementary Fig. S1B), with 70% to 80% inhibition following 2 μmol/L doses (P < 0.0001). Cleaved Notch1 levels also decreased dramatically with MRK-003 treatment, dropping to almost undetectable levels (Fig. 1B) as measured by 2 different antibodies. We confirmed dose-dependent inhibition of HSR-GBM1 and DAOY cell growth following application of MRK-003 in relatively short-term 6- to 9-day growth assays (Fig. 1C; Supplementary Fig. S1C). Interestingly, although neurosphere lines HSR-GBM1 and HSR-GBM2 showed a short-term response to Notch inhibition, they continued to grow even after 3 or more passages with continuous MRK-003 treatment (Fig. 1D; data not shown). These experiments were performed 3 or more times with similar results, indicating the capacity for long-term growth was a reproducible phenomenon. Notch signaling was still quite pronounced at the end of long-term MRK-003 treatment as demonstrated by very low Hes1 and Hes5 levels (Fig. 1D), suggesting that ongoing growth was not due to reactivation of the Notch pathway. Higher concentrations of MRK-003 (2–10 μmol/L) did result in complete cessation of cell growth over the course of 10 to 14 days, indicating that at sufficiently high drug levels cells do not easily develop resistance.

Upregulation of Hedgehog and Wnt signaling following Notch inhibition

Given the ability of a subset of malignant brain tumor cells to survive long-term MRK-003 treatment, we performed a microarray assay on 4 GBM-derived neurosphere lines with 2 different doses of MRK-003 to identify Notch targets and determine whether other pathways might be upregulated to compensate for the loss of Notch activity (HSR-GBM1, n = 3 each for 2 doses; HSR-GBM2, n = 3; JHH-GBM10, n = 3; and JHH-GBM14, n = 2). As expected, canonical Notch targets including Hes1, Hes5, and Hey1 were suppressed 2.7- to 28-fold following MRK-003 treatment. A list of the top differentially regulated genes seen in common across all lines is included in Supplementary Table S2. We performed a gene set enrichment analysis comparing our data against literature-cited, manually curated pathway lists with genes up- and downregulated by pathway activation and found that, as expected, Notch was significantly changed (P = 0.013). We found that 2 other developmental and proliferative pathways were significantly altered: Wnt (P = 0.00013) and Hedgehog (P = 0.0027; Table 1). Closer analysis of specific Hedgehog and Wnt targets indicated that there was an overall trend toward upregulation of canonical targets and pathway components in the presence of MRK-003.

Because Wnt and Hedgehog play an important role in stem cell maintenance and proliferation during normal brain development and can be dysregulated in tumors, we hypothesized that upregulation of these pathways might compensate for MRK-003 induced loss of Notch signaling. Using qPCR to validate our microarray data, we found that the Hedgehog targets Patched1B and Gli1 were both significantly upregulated by up to twofold in neurosphere lines following MRK-003 treatment (2–5 μmol/L; Fig. 2A). The Wnt signaling target Axin2 also showed significant upregulation (Fig. 2A). In contrast, medulloblastoma cell line DAOY showed a 40% decrease in Ptc1B mRNA and no significant change in Gli1 or Axin2 (Supplementary Fig. S1D).

As GSIs are able to cleave proteins other than Notch, we used shRNA to confirm the effect of Notch inhibition on Hedgehog signaling. Infection of HSR-GBM1 neurospheres with lentivirus encoding shRNA targeting either Notch1 or Notch2 resulted in significant reductions in receptor mRNA levels (data not shown). However, inhibiting either Notch1 or Notch2 alone resulted in an overall increase in Notch signaling as evidenced by upregulation of the Notch targets Hes1 and Hes5, suggesting compensation by other Notch receptors (data not shown). We therefore simultaneously used shRNAs against both Notch1 and Notch2, and saw a decrease in mRNA encoding the 2 Notch receptors of approximately 30% to 50%, along with a decrease in Notch targets by a similar amount (Fig. 2A). Inhibition of Notch signaling using shNotch1 and shNotch2 induced Gli1 expression by approximately twofold (Fig. 2A; P = 0.02).

Hes1 regulates Hedgehog signaling via direct binding to Gli1

As a previous work has suggested the potential for cross-talk between the Notch and Hedgehog signaling cascades (14), we focused on the upregulation of Hedgehog signaling in response to MRK-003. Increased levels of Notch pathway components are seen in Hedgehog-driven medulloblastoma models (15, 42) and it was initially suggested that these tumors may be dependent on Notch signaling for survival (15). More recent studies, however, indicate that Hedgehog-driven medulloblastomas can grow in the absence of canonical Notch activity (43, 44). Additionally, several groups have demonstrated that Hedgehog pathway
Fig. 1. Long-term pharmacologic Notch inhibition causes resistance. A, Hes1 and Hes5 levels measured by qPCR in response to 0.4 μmol/L MRK-003. B, Western blot and quantification showing Hes1 and cleaved Notch1 protein levels in response to MRK-003. C, MTS assay measuring cell growth after treatment with MRK-003. Data are representative of n = 5. D, MTS assay measuring cell growth after treatment with 0.4 μmol/L MRK-003 normalized to vehicle (top) and Hes1 mRNA levels after 3 weeks of MRK-003 treatment (bottom). Experiment was done in triplicate for n = 2, and data shown are representative. *, P < 0.02; **, P < 0.001; ***, P < 0.0001 using Student’s t test.
components Gli1 and Gli2 are able to positively regulate Hes1 independently of Notch (45, 46). However, when we treated several GBM neurosphere lines with the Hedgehog inhibitor cyclopamine we did not observe decreases in Hes1 or other Notch pathway targets, suggesting that Hedgehog does not play a significant role regulating Notch targets in malignant gliomas (Supplementary Fig. S2A).

We investigated the possibility of direct Gli1 regulation by Hes1, as potential Hes1 binding sites were previously identified in the first Gli1 intron using in silico analysis (47). Hes1 negatively regulates transcription of targets, thus loss of Hes1 following Notch blockade would be predicted to relieve repression of Gli1 expression and activate the Hedgehog cascade (48). To investigate whether this mechanism occurs in brain tumors, we used ChIP to examine whether Hes1 bound to the 5 N-boxes present in the Gli1 first intron (Fig. 2B). In HSR-GBM1, we found using qPCR that Hes1 interacted with all 5 N-boxes as strongly as with a site in the p27 promoter previously shown to be bound by Hes1 as a positive control (34).
We also used an independent set of PCR primers and an alternate ChIP protocol to confirm binding to the 5 N-boxes in a different neurosphere line, JHH-GBM10 (Supplementary Fig. S2B). In contrast to the GBM lines, Hes1 did not bind N-box 1, 4, or 5 in DAOY cells, and showed only moderate affinity for N-boxes 2 and 3, demonstrating the degree of binding to these N-boxes is context dependent (Supplementary Fig. S2C). This is consistent with our expression data demonstrating that Hedgehog pathway targets Gli1 and Ptc1B increase in response to Notch pathway inhibition in HSR-GBM1, but show no change in response to MRK-003 in DAOY. Finally, we evaluated 3 primary human GBM cultures (passage 0), and found that Hes1 bound the Gli1 first intron Nboxes in one of these (Fig. 2C), suggesting that our finding can be expanded to include some primary GBMs.

When we treated neurosphere lines with MRK-003, Hes1 binding to the Gli1 first intron was reduced, suggesting decreased ability to repress Gli1 expression (Fig. 2B; Supplementary Fig. S2C). Hes1 also bound less to its own promoter at a site of autoregulation previously documented (31, 32), indicating that Hes1 binding may be globally decreased. These findings suggest a direct negative regulatory relationship between Notch and Hedgehog signaling in some GBMs, whereby cells can upregulate Hedgehog signaling in response to pharmacologic Notch pathway inhibition.

To help confirm the presence of such a regulatory mechanism, we looked at the effect of Notch pathway activation on Gli1 and other Hedgehog pathway targets. We infected HSR-GBM1 with retrovirus expressing activated Notch2 (NICD2) or control retrovirus and evaluated Notch pathway activity. Consistent with our model, we found that Notch signaling targets were upregulated (Supplementary Fig. S2D) whereas the Hedgehog targets Gli1 and Ptc1B were significantly downregulated by 50% and 30%, respectively (P = 0.007 and 0.002; Fig. 2D). Experiments using retrovirus encoding activated Notch1 or Notch3 gave very similar results (data not shown). Next, we sought to determine whether the effect of Notch overexpression could be mediated through Hes1. After nucleofecting HSR-GBM1 with Hes1 or a control plasmid, we found a significant 30% reduction (P = 0.02) of Gli1 in response to Hes1 overexpression (Fig. 2D). The modest decrease we observed may be due to limited transfection efficiency (30%-50%), as it is difficult to introduce plasmids into neurosphere lines. We sought to further confirm that the upregulation in Gli1 with MRK-003 treatment was due to Notch pathway inhibition rather than other effects of the GSI by treating cells with MRK-003 1 day after infecting them with control or NICD2-expressing retrovirus. Although Gli1 levels increased in response to MRK-003 with the control virus, they remained at baseline when NICD2 was present (Fig. 2D), suggesting that Notch2 activity is able to rescue the inhibition effect of MRK-003. Taken together, our data suggest that increased expression of Hedgehog targets following Notch blockade is due at least in part to the loss of Hes1 binding at the Gli1 locus (Fig. 2D).

Hedgehog inhibition by Notch is seen in other cancers

Regulation of Gli1 expression by Hes1 has not been previously reported, and we wanted to determine whether other cancer types demonstrated a similar feedback mechanism. We screened 8 cell lines derived from prostate, lung, ovarian, skin, and hematopoetic cell cancers (22RV1, H157, KMS12, L428, Mel10, Reh, TOV-112D, U937) and found that Notch signaling was inhibited by MRK-003 in 2. TOV-112D, an ovarian-derived line, showed a 60% decrease in Hes1 expression on treatment with 2 μmol/L MRK-003 (P = 0.0002) and Mel10, a melanoma-derived line, showed a moderate decrease in Hes1 expression of 20% (P = 0.002). Interestingly, only Mel10 showed an upregulation in Gli1 and Ptc1B with MRK-003 treatment (P = 0.031 and 0.05, respectively; Fig. 3A). Axin2 remained unchanged in both cell lines following MRK-003 introduc-fourth
tion. ChIP showed that Hes1 consistently \((n = 3)\) bound the Gli1 N-boxes 2 and 3 in Mel10 (Fig. 3B), along with other N-boxes to a varying degree (data not shown).

**Coinhibition of Notch and Hedgehog decreases growth and clonogenicity**

We next evaluated whether inhibiting Hedgehog signaling in addition to Notch would augment antitumor effects in GBM neurosphere lines. A Hedgehog antagonist (cyclopamine) and MRK-003 were administered to HSR-GBM1 alone or together in order to detect potential interactions. We observed that cell growth over 11 days decreased slightly with MRK-003 or cyclopamine monotherapy as compared with vehicle, but decreased by approximately 90% in the presence of both drugs (Fig. 3C). Despite the absence of Hes1 binding to the Gli1 intron in DAOY, similar results were seen with cotreatment (Supplementary Fig. S3A).

Because the main effect seemed to be accumulation of dead cells, rather than elongation of processes suggesting differentiation, we performed an Annexin V assay to evaluate the percentage of apoptotic cells. Doing so, we found that the percentage of apoptotic cells doubled (13%) with cotreatment as compared with either drug alone (7%; Fig. 3D).

We next investigated whether cotreatment would decrease the number of clonogenic cells using an anchorage-independent growth assay. HSR-GBM1, HSR-GBM2, and U87 were dissociated to single cells, plated in soft agar, and treated continuously with vehicle, monotherapy, or cotreatment. Cotreatment was significantly more effective than monotherapy for the latter 2 lines, with up to 90% reduction in colony number as compared with cyclopamine alone, and up to 50% reduction as compared with MRK-003 alone (Fig. 4A–C). For HSR-GBM1, the difference between MRK-003 alone and MRK-003 plus cyclopamine was more modest and not statistically significant \((P = 0.077)\), although this trend was repeatable across independent experiments \((n = 3)\).

To assess our ability to specifically deplete clonogenic cells, we examined whether pretreatment would lead to a more pronounced reduction in colony formation on cotreatment. Neurospheres were grown with treatment for 7 days in suspension, and then washed and equal numbers of viable cells plated in soft agar. Even though there was no further drug treatment, the number of colonies in the cotreatment cohort was reduced by 90% as compared with vehicle or cyclopamine, and by 50% as compared with MRK-003 alone (Fig. 4B). This shows that colony-forming cells are more sensitive to combined drug treatment and are eliminated from the population somewhat selectively. We also assessed expression of CD133, a putative tumor stem-cell marker, via fluorescence-activated cell sorting analysis in HSR-GBM1 and DAOY treated for 2 days with vehicle, monotherapy, or both drugs. However, in these 2 lines cotreatment did not decrease the percentage of CD133-positive cells to a greater degree than monotherapy (data not shown). This may reflect the imperfect ability of CD133 alone to prospectively identify stem-like clonogenic cells, a fact highlighted in several recent reports (49).

**Primary human-derived GBMs respond strongly to coinhibition of Notch and Hedgehog**

As a final test for the efficacy of combined inhibition, we treated several freshly resected primary human GBMs cultured in neurosphere media. First, we investigated whether MRK-003 was able to inhibit Notch signaling in primary GBM cultures and found that both Hes1 and Hes5 were
decreased in primary GBM-derived low-passage neurosphere cultures (Supplementary Fig. S3B), and that baseline expression of Notch and Hedgehog signaling was similar to that of GBM neurosphere cultures. Next, we looked at the ability of cotreatment to prevent colony formation. We dissociated the tumors, plated them in serum-free neurosphere media, and treated the primary cultures. Although some variation was observed, most likely due to the heterogeneous nature of clinical samples, overall we saw a dramatic decrease in the number and size of spheres forming over a period of 2 to 4 weeks in the cotreatment cohort as compared with either monotherapy or vehicle (Fig. 5A). Similar results were seen in primary passages from 3 GBMs (JHH-GBM17, JHH-GBM18, and JHH-GBM20) and in passage 2 cells from JHH-GBM14. A significant decrease of 50% to 80% in the number of colonies formed was seen in the lines with sufficient material for multiple replicates (Fig. 5B). The fourth line, JHH-GBM20, showed results similar to JHH-GBM14, but the assay was only performed once due to limited starting material. We also observed a decrease in the average size of tumor neurospheres formed in cotreated cultures as compared with vehicle or monotherapy, ($P < 0.05$), suggesting a limited proliferative capacity in remaining cells (Fig. 5C).

**Discussion**

GBMs are highly resistant to current treatments such as chemotherapy and radiation, and a deeper understanding of GBM biology is necessary for effective tumor elimination. In light of this, large-scale efforts characterizing genetic alterations in GBM have shown that GBM subtypes exist and suggested that multiple pathways could be targeted to treat tumors more effectively (3, 50, 51). We investigated whether resistance could emerge in response to treatment with a Notch inhibitor *in vitro* and found a significant number of cells were able to grow in the presence of long-term MRK-003 treatment. We found Hedgehog signaling was upregulated in response to Notch inhibition and that direct interaction between Hes1 and Gli1 occurs in GBM neurosphere lines and primary GBM samples. This interaction could account for the increase in Hedgehog signaling during Notch suppression and is a potential mechanism of resistance. We demonstrated that targeting both Notch and Hedgehog simultaneously increases apoptosis and inhibits colony-forming ability more dramatically than either monotherapy. Moreover, freshly dissected human GBMs are also highly susceptible to coinhibition. These findings indicate that targeting both pathways is more effective than monotherapy at eliminating GBM cells in some neurospheres *in vitro*, and that cotreatment should be considered in patients after additional preclinical *in vivo* studies are performed.

The finding that Hes1 binds to the Gli1 locus and may regulate its expression at a transcriptional level is both novel and unexpected. The fact that only a subset of cell lines, primary GBM specimens, and cancer types exhibit this relationship suggests other factors, such as binding partners, heterochromatin structure, or methylation, may also be important. We investigated whether inverse expression levels between Hes1 and Gli1 were seen in human GBMs by analyzing public databases (www.rembant.org) and previously published data sets (52), but found no significant relationship between the two (data not shown). This may be due to the fact that this regulatory relationship is only present in a subset of human GBMs. The molecular mechanism and functional role of this feedback mechanism in cancer requires further investigation, as does the question of whether this regulatory mechanism occurs in normal development.

In summary, cotreatment with Hedgehog and Notch inhibitors clearly increases cell death and decreases colony-forming ability *in vitro*, suggesting the potential as a
combinatorial chemotherapy agent. In vivo studies will be required to evaluate whether or not this is a feasible treatment in mouse xenografts prior to any clinical trials. A study evaluating Hedgehog and Notch coinhibition in advanced breast cancer is currently underway (NCT01071564) and may pave the road for determining the safety of cotreatment. Our data support the increasing awareness of cell signaling complexity in tumors, and the potential for adaptation and evasion following individual pathway blockade. Further evaluation of the molecular links between the Notch, Hedgehog, and Wnt pathways seems indicated, and successful tumor elimination may require broader approaches targeting several pathways.

Disclosure of Potential Conflicts of Interest

C.G. Eberhart discloses a patent license and work as a consultant for Stemline Therapeutics.

References


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Correction: The Notch Target Hes1 Directly Modulates Gli1 Expression and Hedgehog Signaling: A Potential Mechanism of Therapeutic Resistance

In this article (Clin Cancer Res. 2010;16:6060–70), which was published in the December 15, 2010, issue of Clinical Cancer Research, a reader informed us of several mislabeled figures. Specifically, in Figs. 2 and 3, "Gli" is incorrectly displayed as "Gil." The correctly labeled figures are provided below. The authors regret this error.

Figure 2.

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The Notch Target Hes1 Directly Modulates Gli1 Expression and Hedgehog Signaling: A Potential Mechanism of Therapeutic Resistance


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