Targetable Signaling Pathway Mutations Are Associated with Malignant Phenotype in IDH-Mutant Gliomas

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Abstract

**Purpose:** Isocitrate dehydrogenase (IDH) gene mutations occur in low-grade and high-grade gliomas. We sought to identify the genetic basis of malignant phenotype heterogeneity in IDH-mutant gliomas.

**Methods:** We prospectively implanted tumor specimens from 20 consecutive IDH1-mutant glioma resections into mouse brains and genotyped all resection specimens using a CLIA-certified molecular panel. Gliomas with cancer driver mutations were tested for sensitivity to targeted inhibitors in vitro. Associations between genomic alterations and outcomes were analyzed in patients.

**Results:** By 10 months, 8 of 20 IDH1-mutant gliomas developed intracerebral xenografts. All xenografts maintained mutant IDH1 and high levels of 2-hydroxyglutarate on serial transplantation. All xenograft-producing gliomas harbored “lineage-defining” mutations in CIC (oligodendroglia) or TP53 (astrocytoma), and 6 of 8 additionally had activating mutations in PIK3CA or amplification of PDGFRα, MET, or N-MYC. Only IDH1 and CIC/TP53 mutations were detected in non-xenograft-forming gliomas (P = 0.0007). Targeted inhibition of the additional alterations decreased proliferation in vitro. Moreover, we detected alterations in known cancer driver genes in 13.4% of IDH-mutant glioma patients, including PIK3CA, KRAS, AKT, or PTEN mutation or PDGFRα, MET, or N-MYC amplification. IDH1/CIC mutant tumors were associated with PIK3CA/KRAS mutations whereas IDH1/TP53 tumors correlated with PDGFRα/MET amplification. Presence of driver alterations at progression was associated with shorter subsequent progression-free survival (median 9.0 vs. 36.1 months; P = 0.0011).

**Conclusion:** A subset of IDH1-mutant gliomas with mutations in driver oncogenes has a more malignant phenotype in patients. Identification of these alterations may provide an opportunity for use of targeted therapies in these patients. *Clin Cancer Res; 20(11); 2898–909. ©2014 AACR.*
be associated with higher grade or progressive
tumors are unlikely to be the triggers of more malignant
tumors (2, 12). Therefore, how these genetic changes
are associated with more rapid subsequent
progression. We also find that genetic subtypes of
IDH-mutant gliomas utilize distinct oncogenic
pathways during transformation to more malignant tumors.
Moreover, IDH-mutant gliomas with driver mutations
preferentially establish orthotopic xenograft tumors in
mouse brain and are sensitive to targeted inhibition of
the mutant gene product. Identification of targetable
recurrent driver mutations provides novel therapeutic
possibilities for the patients with IDH-mutant glioma
who are most in need of new treatments.

malignant phenotype and become lethal. A fundamental
paradigm in cancer progression imparts that morphologic
changes during the process of malignant transformation
reflect the sequential acquisition of genetic alterations (14).
IDH1/2 mutation and widespread hypermethylation of
CpG islands (CpG island hypermethylator phenotype or
CIMP) are the earliest known events in glioma development, preceding the ’lineage-defining’ acquisition of TP53
mutation in astrocytomas or 1p/19q codeletion in oligo-
dendrogliomas (5, 10, 15–18). Mutant IDH1/2 represents a
’trunk’ mutation (19) in the molecular evolutionary tree of
gliomas because it is ubiquitously present throughout the
tumor cell mass (15, 20) and retained on progression from
low- to high-grade with few exceptions (2, 10, 15, 20, 21).
The lineage-defining or ’secondary’ genetic alterations in
IDH-mutant gliomas (TP53/ATRX mutations or 1p/19q
codeletion/CIC mutations) are also early events in tumor
development, as they are present in the vast majority of low-
grade (WHO grade II) diffuse gliomas (2, 12). Therefore,
’primary’ IDH1/2 mutation and ’secondary’ genetic alterations are unlikely to be the triggers of more malignant
behavior. A few genetic alterations have been reported to
be associated with higher grade or progressive IDH-mutant
gliomas, however the alterations that drive transformation to a more malignant phenotype remain largely unknown
(2, 5, 13, 15).

One limitation in the study of IDH-mutant glioma has
been the scarcity of experimental models harboring endog-
enous IDH1/2 mutation. Successful propagation of tumor-
initiating cells (TIC), cancer cells that display stem cell
capabilities, and generation of intracerebral glioma xenografts from IDH-mutant patient gliomas are rare (22–25).
The reasons for the difficulty in establishing models from
patient IDH-mutant gliomas are unknown.

Herein, we hypothesized that additional ‘tertiary’ genetic
alterations, which have been noted to occur in IDH-
mutant gliomas (7, 15, 26, 27), could be the drivers of the
progressive malignant phenotype of IDH-mutant gliomas.
We therefore tested 20 consecutive IDH-mutant glioma
specimens from patients undergoing surgery at our institu-
tion for the ability to establish intracerebral xenografts in
mice. We performed a comparative genetic analysis of all
primary tumor specimens using a CLIA-certified molecular
panel and discovered that the IDH-mutant gliomas that
were enriched with additional tertiary oncogenic genetic
alterations, including PIK3CA mutation and amplification of
the PDGFRA, MET, and N-MYC genes. IDH-mutant
glioma TICs generated from xenograft-forming tumors
exhibit oncogenic addiction to tertiary mutations. In
patients with IDH-mutant glioma, tertiary alterations seem
to be acquired at the time of tumor progression and also
associated with higher pathologic grade and shorter pro-
gression-free survival (PFS). These data indicate acquisition of
tertiary alteration is associated with more aggressive
tumor behavior and may predict the ability to establish
intracerebral xenografts in mice.

Materials and Methods

Biologic samples and clinical data

From September 2011 to October 2012, we prospectively
acquired 20 consecutive untreated (9 patients) and previ-
ously treated (11 patients) patients with IDH-mutant glioma
undergoing resection at the Massachusetts General Hospital
(MGH). Patients either had previously confirmed
IDH mutation or were accrued if clinical suspicion of IDH-
mutant glioma was high based on characteristic features
such as young age, frontal location, and lesser degree of
contrast enhancement and necrosis on neuroimaging (5).
Progression of disease was confirmed by either tissue diag-
nosis or standard response criteria (28). All tumor samples
and clinical information were collected under MGH insti-
tutional review board approved protocols, and informed
consent was obtained from all patients. All mouse proce-
dures were approved by the Subcommittee on Research
Animal Care at MGH.

Glioma neurospheres and orthotopic xenografts

Fresh surgical specimens were enzymatically dissociat-
ed, and 2 to 5 x 10^6 cells were stereotactically implanted
into the right striatum of the brains of 7- to 10-week-old
female severe combined immunodeficient mice as
described (29). In some cases when an excess of tumor
tissue was available, cells were briefly cultured in neuro-
sphere medium as described (30) to enrich TIC neuro-
spheres, and a similar number of cells were implanted
within 48 hours of in vitro culture. There was no notable
difference in xenograft formation with either method.
Mice were monitored for status twice per week and sacri-
ficed when neurologic deficits became significant. A min-
imum 10-month observation period after implantation
was required to determine whether orthotopic xenografts developed, although all animals were sacrificed after 1 year to assess for tumor formation. Brains were removed for pathologic studies and tumors were excised to re-establish TIC neurosphere cultures. TICs were then either implanted into the brains of new mice or used for in vitro assays as described (29, 31).

**Histology and immunostaining**

Hematoxylin and eosin staining and immunohistochemistry (IHC) were performed on formalin-fixed paraffin-embedded (FFPE) sections as described (29, 31). Primary antibodies used for IHC were anti-IDH1 R132H (Dianova; 1:100), Ki-67 (MIB-1; Dako; 1:150), anti-CD31 (BD Pharmingen; 1:150), and anti-nectin (Santa Cruz; 1:400).

**Genotyping and FISH data**

Clinical molecular profiling was performed as described (32, 33). Briefly, the MGH SNapshot assay is a multiplexed, PCR-based, single-base extension assay that interrogates 73 commonly located loci from 23 genes (AKTI, APC, BRAF, CTNNBI1, EGFR, EMLA-ALK, HER2, FGFR3, GNA11, GNAQ, GNAS, HRAS, IDH1, IDH2, KIT, KRAS, MEK1, NOTCH1, NRAS, PIK3CA, PTEN, RET, TP53). Genomic PCR-based sequencing was used to sequence all coding exons of the IDH1, CIC, TP53, PIK3CA, and PIK3R1 genes. PCR products were amplified from genomic DNA templates with Platinum Taq polymerase per manufacturer's protocol using intron-based primers spanning the coding sequences (Supplementary Table S2) then Sanger sequenced (Beckman Coulter Genomics). FISH assays for the EGFR, MET, and PDGFRα genes were performed using BAC probes CTD-2113A18 (7p EGFR locus), CTB-13N12 (7q MET locus), CEP7 (centromere 7 control), RP11-58C6 (4q PDGFRα locus), and CEP4 (centromere 4 control) (Abbott) as described (32). BAC clone RP11-480N14 (chr2:15991148-16158895) was used to make the N-MYC probe and ALK (2p23) Proximal Probe (Kreatech) was used for centromere 2 control. Gene/control probe copy number ratios of >2.0 were considered amplified. 1p and 19q status was determined using the Vysis 1p36/1q25 and 19q13/19p13 FISH Probe Kit (Abbott). 1p/1q and 19q/19p ratios of <0.75 were considered loss and >0.75 as maintained.

**Gas chromatography-mass spectroscopy data**

Ten to 20 mg of frozen tumor tissue was homogenized and extracted with methanol/chloroform. Metabolites were derivatized with N-(tert-butylimidethylsilyl)-N-methyl-trifluoroacetamide, with 1% tert-butylimidethylchlorosilane (Sigma) and analyzed on a 6890N GC system (Agilent Technologies) combined with a 5975B Inert XL MS system (Agilent Technologies). 2-Hydroxyglutarate (2HG) fragment 433 m/z and the glutamate fragment 432 m/z were used for further analysis (34). 2HG and glutamate concentrations were normalized to the internal standard norvaline and tissue weight as described (35).
## Table 1. Orthotopically Implanted Patient IDH-mutant Gliomas

| IDH1 Mutation | Confirmed secondary (lineage) alteration | Tertiary alteration | Time to xenograft (Mos.) | MGG Histology | Sex | Age at Dx | Prior treatment | GBM-O, AOA, AO, LGO, LGOA | Promyeloy, M, U, n.t. | R132H | TP53 | MET | PIK3CA | CIC | Gliadin, TMZ chemotherapy, RT, SRS, BEV, CPT-11, TMZ cycles, PCV, C2, isotretinoin, gefitinib followed by gefitinib 

### **Driver Mutations in IDH1-Mutant Gliomas**

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Driver Mutations in IDH1-Mutant Gliomas

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Genetic alterations associated with ability to generate intracerebral xenograft

We sought to identify the mechanisms accounting for the ability to generate orthotopic xenograft in our set of IDH-mutant gliomas. There was no clear distinction in host factors such as patient age, sex, or prior treatment (radiation or various combinations of radiation and different chemotherapies; Table 1) between gliomas that formed xenograft versus those that did not. Generally, tumors that were able to form xenografts had GBM (WHO grade IV) histology (6/8 xenografts vs. 2/12 in the non-xenograft-forming subset) and lacked 1p/19q codeletion (7/8 xenografts).

We conducted a comparative genetic analysis on the primary tumor specimens to assess whether additional oncogenic alterations might account for differences in the ability to generate xenograft. All 8 xenograft-forming tumors and 10 of 12 non-xenograft-forming tumors harbored the IDH1 R132H variant, which accounts for ~90% of the IDH1 mutations in gliomas (2, 12, 36), and the remaining 2 non-xenograft-forming gliomas harbored IDH1 R132C. Interestingly, one glioma xenograft (MGG79) was homozygous for IDH1 R132H mutation and the corresponding orthotopic xenograft produced high levels of 2HG (Supplementary Fig. S4 and Table S1). This finding is in contrast with a previous report suggesting a wild-type IDH1 allele is necessary for 2HG production (37).

Focused genotyping analysis of all implanted primary tumors was conducted with our CLIA-certified clinical molecular profiling platform (32), which surveys 25 commonly mutated cancer-associated genes. We specifically assessed for "tertiary" genetic alterations, which we defined as nonlineage mutations, because lineage-associated mutations (astrocytic ATRX/TP53 mutations or oligodendrogial...
CIC/TERT mutations and 1p/19q codeletion) occur in virtually all low-grade IDH-mutant gliomas. Strikingly, 6 of 8 xenograft-forming tumors harbored tertiary mutations whereas none were detected in non–xenograft-forming patient gliomas (P = .0007; Table 1).

The detected tertiary alterations included hotspot-activating mutations in PIK3CA (2/6) and high-level focal amplifications in the PDGFRα (2/6) and MET (1/6) genes (Table 1). In addition, we sequenced the entire coding regions of PIK3CA, which encodes p110α, and PIK3R1, which encodes the phosphoinositide 3-kinase (PI3K) regulatory subunit p85α, in all xenograft-forming tumors and detected no other mutations. Notably, one GBM had focal primitive neuroectodermal tumor (PNET) histopathology (MGG152; Fig. 1A) and was unusually malignant in both the patient (5-month overall survival) and in orthotopic xenograft (lethal within 1 month; Table 1). A previous study detected C-MYC or N-MYC amplification in a significant proportion of malignant gliomas-harboring PNET-like components (38); therefore, we interrogated these genes in MGG152 and identified high-level N-MYC amplification (Fig. 2A). We confirmed that all the tertiary genetic alterations detected in the primary tumors were maintained in the respective orthotopic xenografts (Fig. 2A), suggesting these mutations play a role in the tumor initiating capability of IDH1-mutant gliomas.

Tertiary genetic alterations are drivers in IDH-mutant glioma xenografts

We then tested the effect of small molecule inhibitors targeted at the identified tertiary mutations on in vitro proliferation. We examined the impact of BYL719, a
highly selective inhibitor of p110α (39), on the viability of MGG108 (PIK3CA R93Q) and MGG152 (PIK3CA/PIK3R1 wild type) TICs. We observed more potent inhibition of MGG108 than MGG152 cells (IC₅₀ = 7.5 μmol/L for MGG108 vs. 20.1 μmol/L for MGG152), indicating PIK3CA mutation functions as a driver of proliferation in MGG108 cells (Fig. 2B). We then examined the effect of the Myc pathway small molecule inhibitor JQ1 (40) in MGG108 and MGG152 (N-MYC amplified). As expected, MGG152 was significantly more sensitive to JQ1 in cell viability assays relative to MGG108, which lacks N-MYC or C-MYC amplification (IC₅₀ = 0.04 μmol/L for MGG152 vs. 2.08 μmol/L for MGG108; Fig. 2B). Furthermore, shRNA knockdown of N-myc expression in MGG152 suppressed cell proliferation and nearly eliminated sphere formation ability (Fig. 2C and Supplementary Fig. S6). We also tested sunitinib and crizotinib, small molecule inhibitors of PDGFR and c-Met, respectively, in several lines with known PDGFR and MET copy number status. We found that sunitinib was more potent against a line with high-level PDGFR amplification (MGG117) than those without (MGG108 and MGG119), whereas crizotinib was most effective in a line harboring MET amplification (MGG132) (Supplementary Fig. S7). These data suggest that tertiary alterations are oncogenic drivers in IDH-mutant glioma xenografts.

Acquisition of tertiary mutations during malignant transformation

We then asked whether tertiary alterations are acquired when lower-grade IDH-mutant gliomas progress or transform to higher grade tumors in patients. We examined our dataset of 149 patients with IDH-mutant glioma who had clinical molecular profiling at our center and identified 20 tumors with tertiary alterations (13.4%). Tertiary alterations were nearly exclusively present in progressive low-grade (WHO grade II) or high-grade (WHO grade III or IV) tumors (Table 2); specifically 6 grade II (4 progressive), 6 grade III, and 8 grade IV tumors. Presence of a tertiary alteration was associated with grade IV (GBM) versus lower grade (grade II or III) histology (P = 0.027).

We then analyzed a subset of 56 patients who underwent biopsy and genotyping at the time of radiographically defined disease progression. Presence of tertiary alteration in the progressive tumor (14 patients, 25%) was associated with significantly shorter subsequent PFS (median 9.0 months; 95% CI, 4.4–49.3, with tertiary alteration versus 36.1 months; 95% CI, 18.7–52.8, without, P = 0.0011; Fig. 3A and B). Notably, there was no difference in PFS from the time of initial diagnosis (median 55.6 months; 95% CI, 24.6–93.1, with tertiary alteration vs. 54.1 months; 95% CI, 35.7–73.0, without, P = 0.76; Fig. 3A), implicating the tertiary alteration detected at progression as the driver of malignant degeneration in these patients. There was no detectable difference in overall survival; however, there were few deaths in either group (13/56 total patients), therefore longer follow-up time is needed to assess this endpoint.

Several tertiary genetic events were recurrently identified (Table 2), including activating mutations in PIK3CA (9 tumors) and KRAS (4 tumors) and PDGFRA amplification (4 tumors). PIK3CA and KRAS mutations were most often detected in tumors with at least a component of oligodendroglia histology (7/9 PIK3CA mutant and 3/4 KRAS mutant tumors). Interestingly, all 4 PDGFRA-amplified tumors were purely astrocytic (P = 0.026). When specific oncogenes were compared by IDH genetic lineage rather than histopathology (within the set of tumors with tertiary mutations and confirmed lineage mutations), we identified significant associations between 1p/19q codeleted tumors and intracellular signaling pathway gene mutations (KRAS or PIK3CA, P = 0.002) and between receptor tyrosine kinase amplification (PDGFRα or MET) and non–1p/19q codeleted (TP53 mutant) tumors (P = 0.029).

To assess whether tertiary alterations are acquired at tumor progression, we examined paired tumor specimens from newly diagnosed and progressive tumors from 6 patients in whom we detected tertiary alterations. For 2 patients with PDGFRα amplification and 1 patient with focal MET amplification, we confirmed these alterations were present in the progressive but not in the initial tumor specimens (Fig. 3C). In 2 of 3 patients with PIK3CA mutant, the PIK3CA mutations were present only in the progressive tumor (Fig. 3C). The third patient (Patient 6 in Table 2) had PIK3CA E545G mutation in both the diagnostic and progressive tumor specimens. This patient was treated with 12 cycles of temozolomide and progressed just 24.6 months after diagnosis, a relatively rapid time to progression for low-grade oligodendrogliomas with 1p/19q codeletion.

Discussion

IDH-mutant diffuse gliomas nearly always progress after radiation therapy and chemotherapy and eventually transform to more malignant tumors. Effective therapeutic options at that stage are lacking. Herein we demonstrate that the subset of IDH-mutant gliomas that acquire an aggressive phenotype late in the disease are driven by specific tertiary oncogenic alterations. These tertiary alterations are associated with more malignant tumors in patients and increased tumor-forming ability in mice. Importantly, these tertiary alterations represent potential therapeutic targets for patients with IDH-mutant gliomas who are most in need of treatment.

Our data suggest that after acquisition of lineage-defining mutations, IDH-mutant gliomas may follow multiple pathways to transformation (Fig. 4). 1p/19q codeleted tumors tend to activate the PI3K/mTOR or Ras intracellular signaling pathways and TP53-mutant tumors tend to amplify growth factor receptor tyrosine kinases. Our findings are consistent with prior reports; recurrent PIK3CA mutations have been detected in a subset of IDH-mutant, 1p/19q codeleted anaplastic oligodendrogliomas (7, 26) and 2 recent reports observed enrichment of PDGFRα amplification in IDH-mutant versus IDH-wild-type primary GBM (27, 41). In addition, we find that activation of N-myc may
Table 2. Genetic alterations in IDH-mutant glioma patients at MGH

<table>
<thead>
<tr>
<th>Pt</th>
<th>Age</th>
<th>Sex</th>
<th>Initial histology</th>
<th>Initial WHO grade</th>
<th>OS (mos)</th>
<th>PFS (mos)</th>
<th>IDH1 mutation</th>
<th>Confirmed secondary (lineage) alteration</th>
<th>Treatment before detection of tertiary alteration</th>
<th>Tertiary alteration (amino acid substitution or copy number ratio)</th>
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<tbody>
<tr>
<td>1</td>
<td>60</td>
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<td>Oligoastrocytoma</td>
<td>II</td>
<td>78.3</td>
<td>21.9</td>
<td>R132H</td>
<td>codel</td>
<td>RT; TMZ (18 cycles)</td>
<td>AKT1 (E17K), KRAS (G12R), PIK3CA (H1047L)</td>
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<td>2</td>
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<td>II</td>
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<td>54.0</td>
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<td>codel</td>
<td>TMZ (12 cycles); RT</td>
<td>PIK3CA (R88Q)</td>
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<td>159.8</td>
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<td>codel</td>
<td>PCV (6 cycles); RT</td>
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<td>GBM-O</td>
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<td>codel</td>
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<td>55.7</td>
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<td>GBM</td>
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<td>113.2</td>
<td>93.2</td>
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<td>N-MYC amplification (&gt;25:1)</td>
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<td>GBM with PNET component</td>
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<td>3.9</td>
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<td>TP53 R273H</td>
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<td>25.6</td>
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<td>PDGFRA amplification (&gt;25:1)</td>
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<td>61</td>
<td>M</td>
<td>GBM-O</td>
<td>IV</td>
<td>9.4</td>
<td>9.4</td>
<td>R132H</td>
<td>TP53 R273C</td>
<td>None</td>
<td>PTEN (R173C)</td>
</tr>
</tbody>
</table>

Abbreviations: Pt, patient; Dx, diagnosis; OS, overall survival; mos, months; GBM-O, glioblastoma with oligodendroglioma component; codel, 1p/19q codeleted; TMZ, temozolomide; ddTMZ, dose dense temozolomide; RT, radiation therapy; NA, not available.

aRatio of specific gene probe to centromere control.

bEvent has not yet occurred.
be a particularly malignant transformation pathway in IDH-mutant glioma. A recent study similarly observed a correlation between c-Myc expression and shorter time to transformation within IDH-mutant gliomas (42). Together with these reports, our data suggests IDH-mutant gliomas may undergo a sequenced genetic evolution analogous to IDH2-mutant acute myeloid leukemia, where stepwise acquisition of distinct classes of mutations results in more aggressive disease (43).

The mechanisms by which IDH-mutant gliomas acquire tertiary mutations are largely unknown. A recent study observed that a subset of IDH-mutant low-grade gliomas developed a hypermutation phenotype (15, 44) after treatment with temozolomide. All of the hypermutated gliomas in their dataset harbored driver mutations, many in the PI3K/mTOR signaling pathway (15). In our dataset, 10 of 20 patients with tertiary mutation were previously treated with alkylating chemotherapy (Table 2). Five of our 10 chemotherapy-treated patients had PI3K/mTOR pathway mutations in their tumors, and interestingly one tumor had activating mutations in 3 oncogenes (PIK3CA, AKT, and KRAS), suggesting it may be hypermutated. However, 9 patients as well as 2 xenograft-forming tumors from our implantation study harbored tertiary alterations and had no prior treatment, indicating that genomic instability resulting from DNA-damaging therapy is not the sole evolutionary path to malignant progression in IDH-mutant gliomas. The drivers of tertiary mutation in untreated IDH-mutant tumors remain to be determined.

The overall frequency of tertiary mutations in our dataset was 13.4%, which may be reflective of the focused nature
of our genotyping panel. Our data suggests resampling of tumor specimens at the time of progression may increase detection frequencies. We also provide rationale for sampling tumor specimens throughout the course of disease as the acquired tertiary mutation may present an opportunity for therapeutic targeting. Future genomic profiling studies that also include paired tumor samples will address important remaining questions including the scope and frequency of recurrent tertiary mutations, the timing of their appearance and the mechanisms that drive their development. Of note, our genotyping panel did not interrogate many genes that also include paired tumor samples will address important remaining questions including the scope and frequency of recurrent tertiary mutations, the timing of their appearance and the mechanisms that drive their development. Of note, our genotyping panel did not interrogate many genes that commonly mutated in gliomas, such as CDK4/6, MDM2, CCND2, AKT3, RB, PARK2, and NFI (1, 45). However, these mutations were detected in datasets consisting mostly of IDH-wild-type gliomas that evolve along a distinct molecular pathway.

By identifying recurrent, functionally significant tertiary genetic alterations, we set the stage for targeted therapy in IDH-mutant gliomas. Pharmacologic inhibitors for all of the tertiary alterations identified in our work are in development. Notably, our data suggests PDGFRA amplification warrants investigation in TP53-mutant, IDH-mutant gliomas. Outcomes for this subgroup are poor relative to the 1p/19q codeleted subtype (6) possibly because of the uncertain efficacy of chemotherapy in these tumors given their lack of 1p/19q codeletion (46, 47). We detected recurrent mutations in KRAS, which have been reported to be rare in glial tumors (45, 48, 49). Recent clinical data suggest that cancers driven by KRAS mutation may be sensitive to MEK inhibitors (50). In addition, our data suggests investigation of Myc pathway inhibitors (40) may be justified for particularly aggressive IDH-mutant gliomas, because these may harbor C-MYC or N-MYC amplification or inappropriate c-Myc expression. Analogously, a recent study reported that Myc pathway inhibition potently reduces viability of acute myeloid leukemia cells driven by mutant IDH2 (43).

Finally, development of anticancer agents in IDH-mutant gliomas has been limited by the scarcity of biologically accurate preclinical models that are serviceable for testing therapeutics. We have established a panel of endogenous IDH-mutant intracerebral glioma xenografts that represent a powerful platform for studying IDH-mutant tumor biology and for answering fundamental questions about treatment of IDH-mutant gliomas. Future work utilizing these orthotopic xenografts may help determine the optimal therapeutic strategy for IDH-mutant gliomas, which may involve inhibition of mutant IDH1, inhibition of tertiary genetic alterations, alteration of metabolic or epigenetic pathways, or a combination thereof.

Disclosure of Potential Conflicts of Interest
D. Dias-Santagata, L.W. Ellisien, and D.R. Borger are consultant/advisory board members for BioReference Laboratories Inc. M. Vander Heiden has ownership interest (including patents) in and is a consultant/advisory board member for Agios Pharmaceuticals. T.T. Batchelor reports receiving commercial research grants from Argenus, AstraZeneca, Kirin, Merck, Millennium, Novartis, Pfizer, Roche, and Spectrum. No potential conflicts of interest were disclosed by the other authors.
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References

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Driver Mutations in IDH1-Mutant Gliomas


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