Inhibition of BET Bromodomain Targets Genetically Diverse Glioblastoma

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Abstract

**Purpose:** Glioblastoma is refractory to conventional therapies. The bromodomain and extraterminal domain (BET) proteins are epigenetic readers that selectively bind to acetylated lysine residues on histone tails. These proteins recently emerged as important therapeutic targets in NUT midline carcinoma and several types of hematopoietic cancers. In this study, the therapeutic potential of a novel BET bromodomain inhibitor, JQ1, was assessed in a panel of genetically heterogeneous glioblastoma samples.

**Experimental Design:** The antineoplastic effects of JQ1 were shown using *ex vivo* cultures derived from primary glioblastoma xenograft lines and surgical specimens of different genetic background. The *in vivo* efficacy was assessed in orthotopic glioblastoma tumors.

**Results:** We showed that JQ1 induced marked G1 cell-cycle arrest and apoptosis, which was phenocopied by knockdown of individual BET family members. JQ1 treatment resulted in significant changes in expression of genes that play important roles in glioblastoma such as c-Myc, p21^CDKN1A/WAF1, hTERT, Bcl-2, and Bcl-xl. Unlike the observations in some hematopoietic cancer cell lines, exogenous c-Myc did not significantly protect glioblastoma cells against JQ1. In contrast, ectopically expressed Bcl-xl partially rescued cells from JQ1-induced apoptosis, and knockdown of p21^CDKN1A/WAF1 attenuated JQ1-induced cell-cycle arrest. Cells genetically engineered for Akt hyperactivation or p53/Rb inactivation did not compromise JQ1 efficacy, suggesting that these frequently mutated signaling pathways may not confer resistance to JQ1. Furthermore, JQ1 significantly repressed growth of orthotopic glioblastoma tumors.

**Conclusion:** Our results suggest potentially broad therapeutic use of BET bromodomain inhibitors for treating genetically diverse glioblastoma tumors. *Clin Cancer Res; 19*(7); 1–12. ©2013 AACR.

Introduction

Glioblastoma is the most common and aggressive primary malignant brain tumor. Despite advances in the multimodal treatments including surgery and chemoradiotherapy, the overall survival of patients with glioblastoma has remained largely unchanged for decades (1). The dismal prognosis makes this disease an upfront challenge for development of novel therapeutic strategy. Over the past decade, a variety of molecular-targeted agents has been clinically tested for treating glioblastoma. The majority are kinase inhibitors that target signaling pathways recurrently activated in glioblastoma (2). These first-generation targeted agents, however, show at best modest and infrequent efficacy (2). While various mechanisms can be implicated, the widespread and heterogeneous genetic aberrations found amongst glioblastoma cases represent a major challenge for improving glioblastoma response to therapies targeting those heavily altered signaling pathways.

Bromodomains are protein motifs that primarily bind to acetylated lysine residues, including those on histone tails (3). Through this interaction, bromodomain-containing proteins direct the assembly of nuclear macromolecular complexes to specific sites on chromatin that regulate key biologic processes including DNA replication, DNA damage repair, chromatin remodeling, and transcription regulation (3, 4). The BET family proteins (Brd2, Brd3, BRD4, and Brd7) contain 2 amino-terminal bromodomains and are best known for their roles in transcriptional regulation (5). Recently, these proteins emerged as attractive therapeutic targets in the treatment of inflammation and cancer following development of several small-molecular inhibitors that selectively bind to BET bromodomains including benzodiazepine derivatives, I-BETs, and JQ1 (6–9). The oncogenic functions of BET proteins were first identified...
Translational Relevance

Glioblastoma is a highly heterogeneous cancer, characterized at diagnosis by complex genetic and signaling aberrations. Experimental targeted agents, mostly inhibitors of kinases aberrantly activated in glioblastoma, have shown limited efficacy in clinical trials. A novel class of small-molecule inhibitors selectively targeting the bromodomains of BET epigenetic readers recently displayed therapeutic potential in several types of hematopoietic cancers and NUT midline carcinoma. One of these compounds, JQ1, exhibits excellent brain penetrating capacity. In this study, we showed that JQ1 induced significant antineoplastic effects in glioblastoma samples of different genetic background and further confirmed its in vivo efficacy. Our observations suggest that certain epigenetic mechanisms, such as the one mediated by BET proteins, may be commonly required by glioblastoma. Therefore, targeting BET epigenetic readers holds promise to provide benefits for a considerable percentage of patients with glioblastoma.

in NUT midline carcinoma, which is commonly driven by fusion of the bromodomains of BRD3 or BRD4 and the NUT (nuclear protein in testis) protein (10). More recently, an RNA interference screening found that knockdown of BRD4 in acute myeloid leukemia led to downregulation of c-Myc, depletion of leukemia stem cells, and disease regression (11). JQ1 competitively binds to BET bromodomain and displaces BET proteins from acetylated lysines on chromatin (7). Inhibition of the BET bromodomain with JQ1 showed potent anti-cancer effects both in vitro and in vivo in several different hematopoietic cancers as well as in NUT midline carcinoma (7, 11–14). However, cell lines derived from solid tumors, such as lung cancer, breast cancer and cervical cancer, appear to be less sensitive (14, 15). Several studies found that inhibition of BET bromodomain by JQ1 resulted in significant downregulation of c-Myc (11–14). The ability of BET bromodomain inhibition to reduce expression of c-Myc, until now a theoretically penetrant capacity. In this study, we showed that JQ1 induced significant antineoplastic effects in glioblastoma samples of different genetic background and further confirmed its in vivo efficacy. Our observations suggest that certain epigenetic mechanisms, such as the one mediated by BET proteins, may be commonly required by glioblastoma. Therefore, targeting BET epigenetic readers holds promise to provide benefits for a considerable percentage of patients with glioblastoma.

Materials and Methods

Tumor samples and cell culture

T4105, T4302, and T4597 primary glioblastoma xenograft lines were generous gifts from Jeremy Rich at Cleveland Clinic (Cleveland, OH). Primary glioblastoma xenograft lines with a "GBM" prefix were kindly provided by Jann Sarkaria at Mayo Clinic (Rochester, MN). These tumor samples were originally derived from patient surgical specimens and serially passed as subcutaneous xenograft tumors. Primary glioblastoma neurosphere cultures were directly derived from de-identified surgical specimens obtained from patients undergoing resection at Vanderbilt University Medical Center (Nashville, TN) in accordance with protocols approved by the Institutional Review Board. Cells were enzymatically dissociated from either surgical specimens or subcutaneous xenograft tumors as previously described (17, 21). For T4105, T4302, and T4597, matched cellular fractions enriched or depleted for cancer stem cells were separated by magnetic sorting using the CD133 Microbead Kit (Miltenyi Biotec). CD133+ glioblastoma stem cells or unsorted neurospheres were maintained in neurobasal media supplemented with the B27 serum substitute, in addition to 20 ng/mL EGF and 20 ng/mL basic fibroblast growth factor (bFGF; Invitrogen). CD133− cells were maintained in Dulbecco’s Modified Eagle’s Medium supplemented with 10% FBS (Invitrogen) but were cultured in stem cell media at least 24 hours before experiments to control differences in cell media.

DNA constructs and lentivirus production

The coding sequence of Myr-Akt1 was amplified by PCR from pcDNA3-HA-Myr-Akt1 (Addgene; #9008) and subcloned into the XbaI and EcoRI sites of the pCDH-CMV-MCS-EF1-Puro lentiviral vector (System Biosciences). Bcl-xL was amplified from pSFV-neo-Bcl-xL (Addgene #8749) and subcloned into the EcoRI sites of pCDH-CMV-MCS-EF1-Puro. The pLKO.1 lentiviral vectors directing expression of p53 short hairpin RNA (shRNA; #19119) and Bb shRNA (#25641) were purchased from Addgene; shRNA sequences specific to p21 (TRCN0000040127), BRD2 (clone 1-TRCN00006110, clone 2-TRCN00006110), BRD3 (clone 1-TRCN0000021374, clone 2-TRCN0000021376), and BRD4 (clone 1-TRCN0000196576, clone 2-TRCN0000199427) were purchased from Sigma-Aldrich. The lentiviral vectors were co-transfected with the packaging vectors psPAX2 and pCI-VSVG (Addgene) into 293FT cells by Lipofectamine 2000 (Invitrogen) to produce virus. Two days following transfection, viral supernatants were collected and used to infect cells at an approximate MOI of 5. Two days after infections, cells were selected with 1 μg/mL puromycin for at least 48 hours before experiments.
Antibodies and other reagents

The antibodies used in this study include BRD4 antibody from Bethyl Laboratories; c-Myc (9E10) and p53 (DO-1) from Santa Cruz Biotechnology; and p21 (#2947), phospho-S473 Akt (#9271), total Akt (#2920), Bcl-2 (#2870), and Bcl-xl (#2764) from Cell signaling Technology. Actin antibody was purchased from Sigma-Aldrich. PFI-1 was purchased from Millipore.

Cell viability, cell-cycle distribution, and neurosphere formation

To determine dose response, cells were aliquoted into 96-well plate at 5,000 cells per well in triplicates. JQ1 or PFI-1 was added by 2- or 4-fold serial dilutions. Cell number was measured 5 days after plating using the CellTiter-Glo Kit (Promega) and normalized to corresponding vehicle-treated groups. IC_{50} values were calculated by the GraphPad Prism 5 software using the 4-parameter logistic nonlinear regression model. To calculate the relative growth of cells, averaged cell titer of each group on day 1 were assigned a value of 1. All subsequent cell titer values were normalized accordingly.

Activation of caspase-3/7 was measured by the Caspase-Glo 3/7 Assay Kit (Promega) according to the manufacturer’s instructions. Values of caspase activities were normalized to the corresponding cell titer to determine the relative caspase-3/7 activities. Alternatively, cells were labeled by the fluorescein isothiocyanate (FITC)-conjugated Annexin V Staining Kit (BD Biosciences) according to manufacturer’s instructions, and the apoptotic subpopulation was analyzed by flow cytometry.

Cell-cycle distribution was analyzed by flow cytometry using cells stained by 10 μL PBS were implanted into a concentration-dependent manner (Fig. 1A and Supplementary Fig. S1B). Consistent with apparent symptoms, such as lethargy or hunched posture. The median survival was determined by the Kaplan-Meier estimator using the GraphPad Prism 5.0 Software.

In vivo bioluminescence imaging

Tumor progression was monitored by bioluminescence imaging weekly beginning 1 day before JQ1 treatment. Animals were intraperitoneally administrated with 150 mg/kg d-luciferin (Gold Biotechnology). Ten minutes after luciferin administration, bioluminescence was read for 50 seconds on a Xenogen IVIS 200 imaging system (Caliper Life Sciences). Bioluminescence was quantified using the Living Images software (Caliper Life Sciences).

Statistics

GraphPad Prism 5.0 was used to determine statistical significance by the Student t test. Significance of survival assays was determined by the log-rank test. P < 0.05 was considered significant.

Results

Inhibition of BET proteins by small-molecule inhibitors or shRNA reduces proliferation and survival in glioblastoma

We have previously reported that knockdown of c-Myc significantly reduced proliferation, survival, and the tumorigenic potential of glioblastoma stem cells (17). The BET bromodomain inhibitor JQ1 recently emerged as a novel modulator that potently downregulates c-Myc expression in certain hematopoietic cancers (13, 14), suggesting that JQ1 has the potential of targeting other c-Myc–dependent tumors. We first assessed whether JQ1 affected proliferation and survival of functionally validated glioblastoma stem cells, enriched from freshly dissociated glioblastoma xenograft tumors by selection for expression of CD133 surface marker (17, 21–23). In the present study, we focused on the short-term glioblastoma stem cell cultures and primary neurosphere cultures for samples of which the stem cell fraction has not been validated, as these ex vivo models more faithfully phenocopy and genocopy the original human tumors than the traditional serum-supplemented monolayer cultures (21, 22, 24). Treatment with JQ1 [abbreviation for the active enantiomer (+)-JQ1] reduced the viability of T4302 CD133+ cells and CD133+ glioblastoma stem cells derived from other primary xenograft lines in a concentration-dependent manner (Fig. 1A and Supplementary Fig. S1A). In addition, formation of neurospheres and growth by T4302 CD133+ cells were markedly decreased in the presence of JQ1 at various concentrations (Fig. 1B and Supplementary Fig. S1B). Consistent with
previous studies, the enantiomer \((-\rangle\)-JQ1 incapable of recognizing BET bromodomain displayed limited effects (Supplementary Fig. S1C; ref. 7). Finally, another selective but less potent BET bromodomain inhibitor, PFI-1, also induced dose-dependent reduction of cell viability in T4302 CD133\(^+\) cells (Supplementary Fig. S1D). Taken together, these results suggest that the antineoplastic effects of JQ1 and PFI-1 are specifically dependent on targeting the BET bromodomain. Matched CD133\(^+\) non-stem glioblastoma cells showed comparable sensitivity to JQ1 (Fig. 1A and Supplementary Fig. S1A), suggesting similar dependency on the functions of BET proteins across different cell lineages of glioblastoma.

Inhibition of BET bromodomain in hematopoietic cancers and NUT midline carcinoma consistently induces G\(_1\) cell-cycle arrest and apoptosis (6, 7, 11–14). In line with
JQ1 Represses Diverse Glioblastoma Tumors

Figure 2. Knockdown of BET proteins leads to antiproliferative and antisurvival effects resembling JQ1 treatment. A, T4302 CD133+ cells were infected with lentivirus directing expression of nontargeting shRNA (NT) or shRNA sequences specific to BRD2, BRD3 or BRD4 (clone 2). After selection with 1 μg/ml puromycin for 2 days, relative cell growth was determined for the following 5 days. B, three days after puromycin selection, relative caspase-3/7 activity was determined by normalizing the activity of caspase-3/7 to the corresponding cell titers. *, P < 0.001 by Student t test.

these observations, we showed that JQ1 induced a significant G1 cell-cycle arrest in T4302 CD133+ cells (Fig. 1C). In addition, JQ1 activated caspase-3/7 (Supplementary Fig. S1E) and resulted in accumulation of cellular subpopulations positively labeled for the early apoptosis marker, Annexin V (Fig. 1D). Similar observations were made with glioblastoma stem cells derived from multiple xenograft lines (data not shown). JQ1 also compromised proliferative potential in normal human neural progenitors but only induced modest caspase activation in comparison to that in glioblastoma stem cells (Supplementary Fig. S2).

We next asked whether genetic targeting of BET proteins led to similar repression of proliferation and survival by lentivirus-mediated expression of shRNA sequences specific to BRD2, BRD3, or BRD4. Interestingly, knockdown of any one of these BET genes significantly decreased cell growth of T4302 CD133+ cells, associated with potent caspase activation (Fig. 2 and Supplementary Fig. S3). Although a BRD3 knockout mouse model has not been reported, loss of either BRD2 or BRD4 in mouse results in embryonic lethality (25, 26). In particular, BRD2-null embryos display significant defects in neural tubes (26). Taken together, our results suggest that BET proteins possess nonredundant functions in glioblastoma, which are consistent with their proliferative and prosurvival roles in developing neural tissues.

JQ1 alters c-Myc–dependent and -independent transcription regulations

The BET proteins are important transcription regulators. For example, BRD4 promotes transcription by recruiting the positive transcription elongation factor b (P-TEFb) to the RNA polymerase II complex (27, 28) or by acting as an atypical kinase that phosphorylates the carboxyl-terminal domain of RNA polymerase II (29). Studies in several types of c-Myc–driven hematopoietic cancers suggest that, upon JQ1 treatment, downregulation of c-Myc plays a major role in mediating transcriptional changes and repression of cell-cycle progression. However, JQ1 also affects c-Myc–independent mechanisms, as ectopic c-Myc expression does not effectively attenuate JQ1-induced cell death (11, 13, 14). We therefore asked whether c-Myc was the primary downstream target of BET proteins in glioblastoma stem cells. We first showed that c-Myc was downregulated at both mRNA and protein levels upon treatment with JQ1 in T4302 CD133+ cells as well as in matched CD133− cells (Fig. 3A and Supplementary Fig. S4), albeit to a lesser degree in comparison to that observed in hematopoietic cancer cell lines (12–14). In addition, we also found that JQ1 treatment reduced expression of hTERT, Bcl-2 and Bcl-xl and modestly induced expression of the CDK inhibitor p21CIP1/WAF1 (p21), which were repetitively described as BET-regulated genes in different types of hematopoietic cancer cell lines (30).

We next determined whether exogenous c-Myc could protect glioblastoma stem cells from JQ1. Expression of c-Myc from a CMV promoter on a lentiviral vector was not altered by JQ1, in contrast to endogenous c-Myc (Fig. 3B and C). However, T4302 CD133+ cells expressing exogenous c-Myc remained sensitive to JQ1 (Fig. 3D). In addition, JQ1-induced p21 upregulation was not affected by ectopically expressed c-Myc (Fig. 3C), in contrast to previous observations in a multiple myeloma cell line (14). Analysis of other JQ1-targeted genes showed that exogenous c-Myc partially rescued Bcl-2 expression but not Bcl-xl (Fig. 3C), whereas expression of hTERT was fully restored by exogenous c-Myc in the presence of JQ1 (Fig. 3C). These results suggest that inhibition of BET proteins induces profound changes in gene expression via both c-Myc-dependent and -independent mechanisms in glioblastoma. In consistent with the findings in lung adencarcinoma cell lines (15), our results also suggest that c-Myc plays a minor role in mediating the antineoplastic activities of JQ1 in glioblastoma.

Altering core glioblastoma signaling pathways does not confer resistance to JQ1

Advances in high-throughput profiling technology have led to identification of several core signaling pathways that...
are recurrently altered in glioblastoma, exemplified by multiple receptor tyrosine kinases (RTK) and their downstream RAS/PI3K/AKT signaling axis (31, 32). Dysregulated activation of these pathways can be associated with intrinsic and acquired resistance to targeted therapies (33). We therefore asked whether aberrations of these pathways might affect glioblastoma response to BET bromodomain inhibition. The hyperactivation of the RTKs/RAS/PI3K/AKT signaling axis was modeled by lentivirus-directed expression of a myristoylation signal–linked Akt1 (Myr-Akt1). Expression of this constitutively active Akt1 fusion protein is sufficient to rescue HER2-amplified breast cancer cells from trastuzumab (34). In T4302 CD133+ cells, Myr-Akt1 not only drastically increased the levels of phosphorylated Akt but also surprisingly ablated JQ1-induced c-Myc downregulation (Fig. 4A). However, changes in p21 and Bcl-xL expression were not significantly affected and Myr-Akt1–expressing cells appeared to be equally or even more sensitive to JQ1 than the parental cells (Fig. 4B).

The activities of p53 and Rb tumor suppressors are compromised in essentially all glioblastoma tumors via different mechanisms (31, 32). Glioblastoma tumors with Rb mutations are less susceptible to CDK inhibitors (35). The 2 xenograft lines we used in our study, T4302 and T4597, retain wild-type p53 and Rb. Therefore, we determined whether further reducing the activities of these 2 tumor suppressors by RNA interference affected tumor sensitivity to JQ1. Knockdown of p53 with a previously published shRNA sequence significantly decreased p21 expression (Supplementary Fig. S5A; ref. 36), consistent with the role of p53 as a main transcriptional activator for p21. Yet, JQ1 treatment still resulted in an apparent induction of p21 (Supplementary Fig. S5A). The ability of JQ1 to compromise the viability of T4302 CD133+ cells was not significantly changed in the absence of p53 (Fig. 4C). Similarly, knockdown of Rb with a previously reported shRNA did not alter response to JQ1 (Fig. 4D; ref. 37). The basal levels of Rb protein in T4302 CD133+ cells were too low to be detected by immunoblotting, thus the efficacy of Rb-specific shRNA was shown by quantitative real-time PCR (qRT-PCR; Supplementary Fig. S5B) and validated by immunoblotting in HeLa cells (data not shown). Collectively, our observations suggest that these core glioblastoma signaling pathways may not be critically implicated in response to BET inhibition.

**JQ1 shows broad activity in glioblastoma tumors of diverse genetic background**

The core signaling pathways frequently mutated in glioblastoma exhibit limit impact on tumor sensitivity to JQ1, suggesting that BET inhibition may generate broad response in heterogeneous glioblastoma samples. We therefore assessed the effects of JQ1 on the Mayo Clinic test panel of primary glioblastoma xenograft tumors that are known to carry different genetic lesions altering p53, Rb, PTEN, and EGFR (35, 38). These tumors belong to different molecular subtypes as characterized by the Cancer Genome Atlas (TCGA) research network (32). The response to JQ1 of these tumors was also compared with early-passage primary cultures established in our laboratory. All samples were derived from enzymatically dissociated tumor masses and maintained as neurospheres in media that support enrichment of stem cell–like glioblastoma cells (24). In 10 of 15 of these samples, JQ1 reduced cell viability by more than 50% at 5 μmol/L concentration, with IC50 values largely ranging between 60 and 500 nmol/L (Table 1). These results were...
comparable to previous observations in hematopoietic cancers (12–14). Consistent with the results using genetic targeting methods, tumor responsiveness to JQ1 was not specifically associated with any mutational status characterized for these samples (Table 1). Several samples were examined for changes in protein levels of c-Myc and several other JQ1-targeted genes (Fig. 5A). Induction of p21 and downregulation of Bcl-xL upon JQ1 treatment was found in nearly all samples, although to different extents (Fig. 5A). Interestingly, significant downregulation of c-Myc was only observed in those JQ1-sensitive samples (Fig. 5A). Among the 3 modestly responsive samples, c-Myc was barely detectable in GBM8, highly expressed but not affected by JQ1 in GBM22, and even increased upon JQ1 treatment in GBM10 (Fig. 5A). Cells derived from these 3 primary xenograft lines also expressed considerably more Bcl-2 and Bcl-xL than other lines (Fig. 5A). Taken together, our results show widespread and significant responsiveness to BET bromodomain inhibition in a set of genetically heterogeneous glioblastoma samples. Although these samples are not sufficient to identify any markers predictive of JQ1 sensitivity, our results suggest that these 2 proteins play broad and important roles in mediating the ability of BET proteins to regulate glioblastoma proliferation and survival.

**JQ1 represses glioblastoma progression in an orthotopic tumor model**

Matzuk and colleagues recently report that JQ1 shows excellent permeability across the blood–brain barrier ($\text{AUC}_{\text{brain}}/\text{AUC}_{\text{plasma}} = 98\%$; ref. 40). We therefore assessed its therapeutic effects on an orthotopic glioblastoma model that recapitulated the pathologic hallmarks of glioblastoma (21). In a preliminary test, mice bearing T4302 intracranial tumors were sacrificed at 2, 4, or 8 hours after a single intraperitoneal injection of 100 mg/kg JQ1. RNA was extracted from grossly dissected tumor masses and subjected to qRT-PCR with human-specific primers. A decrease of c-Myc and Bcl-xL expression was detected as early as 2 hours after JQ1 administration, followed by apparent represen...
hTERT and Bcl-2 reduction at 4 hours (Fig. 6A). Significant p21 upregulation, which may require precedent degradation of existing c-Myc protein, was not seen until 8 hours after drug administration (Fig. 6A). These results recapitulated observations in ex vivo cultures and thus confirmed JQ1 activities in intracranial tumors. In the first in vivo assay, intracranial tumors were established using 5,000 T4302 CD133+ cells per mouse. Ten days after tumor implantation, mice received 50 mg/kg JQ1 twice a day via intraperitoneal injection for 20 days. The median survival of the JQ1-treated arm was 37 days in comparison to 31 days of the vehicle-treated arm ($P = 0.0026$ by the log-rank test; Fig. 6B). The second experiment was carried out with tumors established using 5,000 T4597 CD133+ cells infected with lentivirus directing expression of firefly luciferase. JQ1 was administrated from day 11 to 45 after tumor implantation, resulting in an extension of the median survival from 37 to 48 days ($P = 0.0089$ by the log-rank test; Fig. 6C). Tumor progression was monitored weekly by bioluminescence imaging in the second test (Fig. 6D). Interestingly, 1 week after JQ1 administration, the growth rate and the sizes of JQ1-treated tumors were slightly higher than those of the control arm, as determined by bioluminescence intensity (Supplementary Fig. S6). Nevertheless, JQ1-treated tumors appeared to progress at a slower rate while treatment continued and thus were soon overgrown by tumors in the control arm (Supplementary Fig. S6). In both in vivo experiments, no significant weight loss or other toxicity was observed in association with drug administration. These results establish in vivo the feasibility of BET bromodomain inhibitors as a novel therapeutic approach for treating glioblastoma.

### Discussion

Epigenetic regulation is a rapidly evolving central theme to oncology. Aberrations in epigenetic regulation are increasingly identified in human cancers (41). Targeting epigenetic modulators holds great promise as cancer therapies, exemplified by vorinostat and romidepsin for treating cutaneous T-cell lymphoma (41). However, successful efforts for developing epigenetic therapy have been largely restricted to hematopoietic cancers via targeting chromatin-modifying enzymes and also obscured by concerns over the lack of specificity of these enzymes and their drugs (41, 42). Recently developed small-molecule inhibitors against BET bromodomain appear to be highly selective for a few closely related targets and affect only a few hundred of genes in different context, thus promoting epigenetic therapy to a new level (4). In the present study, we showed that inhibition of the BET epigenetic readers with JQ1 compromised cellular proliferation and survival of glioblastoma cells. Our complementary genetic and pharmaceutical approaches validated that the antineoplastic effects of JQ1 were mediated by selectively targeting the BET proteins. Remarkably, JQ1 displayed broad efficacy across a panel of genetically diverse glioblastoma samples, highlighting the therapeutic potential of BET bromodomain inhibitors for treating complex solid tumors, such as glioblastoma, in addition to NUT midline carcinoma and hematopoietic cancers.
Pharmaceutical inhibition of BET bromodomain has attracted extensive interest as a novel anti-cancer strategy since its invention 2 years ago (7, 8). One compelling feature of this approach is its ability to induce effective downregulation of c-Myc (11, 13), a long pursued “undruggable” cancer target. Several types of hematopoietic cancers, such as acute myeloid leukemia, Burkitt lymphoma, and multiple myeloma, are well characterized by recurrent c-Myc amplification, translocation, and activation (16). In these largely c-Myc–driven cancers, ectopically expressed c-Myc protected cells from BET inhibition–induced growth suppression in selected cell lines, although protection against cell death is limited (11, 13, 14). Our results also showed that BET inhibition decreased c-Myc expression in glioblastoma. However, in glioblastoma, downregulation of c-Myc upon BET inhibition was rather modest and appeared to only play a minor role in mediating the effects of JQ1. Although c-Myc may not be the primary BET target in glioblastoma, we noticed that c-Myc levels were not significantly reduced by JQ1 in tumors showing relatively moderate response to JQ1 such as GBM8, GBM10, and GBM22. In contrast, JQ1-induced c-Myc downregulation were significant in JQ1-sensitive samples. These results suggest that the ability of JQ1 to downregulate c-Myc expression may be associated with sensitivity to BET inhibition. Among other targets affected by BET inhibition, p21 and Bcl-xL provided partially protection against JQ1 when genetically manipulated. These 2 genes were also widely responsive to JQ1 in various glioblastoma samples. Therefore, it appears that p21 and Bcl-xL play important roles in BET-mediated regulation of cellular proliferation and survival in glioblastoma. However, the BET-targeted gene expression profiles and the precise molecular mechanisms mediating the actions of BET inhibitors in glioblastoma, a
highly complex disease, remain to be defined and warrant future studies on a broader scale.

BET bromodomain inhibition displayed broad antineoplastic effects in a range of glioblastoma tumors carrying different genetic lesions. Some of these samples significantly differ in response to conventional chemoradiotherapy or molecular targeted agents that block signaling pathways frequently activated in glioblastoma. For example, Sarkaria and colleagues report that the EGFRvIII-expressing GBM6 is resistant to EGFR inhibition by erlotinib, whereas GBM12 is sensitive (43). Nonetheless, ex vivo cultures derived from these 2 xenograft lines were both highly sensitive to JQ1. In addition to these samples, glioblastoma stem cells genetically engineered to alter the core glioblastoma signaling pathways, such as Akt, p53, or Rb pathways, maintained sensitivity to JQ1. In glioblastoma and most other solid cancers, key tumor promoting pathways are often altered by combinations of genetic events, compromising the potential of single-targeted agents in the absence of predictive biomarkers. For example, distinct cellular subclones amplified for EGFR, PDGFR, or MET can co-exist in some glioblastoma tumors, providing one explanation as to why targeting one of these kinases only affects a small subset of patients (44, 45). According to the TCGA database (accessed via the cBio Cancer Genomics Portal), genetic alterations of BET proteins are very rare in glioblastoma. Our results showed that BRD2, BRD3, and BRD4 possessed nonredundant functions in regulating proliferation and survival in glioblastoma. We also showed that BET inhibition compromised proliferation of normal human neural progenitor cells derived from fetal tissues. Data generated from genetically engineered mouse models suggest that BET proteins, particularly BRD2, are critically implicated in neurogenesis (25, 26). Taken together, we speculate that BET proteins are commonly required for both proliferating normal neural tissues and their transformed counterparts. The potential of BET inhibitors to broadly target glioblastoma tumors carrying different genetic lesions has important clinical implication, as it suggests that this novel therapeutic strategy has the potential to generate measurable response in patients with glioblastoma, even in the absence of guidance by BET mutations or other predictive biomarkers.

Another interesting feature of JQ1 is its ability to target both glioblastoma stem cells and matched non-stem cancer cells. Glioblastoma is among several human cancers following a hierarchical organization that stem cell–like cells critically drive the pathology of cancer and give rise to multilineage non-stem cancer cells that have restricted tumorigenic potential (22). Glioblastoma stem cells are particularly important therapeutic targets as they appear to be more resistant to conventional chemotherapy and radiotherapy than their progenies and propel tumor recurrence (21, 46). However, non-stem cancer cells are not simply bystanders. Recent studies provide evidence suggesting that differentiation of non-stem cancer cells can be reversible under certain circumstances so that these cells may confer tumorigenesis (47). It is also reported that non-stem cancer cells participate in microenvironmental support of cancer stem cells (48). Therefore, while eradication of glioblastoma stem cells is greatly desired, it is also important that the non-stem cancer cell subpopulation can be effectively compromised. Normal lineage commitment is associated with epigenetic changes (49). Similarly, the phenotypic difference between cancer stem cells and their differentiated progenies can be driven by epigenetic mechanisms, although direct experimental evidence is lacking (49).
Therefore, our results suggest that BET protein–regulated epigenetic mechanisms are shared by the glioblastoma cell hierarchy despite potentially significant difference in epigenetic regulations among these cellular subpopulations.

Results of this study established the concept and explored the feasibility of treating glioblastoma with a new class of epigenetic agents that targets the BET bromodomain proteins. Notably, this therapy displays broad activity across a set of genetically or epigenetically distinct glioblastoma samples, suggesting that BET family proteins regulate essential functions conserved to a substantial percentage of this heterogeneous disease. While targeting signaling pathways frequently dysregulated in glioblastoma has experienced significant setbacks in clinical development over the past decade, the encouraging preclinical results of BET bromodomain inhibition suggest a new avenue to treat this deadly disease. Given the excellent brain-penetrating capacity of JQ1, further study is warranted to fully explore its potential in additional cancer types or other conditions of the central nervous system.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors’ Contributions
Conception and design: J. Wang
Development of methodology: J. Wang

References

Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): Z. Cheng, Y. Gong, Y. Ma, L.A. Pierce, J. Wang

Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): Z. Cheng, Y. Gong, Y. Ma, R.C. Thompson, J. Wang

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Study supervision: J. Wang

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