Introduction

Malignant glioma remains one of the most deadly cancers (1). Despite improved surgical procedures and newer therapies, no significant improvement of patients’ survival has been observed, underscoring the urgency and importance to identify approaches that are not derivatives of current treatment modalities. One of the subpopulations of glioma cells has been recognized as highly tumorigenic and resistant to various therapies (2, 3). This subpopulation of glioma cells exhibits stem cell–like phenotype—capable of sustaining self-renewal with gene expression profiles that resemble those of multipotent neural stem cells. Owing to their resemblance to normal stem cells, these aggressive cancer cells are referred to as cancer stem cells (CSC; refs. 4, 5). In addition to glioma, CSCs have been shown in several other types of solid tumors, as well as blood cancers (6). Although there are still unanswered issues and questions on the etiology of CSCs, the importance to eliminate glioma stem cells (GSC) for achieving better antitumor efficacy is evident.

One of the most crucial factors underlying cancer is signal transducer and activator of transcription 3 (STAT3). As a signal transducer, STAT3 is a central node for numerous oncogenic signaling pathways involving cytokines and growth factors (7–10). STAT3 is also an important transcription regulator, defining a transcriptional program at multiple levels that facilitates tumor cell proliferation, survival, invasion, cancer-promoting inflammation, and suppression of antitumor immune responses (7, 9, 11–14). Furthermore, an essential role of STAT3 in maintaining expression of genes important for stem cell phenotype has been demonstrated (15). For malignant glioma, persistent activation of a STAT3-regulated gene network is critical for tumor progression, mesenchymal transition, and negatively impacts patient survival (16). Highly relevant to the current study, findings from pioneering work have suggested the importance of targeting STAT3 and/or its critical upstream activators in disruption of GSC maintenance (16–18). However, directly targeting STAT3 with small-molecule drugs for the treatment of patients with cancer remains a challenge, due to the lack of enzymatic activity of transcription factors.

Toll-like receptor 9 (TLR9) is expressed in several types of immune cells (19–21). Stimulation by its ligands, single-stranded unmethylated DNA containing CpG oligonucleotides (CpG-ODN), in the immune subsets has been shown to activate the NF-κB pathway, leading to Th1 immunostimulation and antitumor immune responses, especially in conjunction with other modality of therapies, including radiation (22–24).
However, antitumor immune responses induced by CpG-ODN monotherapy are less than desirable in several preclinical testing models and disappointing in some human trials (22, 25). One of the explanations for the limited antitumor immune responses induced by CpG-ODN treatment is that the CpG–TLR9 signaling axis also activates STAT3, which serves as a brake to constrain CpG-induced Th1 immune responses (23). The ability of STAT3 to potently suppress Th1 immune responses and antitumor immunity has been well documented (10, 26).

We have recently developed an in vivo siRNA delivery technology platform by covalently linking siRNA to the CpG moiety recognized by TLR9. We have demonstrated that CpG-STAT3siRNA treatment in vivo silences STAT3 in dendritic cells, macrophages, and B cells, leading to potent antitumor immunity (27). Our recent data further illustrate that silencing STAT3 in myeloid cells by CpG-STAT3siRNA resulted in antitumor effects at both primary tumor and future metastatic sites (14, 27, 28). Although a role of TLR9 in stimulating immune responses has been recognized (21, 29), expression of TLR9 in tumors, including malignant glioma, correlates with poor patient survival (30, 31). TLR2 and TLR7 have also been shown to promote tumor growth in a STAT3-dependent manner (32). In the current study, we investigate the possibility that TLR9 has a critical role in promoting GSCs, which, in turn, also allows inhibition of essential but difficult targets critical for CSC development and maintenance.

Materials and Methods

Animals and treatments

C57BL/6 and immune-compromised IL-2rg(ko)/NOD-SCID mice were purchased from The Jackson Laboratory. Mice were housed in a pathogen-free animal facility at the Beckman Research Institute at the City of Hope National Medical Center. Required animal procedures were approved by the Institutional Animal Care and Use Committee of the Beckman Research Institute at the City of Hope National Medical Center in compliance with the NIH guidelines. Tumor-bearing mice were treated with 782.5 pmol of CpG-STAT3siRNA. CpG- Luciferase-siRNA, murine CpG1668, or human CpG-D19.

Cell lines and tissue

Mouse glioma cell lines GL261, GL261-luciferase, DBT, as well as human glioma cell lines U251 and U87 (ATCC) were maintained in DMEM (Gibco) supplemented with 10% FBS (Sigma), antibiotics, and antimicrotics (Gibco). Human primary, low-passage, stem-like glioblastoma cell lines GSC003−4, GSC008, GSC024, GSC030, GSC036, GSC017−4 (kindly provided by Dr. Christine Brown, Department of Hematology and Hematopoietic Cell Transplantation, City of Hope Medical Center, Duarte, CA) were cultured in DMEM-F50−50 supplemented with HEPES (Gibco), B-27 (Invitrogen), Heparin-sodium (Sagent), antibiotics and antimicrotics (Gibco), 20 ng/mL FGFb, 20 ng/mL EGF (PeproTech), and GlutaMAX (Gibco). Cell culture was performed in ultra-low adhesion plates (Corning). Human glioblastoma cell lines were treated for 24 hours with 500 pmol/mL CpG-ODN (class A) 5′-GGG GAC GAC GTG GGG GGG-3′, CpG-ODN (class B) 5′-TCG TCG TCG TCG TCG TCG-3′, CpG-ODN (class C) 5′-TCG TCG TCG TCG TCG TCG-3′ GC TGA CTT-3′ purchased from InvivoGen or 500 pmol/mL CpG-ODN-D19 (class A) 5′- GGT GCA TCG ATG CAG GGG GG-3′ kindly provided by Dr. Piotr Swiderski, Department of Molecular Medicine, Beckman Research Institute at City of Hope Medical Center, Duarte, CA. Interferon-γ was purchased from PeproTech; GSCs were treated with 20 ng/mL for 30 minutes at 37 °C. RNAi against human Frizzled-4 (FZD4) was introduced using RNAiMAX according to the manufacturer’s instructions (Invitrogen). Frizzled-4siRNA was obtained from Santa Cruz Biotechnology (sc-39983).

Flow cytometry

Antibodies for flow cytometry were purchased from Santa Cruz Biotechnology (MS1, SOX2, Nestin), Cell Signaling Technology (pJAK2), Abcam (GFAP, Tuj1), R&D Systems (oligodendrocyte marker O4), or BD Pharmingen (pSTAT3, TLR9). Secondary antibodies were coupled to either Alexa Fluor-488 or Alexa Fluor488 (Invitrogen). Intracellular staining was performed after fixation of single-cell suspensions with 2% parafomaldehyde and permeabilization with ice-cold 100% methanol, blocked with PBS/1% BSA for 1 hour at 4 °C, and stained with an antibody diluted at 1:50 in PBS/1% BSA for 30 to 45 minutes at room temperature. ALDH1 detection was performed according to the manufacturer’s instructions (Aldelfluor; STEMCELL Technologies). Stained single-cell suspensions were analyzed using an Accuri C6 cytometer (BD Biosciences), followed by FlowJo 7.6.1 analysis.
Imaging

Indirect immunofluorescence on frozen tissue sections or paraffin-embedded tissue specimen was carried out as previously described (28). Briefly, after deparaffinization and antigen retrieval at low pH citrate buffer (Vector), tissue microsections were fixed with 2% paraformaldehyde, followed by permeabilization with ice-cold 100% methanol, treated with signal enhancer (Image-iT; Invitrogen) for 30 minutes, blocked with PBS containing 10% goat serum and 2.5% mouse serum (Sigma) for 1 hour at room temperature, and stained with a 1:50 dilution of the primary antibody (TLR9, MSI-1, Sox2, Nestin, GFAP, TuJ1; antibodies were obtained from Abcam; pStat3, Frizzled 4 were purchased from Santa Cruz Biotechnology; pJak2, cleaved caspase-3 antibodies were obtained from Cell Signaling Technology; anti-mouse CD31 was purchased from BD Pharmingen; anti-oligodendrocyte marker O4 was obtained from R&D Systems) in PBS/sera overnight at 4°C. After washing with PBS, secondary antibodies were diluted (1:100) in PBS/sera containing 100 ng/mL Hoechst 33342 (Invitrogen). After final washing with PBS, specimens were mounted with Mowiol (Calbiochem).

Indirect immunofluorescence on cultured cells was carried out as described previously (27). Confocal analysis was performed using a LSM 510 Meta (Zeiss). Intravital multiphoton imaging was performed as previously described (27). Blood vasculature of the brain was stained by systemic injection of 100 µg dextran–rhodamine (Invitrogen); cell apoptosis was visualized by systemically injecting 10 µg Annexin V-FITC (BioVision) diluted in sterile HBSS (Gibco). We used an Ultima 2-photon Microscope for IVPM analysis (Prairie Technologies). Acquired Z-stacks were reconstructed to full 3D view using the Amira software (Visualization Sciences Group).

Noninvasive imaging of luciferase-expressing glioma cells using D-luciferin was performed according to the manufacturer’s instructions (Caliper Life Sciences; PerkinElmer). Bio luminescence given by luciferase activity was acquired using IVIS100 imaging systems and analyzed with Living Image 2.50 (Caliper Life Sciences; PerkinElmer).

Chromatin immunoprecipitation assay

Chromatin immunoprecipitation was performed using a ChIP assay kit (Upstate Biotechnology) according to the manufacturer’s instructions. We performed chromatin immunoprecipitation in cells based on the protocol provided by Upstate Biotechnology. The chromatin was prepared from 5 × 10⁶ cells and subjected to the ChIP assay as previously described (13). Of note, 4 µg of anti-STAT3 rabbit polyclonal antibody or control rabbit IgG was used for immunoprecipitation. The primers 5′-TGAAGCTCAGAGTAAGAATGCT-3′, and 5′-GAGACAGATGACTCAAGAGAC-3′ were used to amplify the mouse Tlr9 promoter fragment (−950 to −740 bp, from the transcription start site) that contained the putative STAT3-binding sites as suggested by the TRANSFAC software.

Limiting dilution assay

Cells were cultured for at least 10 days in sphere forming medium. Before sphere assays, cells were placed into single-cell suspension. Cultures free of clumping and being of >90% viability were used. Cells were serially diluted from 500 to 2 cells per well into 96-well plates as previously described (33). Cells were cultured in DMEM-50–50 supplemented with HEPES (Gibco), B-27 supplement (Life Technologies), Pen-Strep Antibiotics (Life Technologies). Every 3 days, fresh EGF and bFGF (PeproTech) were added. Subsequently, cultures were analyzed for spheres in each well. Data were analyzed using the Extreme Limiting Dilution Algorithm (ELDA; ref. 34).

Statistical analyses

Kaplan–Meier analyses were performed using GraphPad Prism 5. Unless otherwise noted, all statistical comparisons were made by the unpaired two-tailed Student t test and were considered significant if P < 0.05.

Results

**TLR9 is overexpressed in glioma stem cells**

Elevated TLR9 expression has been shown to correlate with poor survival of patients with malignant glioma (30, 31). We, therefore, tested TLR9 expression levels in GSC subpopulations of glioblastoma tumors. Overexpression of TLR9 as well as high expression levels of phospho-STAT3 (pSTAT3) could be found in well-characterized primary, low-passage human GSC-like cells derived from high-grade gliomas (Fig. 1A, and data not shown; refs. 35, 36). Increased TLR9 expression was associated with considerably enhanced expression levels of critical factors favoring GSC maintenance and progeny such as SOX2, Musashi-1 (MSH1), and Nestin. Conversely, low expression of TLR9 was concomitant with reduced expression of SOX2, MSH1, and Nestin in primary human GSCs (Fig. 1B). Using sphere formation assays in vitro for the determination of stem-like cells and to phenocopy patient-derived GSCs (37), TLR9 expression was dramatically increased upon induction of tumor cell spheres (Supplementary Fig. S1). In addition, TLR9 expression was associated with enhanced expression of the CSC markers Sox2, Msi1, and Nestin in human as well as in murine models (Supplementary Fig. S1). Furthermore, TLR9 ligandation with CpG-ODN propagated tumor sphere formation. However, TLR9 silencing diminished the formation of spheres as well as self-renewal capacity as shown by a limited dilution assay (LDA) assessing the potential of tumorigenic repopulation (Supplementary Fig. S2; refs. 33, 34). Interestingly, Stat3 was identified to bind to the Tlr9 promoter upon induction of tumor spheres in vitro. These findings from in vitro models indicate a vital role of TLR9 in GSC maintenance. Moreover, SOX2 and MSH1 glioma subpopulations of glioblastoma multiforme (GBM) tumor tissue sections exhibited considerably increased TLR9 expression accompanied by high pSTAT3 expression as assessed by immunofluorescence staining (Fig. 1C). We further showed by Western blotting that TLR9 expression was elevated in various human GSC lines (Fig. 1D).

**Triggering TLR9 with CpG-ODNs induces Frizzled 4-dependent JAK2 activation**

Our data show that CpG-ODNs activate STAT3 (23). Because JAK2 is a tyrosine kinase contributing to STAT3 activation, we examined whether CpG-ODN could activate JAK2. We treated...
Figure 1. TLR9 is elevated in stem cell–like cells in primary human GBM. A, analysis of pSTAT3 and TLR9 expression in primary human glioma CSC-like cell lines using flow cytometry. B, expression of CSC-associated factors as indicated in TLR9high (red) and TLR9low (black) primary human glioma CSC-like cells analyzed by flow cytometry. GSC008, GSC030, GSC003, GSC024, GSC036, and GSC0117 are various primary human glioma CSC-like cell lines. C, TLR9 and pSTAT3 expression in SOX2+/MSI1+ brain tumor tissue sections. Shown are confocal microscopic images. Scale bar, 50 μm or 20 μm, respectively. D, Western blotting analysis showing TLR9 expression in various primary human glioma CSC lines (081024, 081110, 090127, and JHH 136).
Figure 2. CpG-TLR9 signaling-induced GSCs require Frizzled 4/JAK2 interaction. A, JAK2 is activated in primary human GSC008 cells upon stimulation by various classes of CpG-ODNs (classes A, B, C; D19 is class A). FACS showing pJAK2 levels in the GSCs receiving either indicated CpG-ODNs or IFN-γ. Ectopic IFN-γ stimulation of GSCs was included as a positive control for inducing JAK2 activation. B, FACS analysis showing silencing efficacy by Frizzled 4 siRNA introduced into human GSC-like cells. C, FACS analysis showing expression of activated JAK2 (left) or activated STAT3 (right) in U87 human glioma cells grown as spheres and transiently transfected with Frizzled4 siRNA, stimulated with CpG-ODN as indicated. D, effects of silencing Frizzled 4 (FZD4) on GSC-like cells as phenocopied by sphere formation. U87 human glioma cells were first transfected with indicated siRNAs followed by inducing sphere growth and treatment with CpG-ODN. SD and significance are shown; *; P ≤ 0.05; **; P ≤ 0.01. E, phospho-JAK2 and Frizzled 4 colocalize upon CpG-ODN stimulation in GSC-like cells. (Continued on the following page.)
human primary GSCs with various classes of CpG-ODNs, followed by flow cytometric analysis for JAK2 phosphorylation. Data obtained from these experiments showed that treatment with CpG-ODNs for 24 hours activates JAK2 effectively, which was comparable with the immediate early response induced by IFNγ (Fig. 2A). We next explored the molecular mechanism(s) by which CpG-ODN–TLR9 signaling activates JAK2/STAT3. Because Wnt/Frizzled class receptor 4 (Frizzled 4) signaling is critical for CSC maintenance and has been shown to be important for GSC stemness (38, 39), we hypothesized that CpG/TLR9 signaling may, directly or indirectly, stimulate the Wnt/Frizzled pathway. We showed that silencing Frizzled 4 upon CpG-ODN treatment, and silencing Frizzled 4 with CpG–ODN-induced sphere formation (Fig. 2D). To provide additional evidence that CpG-ODNs induce interaction between pJAK2 localized in the same subcellular domains upon CpG–ODN stimulation (Fig. 2E, top). Furthermore, silencing Frizzled 4 and pJAK2 were colocalized with Frizzled 4 upon CpG–ODN treatment, and silencing Frizzled 4 and pJAK2 were localized in the same subcellular domains upon CpG–ODN stimulation (Fig. 2E, bottom). Furthermore, immunoprecipitation with an anti-Frizzled 4 antibody followed by Western blotting to detect Wnt/Frizzled pathway. We showed that silencing Frizzled 4 upon CpG-ODN treatment, and silencing Frizzled 4 with CpG–ODN induced sphere formation (Fig. 2D). To provide additional evidence that CpG-ODNs induce interaction between pJAK2 and pSTAT3 and pSTAT3–induced sphere formation (Fig. 2D). To provide additional evidence that CpG-ODNs induce interaction between pJAK2 colocalized with Frizzled 4 upon CpG–ODN treatment, and silencing Frizzled 4 and pJAK2 were colocalized in the same subcellular domains upon CpG–ODN stimulation (Fig. 2E, top). Interestingly, Frizzled 4 and pJAK2 were localized in the same subcellular domains upon CpG–ODN stimulation (Fig. 2E, bottom). Furthermore, immunoprecipitation with an anti-Frizzled 4 antibody followed by Western blotting to detect JAK2 showed that JAK2 and Frizzled 4 were in the same complex upon CpG–ODN stimulation (Fig. 2F).

**CpG–STAT3siRNA inhibits human GSC-like cells and human glioblastoma growth**

We next investigated whether a human version of CpG–STAT3siRNA (35, 36) diminishes the GSC phenotype in GBM. To assess whether undifferentiated populations can be pushed toward differentiation, human primary GSCs (35, 36) were treated in vitro with CpG–ODN or CpG–STAT3siRNA and analyzed via confocal microscopy for expression of cell differentiation markers. Upon treatment with CpG–STAT3siRNA, the cell differentiation markers O4, GFAP, and TuJ1 were substantially increased compared with those of CpG–ODN and non–treated controls. Interestingly, primary human GSCs treated with CpG–ODN reduced O4 expression (Fig. 3A and B). Moreover, whereas CpG–ODN treatment stimulated tumor sphere growth (Fig. 3A, middle), administration of CpG–STAT3siRNA resulted in disruption of tumor sphere integrity (Fig. 3A, right).

TLR9 is necessary to maintain murine GSC-like phenotype (Supplementary Fig. S2). To determine whether STAT3 is necessary for maintaining human GSC phenotype, primary human GSCs were treated with CpG–STAT3siRNA and placed into a LDA to determine the frequency of CSCs within a tumor cell population (33, 34, 41). Treatment of primary human GSCs with CpG–STAT3siRNA resulted in a significant decrease in the ability of GSC populations to form sphere cultures upon extreme dilution of cells plated, suggesting a reduction in GSC frequency upon treatment (Fig. 3C). We further assessed the effects of CpG–STAT3siRNA on expression of an enzymatic CSC marker, aldehyde dehydrogenase 1 (ALDH1). Using a fluorescent substrate of ALDH1, bodipy–aminocetate, a substantial decrease in ALDH1+ cells was observed upon introduction of CpG–STAT3siRNA as analyzed in two different primary human GSC lines (Fig. 3D).

We next determined the effects of in vivo treatment with CpG–STAT3siRNA of primary human glioma cells enriched for the GSC phenotype ex vivo before engraftment. Primary human GSCs were implanted in immunodeficient (NSG) mice to form tumors. Treatment with CpG–STAT3siRNA resulted in a significant delay in tumor growth compared with the nontreated and CpG–ODN–treated controls (Fig. 3E). When analyzed for inhibition of pSTAT3 via confocal microscopy, pSTAT3 levels were considerably decreased in CpG–STAT3siRNA–treated human GSC primary cells when compared with CpG–ODN–treated and nontreated controls (Fig. 3F, top). Furthermore, tumor apoptosis was increased, as shown by enhanced cleaved caspase-3 expression (Fig. 3F, middle), and proliferative activity indicated by Ki67 was significantly decreased in the CpG–STAT3siRNA–treated cells compared with controls (Fig. 3F, bottom). These data indicate a significant therapeutic effect on glioblastoma highly enriched with GSC-like cells when treated with CpG–STAT3siRNA in vivo. Because the siRNA in the conjugate is against human STAT3, and the mice used in the experiments are severely immune-deficient, the antitumor effects observed are likely due to direct effects on the human glioblastoma/GSC-like cells in vivo, which are also supported by results generated in vitro (Fig. 3A–D). Moreover, the antitumoral efficacy of CpG–Stat3siRNA could be validated in rodent models (Supplementary Fig. S3), and a significantly reduced expression of factors involved in GSC maintenance, such as Sox2 and SSEA1, could be confirmed in mouse tumors when mice were treated with CpG–Stat3siRNA (Supplementary Fig. S4).

**Systemic delivery of CpG–Stat3siRNA targets GSC in orthotopic brain tumor**

Local treatments with CpG–Stat3siRNA of subcutaneous glioma resulted in inhibition of tumor growth and Stat3 activity, induction of tumor cell apoptosis, as well as prolonged survival (Supplementary Fig. S3). The local treatment also decreased expression of CSC-associated factors (Supplementary Fig. S4). However, the blood–brain barrier represents a major obstacle for therapeutic intervention for brain tumors. After systemic injection, fluorescently labeled CpG–Stat3siRNA could be found in an intact, tumor-free brain as fast as 2 hours after administration (Fig. 4A), and appeared to internalize into cells (Fig. 4B). Systemically treating mice bearing luciferase-expressing
Figure 3. Inhibitory effects of CpG-STAT3siRNA on primary human GSCs. A, CpG-STAT3siRNA induces expression of differentiation markers. Confocal microscopic images show expression of differentiation markers O4, GFAP, and Tuj1 as well as changes in morphology of primary human GSC-like cells. Scale bar, 20 μm. B, flow cytometric analyses showing expression levels of differentiation markers O4 and GFAP in primary human GSC-like cells upon treatment with CpG-STAT3siRNA, CpG-ODN, or vehicle control as indicated. C, impact of CpG-STAT3siRNA on human primary GSC-like cells using LDAs. LDA shows effect of CpG-STAT3siRNA on frequency of primary human GSC-like cells. CpG-ODN and vehicle treatments were included as controls. D, flow cytometric analyses to detect ALDH1 activity in primary human GSC-like cells treated with CpG-STAT3siRNA, CpG-ODN, or vehicle control as indicated. E, CpG-STAT3siRNA treatments significantly inhibit growth of human glioma enriched with primary human GSC-like cells. Primary human GSC-like cells, GSC030, were engrafted in immunocompromised (NSG) mice. Tumor-bearing mice were treated locally with CpG-STAT3siRNA, CpG-ODN, or vehicle control as indicated and tumor growth kinetics was monitored. (Continued on the following page.)
tumors with CpG-luciferase-siRNA also showed that the CpG-siRNA could pass the blood–brain barrier to reach the tumor (Supplementary Fig. S5). Furthermore, systemic CpG-Stat3-siRNA–treated mice had a significantly prolonged survival compared with the control groups (Fig. 4C). A concomitant decrease in Stat3 activity and TLR9 expression, compared with CpG-scrambled-RNA treatments, was observed (Fig. 4D). Moreover, systemic treatments of orthotopically engrafted brain tumors with CpG-Stat3siRNA drastically reduced the expression of Nestin, Msi1, as well as pStat3 (Fig. 4E).

Discussion

Our current study identifies TLR9 as a key functional marker for glioma cancer stem–like cells. The role of TLR9 is mostly characterized in immune cells and linked to inflammation (21, 42–44). Although CpG-TLR9 stimulation in immune cells leads to the activation of antitumor immune responses, STAT3 also acts as a brake/checkpoint for this pathway in the immune cells, constraining antitumor immunity (23). The ligands of TLR9, CpG-ODNs, have been extensively studied in animal models and in clinical trials as cancer immunotherapeutics (25, 29). However, evidence has been accumulating that TLR9 can be elevated in tumors and associated with cancer progression (30, 31). Our results suggest that TLR9, an important inflammatory signaling molecule, is crucial for CSC development/maintenance in malignant glioma. Furthermore, CpG-TLR9 and Stat3 form a feed-forward loop in GSCs: CpG-TLR9 activates Stat3, whereas activated Stat3 upregulates TLR9 expression. These results provide a possible molecular explanation about why TLR9 upregulation correlates with poor survival of some patients with cancer, including patients with GBM (30, 31).

STAT3 has been demonstrated extensively to be a crucial transcription factor for the development and maintenance of stem cells and CSCs (45–47). Recently, a role of JAK2 as a target to induce cell-cycle arrest and apoptosis of GSCs has also been indicated (17). Although in immune cells CpG-ODN is known to induce STAT3 (23), the detailed mechanisms underlying CpG-induced STAT3 activation remain to be further explored. A role of Wnt/Frizzled signaling in stem cells/CSCs is evident, and Frizzled 4 has been shown to be important for GSCs (38, 39, 48). Our current studies suggest that CpG-TLR9 signaling induces JAK2 activation in a Frizzled 4–dependent manner, and that activated JAK2 and Frizzled 4 form a complex as demonstrated by coimmunoprecipitation/Western blotting. At this time, how CpG-ODN induces Frizzled 4 expression remains to be demonstrated. However, a role of STAT3 in upregulating expression of Wnt is known (49), suggesting that induction of Frizzled 4 by CpG/TLR9 could be through a STAT3/Wnt connection. Although more mechanistic studies are required to fully understand how CpG-TLR9 signaling supports GSCs, our current studies provide evidence that JAK2 and Frizzled 4 interact, and that Frizzled 4 plays an important role in JAK2-STAT3 activation in glioma stem cells induced by CpG/TLR9.

Several excellent molecular targets to inhibit GSCs have been shown (5, 6, 18). At the same time, broadly targeting...
STAT3 and other GSC targets in patients may cause undesirable effects. Identifying TLR9 as a critical functional marker for GSCs allows the use of the CpG-siRNA technology to more specifically target malignant glioma. First of all, CpG-siRNA is uptaken by immune cells of myeloid origin, such as microglia, in the GBM tumor microenvironment. By silencing STAT3, CpG-STAT3siRNA should reduce tumor-induced immunosuppression and boost antitumor immune responses triggered by CpG-ODN (23, 27, 28). Second, because malignant glioma cells, especially glioma stem cells, display elevated TLR9 expression, CpG-STAT3siRNA can be efficiently internalized by GSCs. When STAT3 is silenced, tumor growth and the GSC-like population are reduced. The experiments done in immune-decient mice using human STAT3-siRNA further show that in the absence of immune responses and other effects from the tumor microenvironment, CpG-STAT3siRNA reduces human stem-like glioblastoma cells. The current study indicates that CpG-siRNA can also pass the blood–brain barrier. Our studies, therefore, provide the proof-of-principle evidence that supports clinical use of CpG-siRNA technology.

Figure 4. Systemic delivery of CpG-STAT3siRNA targets GSCs. A, fluorescently labeled CpG-STAT3siRNA (green) passing the blood–brain barrier (BBB) 2 hours after systemic administration. Ex vivo multiphoton imaging shows CpG-STAT3siRNA in brains of tumor-free mice. Scale bar, 100 μm. B, distribution of fluorescently labeled CpG-STAT3siRNA (green) relative to BBB shown by 3D rendering of ex vivo acquired image z-stack. Dimensions are indicated. C, Kaplan–Meier plot showing survival of DBT brain tumor–bearing C57BL/6 mice systemically treated with CpG-STAT3siRNA, CpG-ODN, or left untreated. Significance is shown: **, P < 0.01; ***, P < 0.001. D, confocal microscopic analyses indicating protein expression levels of pStat3 and TLR9 in GL261 mouse brain tumor upon indicated treatments. Scale bar, 100 μm. E, confocal microscopic images showing levels of pStat3 in Nestin+ and Msi1+ areas of orthotopically implanted GL261 mouse brain tumors. Treatments are as indicated. Scale bars, 50 μm (top) and 10 μm (bottom). Right, mean fluorescent intensity per field of view (FOV) quantified; SD and significance shown (n = 5; ***, P < 0.001).
CpG-STAT3siRNA for treating malignant glioma. Because CpG-STAT3siRNA also modulates the tumor immunologic environment to favor antitumor immune responses, combinatorial therapy with CpG-STAT3siRNA and immunotherapies such as T-cell therapy can be highly desirable.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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