Downregulation of miR-452 Promotes Stem-Like Traits and Tumorigenicity of Gliomas

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Abstract

Purpose: miR-452 is reported to be required for neural crest stem cell differentiation during neural crest development. However, the biologic role of miR-452 in gliomas remains unclear. The aim of the present study was to evaluate the effect of miR-452 on the stem-like properties and tumorigenesis of glioma cells.

Experimental Design: The expression of miR-452 was examined in glioma cells and glioma tissues using real-time PCR. The effects of miR-452 on stem-like traits and tumorigenesis were investigated in vitro and in vivo using patient-derived glioma cells and glioma cell lines. Western blotting and luciferase reporter assays were conducted to examine the negative regulation of Bmi-1, LEF1, and TCF4 by miR-452. The methylation of the miR-452 promoter region was examined by bisulfite genomic sequencing PCR.

Results: miR-452 was markedly downregulated in glioma cells and clinical glioma tissues. miR-452 levels were inversely correlated with World Health Organization (WHO) grades and patient survival. miR-452 directly targeted and suppressed multiple stemness regulators, including Bmi-1, LEF1, and TCF4, resulting in reduced stem-like traits and tumorigenesis of glioma cells in vitro and in vivo. Furthermore, we showed that downregulation of miR-452 in gliomas was caused by hypermethylation of its promoter region.

Conclusions: Downregulation of miR-452 plays an important role in promoting the stem-like traits and tumorigenesis of gliomas and may represent a novel prognostic biomarker and therapeutic target for the disease. Clin Cancer Res; 19(13); 3429–38. ©2013 AACR.

Introduction

Gliomas, one of the most lethal malignant tumors of the central nervous system, have been classified into four grades (I–IV) as a means of reflecting their anticipated biologic behavior (1). More than half of all gliomas are glioblastoma multiforme (grade IV astrocytoma; ref. 2). Despite modern surgical and medical treatments, the prognosis of gliomas remains very poor, with the median survival time for patients with glioblastoma being only 14.6 months (3). Glioblastoma shows a significantly similar gene expression signature and cell phenotype to those of embryonic stem cells, whereas other glioma types show a lower degree of similarity corresponding to their lower grades (4). This suggests that molecular regulators of stem cell function might be implicated in cancer aggressiveness and poor patient survival. Therefore, understanding the precise molecular mechanisms underlying the stem cell–like properties of cancer cells could provide new insights into the pathogenesis of gliomas and lead to more effective anticancer therapeutic strategies.

The molecular pathways controlling the function of stem cells, such as the Bmi-1 and Wnt/β-catenin pathways, have been shown to play important roles in tumor progression (5, 6). For instance, Bmi-1 is essential for the “stemness” of both normal stem cells and cancer stem cells, such as leukemias, gliomas, and hepatocellular carcinoma (7–10). Abdouh and colleagues reported that Bmi-1 maintains glioma stem-like cells in an undifferentiated state, and that knockdown of Bmi-1 induces glioma cell differentiation and prevents tumor formation in xenografts (9). Similarly, the Wnt/β-catenin signaling pathway has been shown to be important for the regulation of the stemness properties and tumorigenicity of glioma cells (11). Silencing β-catenin in FoxM1-overexpressing glioma cells diminishes neurosphere formation and tumor initiation, indicating that Wnt/β-catenin signaling is required for the FoxM1-mediated stem-like phenotype of gliomas (12).

MicroRNAs (miRNA) are small, noncoding RNAs that have recently emerged as important molecules involved in...
transcriptional gene regulation (13). Multiple miRNAs have been reported to play critical roles in the stem-like traits and aggressiveness of cancers (14–16). Overexpression of miR-124 can reduce neuron formation, CD133+ subpopulation, and glioma cell tumorigenicity and invasion (16). Interestingly, the miRNA expression profiles of gliomas are similar to those of neural precursor cells (17), suggesting that the miRNAs involved in stemness regulation may also contribute to glioma pathogenesis.

It has been reported that miR-452 is required for the differentiation of neural crest stem cell–derived tissues, and miR-452 knockdown during neural crest development leads to craniofacial defects (18). Here, we report that miR-452 is downregulated in human gliomas, especially high-grade, undifferentiated gliomas. We find that upregulation of miR-452 suppresses glioma stem-like traits and tumorigenesis, both in vitro and in vivo, through inhibition of multiple stemness regulators, including Bmi-1, LEF1, and TCF4. These results uncover a novel regulatory mechanism underlying the stem-like properties of glioma cells.

Materials and Methods

Cell lines and primary cultured tumor cells

Primary normal human astrocytes (NHA) were purchased from ScienCell Research Laboratories and cultured according to the manufacturer’s instructions. Fresh brain tumor tissues obtained from the First Affiliated Hospital of Sun Yat-sen University were collected and processed within 30 minutes after resection. Primary cultured tumor cells were obtained after mechanical dissociation as previously described (19). Glioma cell lines U87MG, A172, U251MG, LN-340, LN-464, LN-428, LN-18, U118MG, U138MG, LN-443, D247MG, and LN-229 were provided by Dr. Shi-Yuan Cheng’s laboratory at Northwestern University (Chicago, IL), and cultured in Dulbecco’s Modified Eagle Medium supplemented with 10% FBS (HyClone). All cell lines were authenticated by short tandem repeat fingerprinting at IDEXX RADIL or Services at Sun Yat-sen University Forensic Medicine Lab (Guangzhou, China).

Plasmids, virus production, and infection of target cells

The human miR-452 precursor with 500-bp genomic flanking sequences on each side was amplified by PCR from genomic DNA and cloned into a retroviral pMSCV-puro vector. Human Bmi-1, LEF1, and TCF4 open reading frames were amplified by PCR and were cloned into the pMSCV-neo vector (Clontech). The 3′-untranslated regions (3′UTR) of the human Bmi-1, LEF1, and TCF4 genes, generated by PCR amplification from NHA, were cloned into a modified pGL3 luciferase reporter plasmid (Promega). The point mutations in the tentative miR-452-binding seed regions in the 3′UTRs of the Bmi-1, LEF1, and TCF4 genes were created using the QuickChange Mutagenesis kit (Stratagene). pTOP-Flash and pFOP-Flash plasmids were used to determine β-catenin transcriptional activity. miR-452 mimics and negative control oligonucleotides were purchased from Ribobio Tech. Transfection of plasmids or oligonucleotides was carried out using the Lipofectamine 2000 reagent (Invitrogen) according to the manufacturer’s instructions. Stable cell lines expressing miR-452 and vector were generated via retroviral infection using HEK293T cells, as previously described (20), and selected with 0.5 μg/mL puromycin for 10 days. The primers used for plasmid construction are listed in Supplementary Materials and Methods.

Tissue specimens and patient information

Eighty-eight paraffin-embedded, archived clinical glioma specimens, including World Health Organization (WHO) grade I–IV tumors and freshly snap-frozen glioma tissues, were histopathologically diagnosed at the First Affiliated Hospital of Sun Yat-sen University from 2000 to 2010. The clinical information related to the samples has been summarized in Supplementary Table S1. Normal brain tissues were obtained from individuals who died in traffic accidents and confirmed to be free of any preexisting pathologically detectable conditions. Consent from patients and approval from the Institutional Research Ethics Committee were obtained for the use of these clinical materials for research purposes.

Western blotting analysis

Western blotting was conducted as previously described (20) using anti-Bmi-1 (Millipore), anti-TCF4, and anti-LEF1 (Cell Signaling Technology) antibodies. The blotted membranes were stripped and reprobed with an anti-β-tubulin antibody (Sigma).

Intracranial brain tumor xenografts: immunohistochemical and hematoxylin and eosin staining

Indicated glioma cells were stereotactically implanted into the brains of individual mice (n = 5 per group). One
miR-452 Functions as Tumor Suppressor in Gliomas

miR-452 downregulation in gliomas correlates with improved patient prognosis

To investigate the biologic role of miR-452 in the stem-like traits and aggressiveness of gliomas, we first examined miR-452 expression in glioma cells and clinical glioma tissues. The expression of miR-452 was differentially reduced in all 12 glioma cell lines and 2 patient-derived glioma cells (PDGC) compared with that in NHA, and in 13 glioma samples compared with that in normal brain tissues (n = 3), indicating that miR-452 is downregulated in gliomas (Fig. 1A and B).

The expression of miR-452 was further examined in 88 clinical glioma samples. Statistical analysis revealed that miR-452 expression was inversely correlated with the WHO histologic grade (P = 0.018) and patient survival (P = 0.008; Fig. 1C and Supplementary Table S2). Kaplan–Meier analysis and log-rank test revealed that decreased miR-452 expression was correlated with shorter patient survival time (P < 0.001; Fig. 1D and Supplementary Fig. S1).

Importantly, univariate and multivariate analyses revealed that miR-452 expression (P < 0.001) and WHO histologic grade (P < 0.001) were each recognized as an independent prognostic factor for patients with glioma (Supplementary Table S3). Furthermore, through analyzing The Cancer Genome Atlas (TCGA) database, we also found that decreased miR-452 expression was correlated with shorter glioblastoma patient survival time (n = 478, P = 0.0198; Fig. 1E), and that miR-452 expression (P = 0.045) was an independent prognostic factor for patients with glioblastoma (Supplementary Tables S4 and S5). Taken together, these data suggest that miR-452 downregulation might represent a useful independent biomarker for the prognosis of patients with gliomas.

Upregulation of miR-452 reduces glioma cell stem-like traits

To examine the effect of miR-452 dysregulation on glioma stem-like traits, 2 PDGCs and U87MG and LN443 glioma cell lines stably overexpressing miR-452 were established (Fig. 2A and Supplementary Fig. S2A). As shown in Fig. 2B and Supplementary Fig. S2B, overexpression of miR-452 markedly reduced the proportion of side population cells in all 4 glioma cells. However, the proportion of side population cells was increased in glioma cells transfected with a miR-452 inhibitor (Supplementary Fig. S2C). The expression of miR-452 in side population cells was shown to be lower than that in non-side population cells (data not shown). Meanwhile, miR-452 overexpression significantly reduced the mRNA-expression levels of multiple pluripotency factors, including ABCG2, KLF4, SOX2, OCT4, NANOG, and c-Myc (Fig. 2C and Supplementary Fig. S2D; ref. 21). Furthermore, a neurosphere assay showed that miR-452–transduced cells formed smaller and fewer neurospheres than vector controls (Fig. 2D and Supplementary Fig. S2E). To test whether miR-452 is involved in glioma differentiation, the neurospheres formed by miR-452- and vector-transduced cells were cultured under differentiating conditions with 5% serum. Immunofluorescence analysis revealed that overexpression of miR-452 led to decreased Nestin (a neural stem cell marker) expression and increased GFAP (an astrocyte marker) compared with vector controls, indicating that miR-452 induces the differentiation of glioma stem-like cells (Fig. 2E and Supplementary Fig. S2F). Collectively, our results suggest that miR-452 overexpression reduces the stem-like traits of glioma cells.
UTRs of Bmi-1, LEF1, and TCF4, but failed to reduce the luciferase activities of the mutated 3' UTRs of these transcripts (Fig. 3C and Supplementary Fig. S3B). However, the inhibitory effects of miR-452 on the expressions of Bmi-1, LEF1, and TCF4 and luciferase reporter activities were abrogated by miR-452 inhibition (Supplementary Fig. S3C and S3D). Furthermore, miRNP IP analysis revealed that miR-452 was specifically associated with the 3' UTRs of Bmi-1, LEF1, and TCF4, but not with GAPDH (Fig. 3D and Supplementary Fig. S3E), thus providing additional evidence that miR-452 directly targets the 3' UTRs of Bmi-1, LEF1, and TCF4. Importantly, restoration of Bmi-1, LEF1, or TCF4 expression partially, but significantly, rescued the proportion of side population cells in miR-452–transduced cells, indicating that Bmi-1, LEF1, and TCF4 genes are regulatory targets that contributed to miR-452 downregulation mediated-glioma stem–like traits (Fig. 3E).

Notably, miR-452 levels in 9 freshly collected clinical glioma samples were inversely correlated with the expressions of Bmi-1 (r = −0.867; P = 0.002), LEF1 (r = −0.767; P = 0.016), and TCF4 (r = −0.817; P = 0.007), further confirming the inhibitory effects of miR-452 on Bmi-1, LEF1, and TCF4 in gliomas (Fig. 4A and B).

Upregulation of miR-452 decreases tumorigenesis of glioma cells in vivo

To determine the role of miR-452 in modulating glioma tumorigenesis in vivo, we stereotactically implanted miR-452- or vector-transduced PDGCs into the brains of nude mice. As shown in Fig. 5A and Supplementary Table S6, miR-452–transduced cells formed much smaller tumors and displayed lower tumorigenicity, showing that miR-452 overexpression reduces PDGC tumorigenesis in vivo. Kaplan–Meier analysis revealed that mice implanted with miR-452–transduced cells survived significantly longer than control mice (Fig. 5B). Immunohistochemical (IHC) analysis showed that intracranial tumors formed by miR-452–transduced PDGCs had fewer Nestin-positive tumor cells and more GFAP-expressing cells than the control tumors (Fig. 5C). Consistently, these results suggest that...

Figure 1. Reduced miR-452 expression in gliomas is correlated with poor prognosis. A and B, real-time PCR analysis of miR-452 expression in 12 indicated glioma cell lines, 2 PDGCs, and NHA (A), and in 13 glioma tissues and 3 normal brain tissues (B). Transcript levels were normalized to U6 expression. C, statistical analysis of miR-452 expression in normal brain tissues (n = 3) and glioma specimens of different WHO grades (n = 88). D, Kaplan–Meier curves of glioma patients with low- versus high-expression of miR-452 (n = 88; P < 0.001). E, Kaplan–Meier curves of glioblastoma patients with low- versus high-expression of miR-452 in TCGA datasets (n = 478; P = 0.0198). Error bars represent the mean ± SD of three independent experiments. * P < 0.05.
miR-452 overexpression also inhibits the tumorigenicity of U87MG glioma cells in vivo (Supplementary Fig. S5A–S5C).

miR-452 is downregulated by promoter hypermethylation

The miR-452 coding sequence is located in the intron of the GABRE gene at Xq28. In agreement with a previous study (22), we found that miR-452 expression was correlated with GABRE mRNA expression in glioma cell lines (P = 0.003) and glioma tissues (P = 0.001; Fig. 6A and B), suggesting that miR-452 is likely to be cotranscribed with GABRE mRNA. Promoter methylation has been reported to control GABRE expression in gastric cancer and uterine leiomyoma (23, 24). Therefore, we investigated whether the reduced miR-452 in gliomas was a result of promoter hypermethylation. Analysis of the GABRE promoter region using the UCSC genome browser (http://genome.ucsc.edu/) indicated a CpG island located between −404 bp and +470 bp, relative to the transcription start site (Fig. 6C). Furthermore, bisulfite genomic sequencing PCR (BSP) showed that the CpG island within the GABRE promoter was hypermethylated in glioma cell lines and PDGCs, but not in NHA (Fig. 6D). Moreover, we found that miR-452 expression was significantly increased in glioma cell lines and PDGC treatment with the methylase inhibitor 5-aza-dC, but not in NHA (Fig. 6E). Consistent with the data from cultured glioma cells, the CpG island in the GABRE promoter was also found to be hypermethylated in clinical glioma samples (n = 25), but not in normal brain tissue (n = 5; Fig. 6F). These results indicate that the reduced miR-452 expression in gliomas is attributable to promoter hypermethylation.

Discussion

This study establishes an important role of miR-452 in the inhibition of glioma tumorigenesis. We find that overexpression of miR-452 directly suppresses the expressions of Bmi-1, LEF1, and TCF4 in glioma cells, attenuates glioma stem-like phenotypes in vitro, and inhibits glioma tumorigenesis in the brains of animals. Conversely, inhibition of miR-452 induces expression of the above-mentioned stemness regulators. Furthermore, we show that the expression levels of miR-452 are decreased in clinical glioma samples via promoter hypermethylation. Taken together, our results reveal a novel mechanism by which miR-452 regulates glioma stem-like phenotypes through modulation of multiple stemness regulators, suggesting that miR-452 might function as a tumor-suppressive miRNA in human gliomas.

A better understanding of the critical pathways involved in stem-like traits is important for identifying new molecular targets for eradicating gliomas. Bmi-1, a component of the polycomb repressor complex, is reported to be essential for the proliferation and self-renewal of leukemic and hematopoietic stem-like cells through binding to trimethylated H3K27 in the CDKN2A promoter and repressing the expression of p16INK4A and p19ARF (10, 25, 26). However,
it has been also reported that Bmi-1 is highly expressed in
gliomas and promotes glioma stem-like cell proliferation
and undifferentiation in a p16INK4A/p19ARF-independent
manner (27, 28). Furthermore, the constitutive
activation of the Wnt/β-catenin pathway has been shown
to lead to reprogramming and generating a stem-like
phenotype in gliomas through the activation of several
downstream genes, including c-Myc, NANOG, OCT4, and

**Figure 3.** miR-452 directly downregulates multiple stemness regulators. A, predicted miR-452 target sequences in the Bmi-1 3' UTR, LEF1 3' UTR, and TCF4 3' UTR and mutants containing 2 mutated nucleotides in 3' UTR of these transcripts. B, Western blotting analysis of the expressions of Bmi-1, LEF1, and TCF4 in the indicated cells. α-Tubulin was used as a loading control. C, luciferase activities of reporters containing the 3' UTRs or mutated 3' UTRs of Bmi-1, LEF1, and TCF4 in the indicated cells transfected with negative control (NC) or miR-452 mimic. D, top, miRNP IP assay showing the association of miR-452 with Bmi-1, LEF1, and TCF4. GAPDH was used as a negative control, and 5S rRNA was used as a control for overall expression levels. Bottom, Western blotting analysis of HA-Ago1. E, top, restoration of Bmi-1, LEF1, and TCF4 expression partially, but significantly, rescued the proportion of side population cells in miR-452-transduced cells. Bottom, Western blotting analysis of Bmi-1, LEF1, and TCF4 protein expression in the indicated cells. α-Tubulin was used as a loading control. Error bars represent the mean ± SD of three independent experiments. *P < 0.05.
SOX2 (11, 12, 29–31). As both the Bmi-1 and Wnt/β-catenin pathways are critical regulators of stemness, inhibition of these 2 pathways would significantly reduce the stem-like properties of gliomas. Here, we found that miR-452 could directly target and suppress the expressions of Bmi-1, LEF1, and TCF4 and, thereby, reduce
neurosphere formation and decrease the proportion of side population cells. Therefore, our data reveal a novel role of miR-452 downregulation in glioma tumorigenesis through the modulation of glioma stem-like traits. Previously, Fang and colleagues have reported that miR-452 could be downregulated by the stem cell transcription factor SOX2 in glioblastoma (32). In the current study, we found that the expression levels of multiple stem cell factors, including SOX2, were significantly decreased in miR-452-overexpressing glioma cells. Meanwhile, we showed that miR-452 was markedly reduced in gliomas and that the downregulation of miR-452 in gliomas cells was caused by hypermethylation of its promoter region. Thus, integrating results from previous study with our results suggests that there may be a feedback loop in the expressions of miR-452 and SOX2.

Epigenetic modifications, such as DNA promoter methylation, have been shown to play crucial roles in the regulation of gene expression in various physiologic and pathologic processes (33). During development and carcinogenesis, hypermethylation of tumor-suppressor genes and hypomethylation of the CpG islands in oncogenes regulate a number of vital cellular processes. Aberrant site-specific DNA methylation is, therefore, a potentially useful biomarker for detecting cancer and predicting patient survival (34). Emerging evidence also strongly suggests that DNA methylation could lead to dysregulation of miRNAs in cancer (35). The role of miR-452 during development has
been established. miR-452 is essential for the proper development of neural crest cell-derived tissues through regulating an epithelial–mesenchymal signaling cascade by directly targeting Wnt5a in the neural crest cell-derived mesenchyme (18). Moreover, treatment of mouse embryos with the demethylating agent 5-aza-dC resulted in inhibition of development from morula to blastocyst and downregulation of miR-452 (36). These data not only indicate that miR-452 plays a role in cell differentiation during development but also indicate that miR-452 expression is tightly regulated through the methylation of its gene. Herein, we show that treatment of PDGFCs and glioma cells with 5-aza-dC significantly increased miR-452 expression, and the CpG island in the miR-452 promoter was hypermethylated in glioma cells and clinical glioma samples. Importantly, reduced miR-452 levels were significantly correlated with the WHO grades and overall survival of patients with glioma. Thus, our data strongly suggest that miR-452 promoter methylation could be a potential predictor of glioma progression and patient survival.

It has been reported that miR-452 is downregulated in human breast cancer (37). Our result is consistent with this observation. We found that miR-452 was significantly downregulated in glioma cell lines and human primary glioma tissues when compared with that in NHA and normal brain tissues. However, miR-452 has been found to be upregulated in hepatocellular carcinomas (38) and lymph node–positive urothelial carcinomas (39), suggesting that miR-452 could have a tumor-promoting role in distinct types of human cancers. This signifies an important issue that the biologic activities of miRNAs could be determined by the distinct context in various microenvironments. Indeed, accumulating evidence shows that an individual miRNA could have diverse functions under different cellular contexts, likely depending on the availability of specific targets or downstream effectors (40, 41). Nonetheless, our results reveal an important role of miR-452 in inhibiting glioma tumorigenesis, thereby providing new mechanistic insights that could establish miR-452 as a novel and potentially useful biomarker for the prognosis of patients with gliomas. Recently, Kim and colleagues selected 121 miRNAs, including miR-452, to identify clinically and genetically distinct glioblastoma subclasses, and they found that miR-452 had relatively high expression in the "neuro-mesenchymal precursors" subset but had relatively low expression in the "neural," "oligoneural," "astrocytic," and "radial glial" subsets (42). Thus, it is important to further investigate the effect of miR-452 in organizing and maintaining the phenotypic and molecular architecture of glioblastoma subsets.

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

Authors’ Contributions
Conception and design: L. Song
Development of methodology: L. Liu
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): L. Liu, K. Chen, J. Wu
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): K. Chen, J. Wu, L. Shi, B. Hu, S.Y. Cheng, M. Li
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