

Over-expression of Gai3 in human glioma is required for Akt-mTOR activation and cell growth

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ABSTRACT

We have previously identified a unique function of G protein α inhibitory subunit (Gai protein) in transducing Akt-mTOR signaling. Here, we examined the expression and biological functions of Gai protein 3 (Gai3) in human glioma. As compared to the normal brain tissues, mRNA and protein expressions of Gai3 were significantly upregulated in multiple human glioma tissues. Its expression level was associated with receptor tyrosine kinases (RTKs, including EGFR, FGFR and PDGFR α) over-expression and Akt-mTOR hyperactivity. Gai3 formed a complex with above RTKs and the adaptor protein Gab1 in glioma tissues and cells, which was required for downstream Akt-mTOR activation. Gai3 shRNA knockdown or dominant negative mutation largely attenuated Akt-mTOR activation and glioma cell growth. Further, Gai3-knockout (KO) mouse embryonic fibroblasts (MEFs) showed decreased Akt activation and cell growth. Reversely, introduction of a constitutively-active Gai3 in glioma cells enhanced Akt-mTOR activation and cell growth. *In vivo*, Gai3 shRNA-expressing U87MG tumors grew slower than the control shRNA-bearing U87MG tumors in nude mice. Akt-mTOR activation was also inhibited in U87MG tumors with Gai3 shRNA. Collectively, these results indicate that over-expressed Gai3 forms a complex with several RTKs in human glioma to transduce Akt-mTOR activation and tumor cell growth.

INTRODUCTION

Glioma is a main contributor of cancer-related death around the world [1–3]. The prognosis for high-grade glioma (grade III-IV) has been extremely poor [1–3]. Postoperative radiation and temozolomide (TMZ) chemotherapy have become the standard treatments for glioma [4–6]. Yet, the overall survival has not been significantly improved over the years [4–6].

Akt-mammalian target of rapamycin (mTOR) signaling is frequently dysregulated and hyper-activated in glioma, which promotes tumorigenesis, progression and chemoresistance [7–9]. Existing evidences have suggested

that over-expressed and/or constitutively-active receptor tyrosine kinases (RTKs) cause Akt-mTOR over-activation in the glioma [10, 11]. These RTKs, including EGFR (epidermal growth factor receptor), FGFR (fibroblast growth factor receptor) and PDGFR α (platelet-derived growth factor receptor α), along with their downstream Akt-mTOR signalings are thus valuable oncotargets for glioma [11].

G protein α inhibitory subunit (Gai protein) was originally identified by its ability to couple with GPCRs (G-protein coupled receptors) and to inhibit adenylate cyclase (AC) [12]. Intriguingly, our group [13, 14] and others [15] have identified an un-anticipated function of

Gai protein in transducing Akt-mTOR signaling by several RTKs. For example, Gai protein was required for the activation of Akt-mTOR signaling by EGFR and FGFR ligands [13, 14]. Following ligand binding, Gai protein physically associates with RTK to activate the adaptor protein Gab1 (growth factor receptor binding 2 [Grb2]-associated binding protein 1) and downstream Akt-mTOR signaling [13, 14].

Having found the requirement of Gai protein in RTK-activated Akt-mTORC1 signaling, we here examined the expression and biological functions of Gai3 in human glioma cells and tissues. Our results indicate that over-expressed Gai3 forms a complex with several RTKs in human glioma to transduce Akt-mTOR activation.

RESULTS

Gai3 over-expression is associated with RTK upregulation and Akt-mTOR hyperactivity in human glioma tissues

First, we examined Gai3 expression in human glioma tissues. As described, a total of twelve pairs of glioma tissues (“T”) and surrounding normal brain tissues (“N”) were collected. Real-time quantitative PCR assay

was performed to examine Gai3 mRNA expression. As demonstrated in Figure 1A and 1B, Gai3 mRNA expression level in glioma tissues was 3–4 times higher than that in normal brain tissues. Intriguingly, we didn’t detect a significant difference in Gai3 mRNA level between low-grade (grade I–II, Figure 1A) and high grade (grade III–IV, Figure 1B) tumors. Western blotting assay was performed to test Gai3 protein expression in above tissues. As compared to the surrounding brain tissues, Gai3 protein in glioma tissues was again upregulated (see quantified results in Figure 1C and 1D). Once again, Gai3 upregulation was equivalent between low-grade (Figure 1C) and high grade (Figure 1D) tumors. Remarkably, in these glioma tissues, over-expression of Gai3 was positively correlated with upregulation of mentioned RTKs, including EGFR, FGFR and PDGFR α (see quantified results, Figure 1E).

Our previous studies have confirmed that Gai3 is required for Akt-mTOR activation by EGFR [13] and FGFR [14]. Next, we wanted to know if Gai3 expression was associated with Akt-mTOR activation level in these tissues. Indeed, glioma tumors with Gai3 over-expression also showed high level of p-Akt (Ser-473) and p-S6K1 (Thr-389) (see quantified results, Figure 1F). Yet, p-Akt and p-S6K1 levels were much lower in normal

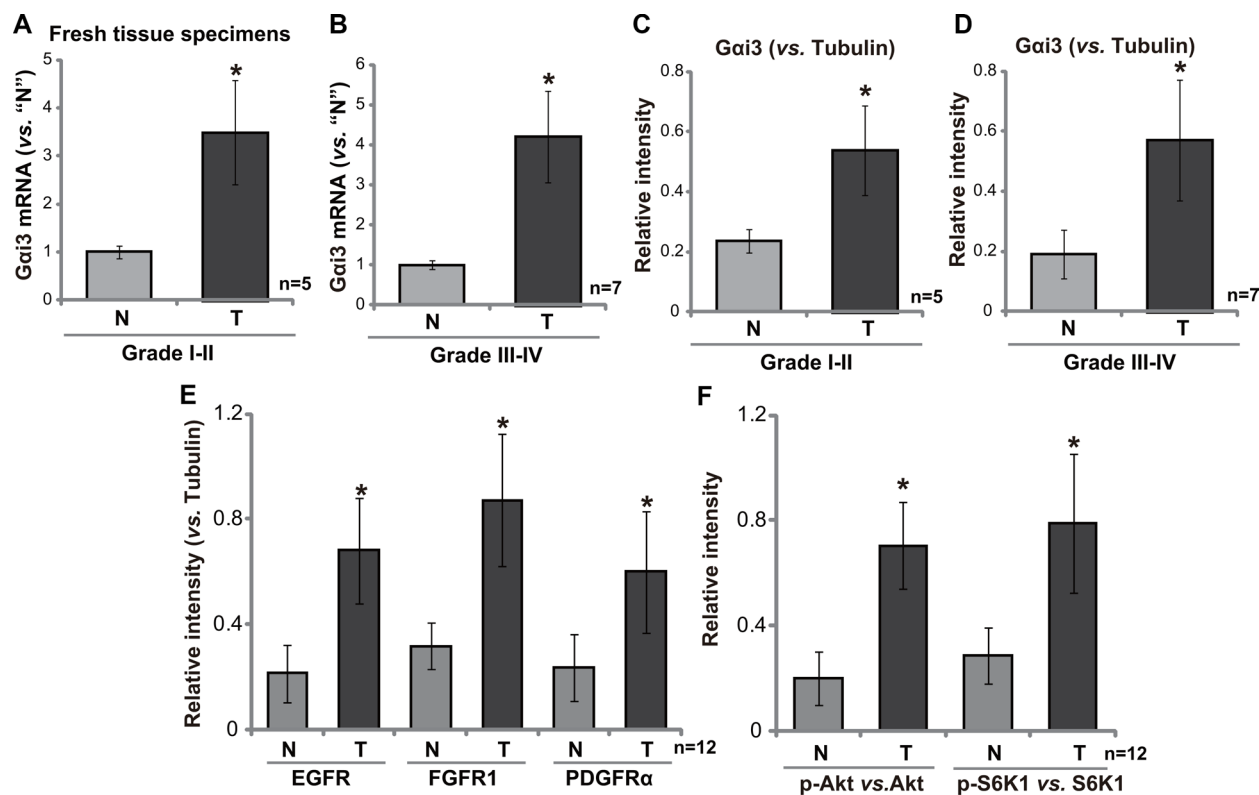


Figure 1: Gai3 over-expression is associated with RTK upregulation and Akt-mTOR hyperactivity in human glioma tissues. Fresh human glioma tissues (“T”, $n = 12$) and the surrounding normal brain tissues (“N”, $n = 12$) were homogenized and dissolved in the tissue lysis buffer, relative Gai3 mRNA expression (vs. GAPDH) was examined by real-time PCR assay (A and B); Quantified western blotting assay results showed expression of Gai3 and other listed proteins in above patients’ tissues (C–F). “MW” stands for molecular weight (Same for all figures). Bars stand for mean \pm SD. * $p < 0.05$ vs. “N” group.

brain tissues (Figure 1F). Collectively, these results demonstrated that *Gai3* was over-expressed in multiple human glioma tissues, and its level was associated with RTKs upregulation and Akt-mTOR hyperactivity.

Over-expressed *Gai3* associates with several RTKs and the adaptor protein *Gab1* in human glioma cells and tissues

Next, we tested *Gai3* expression in cultured human glioma cells. As compared to the primary human astrocytes (“Astrocytes”), *Gai3* protein (Figure 2A) and mRNA (Figure 2B) were up-regulated in U87MG glioma cells and primary human glioma cells (Patient-4-derived, “Glioma cells”). Further, *Gai3* over-expression was again correlated with high level of p-Akt/p-S6K1 in the glioma

cells (Figure 2A). Similar results were also obtained in other patient-derived primary glioma cells (Data not shown). Importantly, co-immunoprecipitation (Co-IP) assay results showed that *Gai3* formed a complex with the mentioned RTKs (EGFR, FGFR and PDGFR α) and the adaptor protein *Gab1* in U87MG cells (Figure 2C). Notably, the *Gai3*-RTK-*Gab1* association required FBS stimulation, and was not observed in phosphate-buffered solution (PBS)-starved cells (“starvation”, Figure 2C).

Significantly, as shown in Figure 2D, the *Gai3*-RTK-*Gab1* association was also observed in multiple human glioma tissues. “T1/T4/T8” stand patient-1/-4/-8’s glioma tissues (Figure 2D). Similar *Gai3*-RTK-*Gab1* association was also observed in other glioma tissues (Data not shown). Therefore, these results demonstrated that over-expressed *Gai3* associated with several RTKs

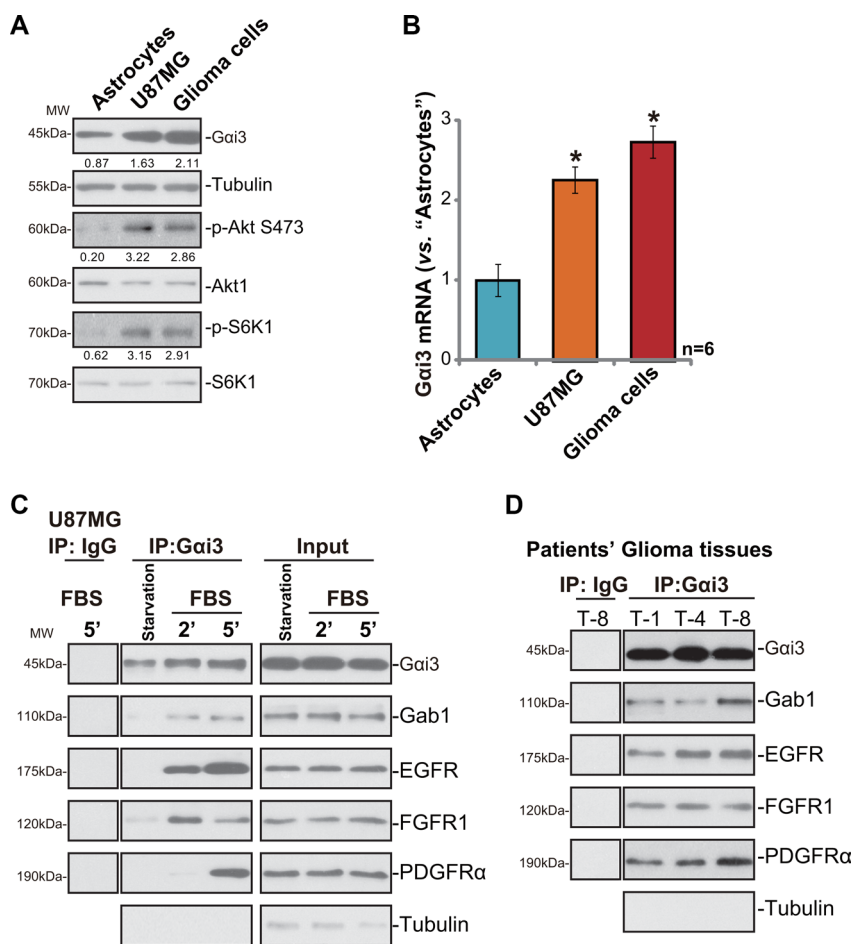


Figure 2: Over-expressed *Gai3* associates with several RTKs and the adaptor protein *Gab1* in human glioma cells and tissues. Western blotting analysis showed expression of *Gai3* and listed kinases in primary human astrocytes (“Astrocytes”), U87MG glioma cells (“U87MG”) and primary human glioma cells (“Glioma cells”, Patient-4-derived) (A); *Gai3* mRNA expression (vs. GAPDH) in above cells was examined by real-time PCR assay (B). U87MG cells were phosphate-buffered solution (PBS)-starved (15 min, “starvation”) or stimulated with 10% FBS for applied time, *Gai3* association with several RTKs (EGFR, FGFR and PDGFR α) and *Gab1* was tested by co-immunoprecipitation (Co-IP) assay (C); “Input” showed expression of above proteins (C). Fresh glioma tissue lysates from patient-1/-4/-8 (named T-1/-4/-8) were subjected to same Co-IP assay of *Gai3*-RTK-*Gab1* association (D). *Gai3* protein expression (normalized to tubulin), p-Akt (normalized to Akt1) and p-S6K1 (normalized to S6K1) were quantified (A). For Western blotting assay, same set of lysate samples were run in sister gels. Experiments in this figure were repeated three times, with similar results obtained. Bars stand for mean \pm SD. * $p < 0.05$ vs. “Astrocytes” group (B, $n = 6$).

(EGFR, FGFR and PDGFR α) and the adaptor protein Gab1 in human glioma cells and tissues.

In glioma cells, *Gai3* shRNA knockdown inhibits Akt activation and cell growth

To study the potential involvement of *Gai3* on glioma cell functions, lentiviral shRNA strategy was applied to stably knockdown *Gai3* in glioma cells. As shown in Figure 3A, the two non-overlapping *Gai3* shRNAs (-a/-b) downregulated *Gai3* expression in U87MG cells. As a result, p-Akt was inhibited (Figure 3A), indicating the requirement of *Gai3* in Akt-mTOR activation. Further, U87MG cell growth, tested by the MTT assay (Figure 3B) and clonogenicity assay

(Figure 3C), was also inhibited by *Gai3* shRNAs. On the other hand, histone-DNA apoptosis ELISA assay results suggested a high basal apoptosis level in the *Gai3* knockdown cells (Figure 3D). Intriguingly, in U87MG cells, *Gai3* shRNA-b was more potent than *Gai3* shRNA-a in downregulating *Gai3* and pAkt (Figure 3A). Consequently, growth inhibition and apoptosis activation were also more significant in *Gai3* shRNA-b-expressing cells (Figure 3B–3D). To further study the function of *Gai3* in cell growth, *Gai3* knockout (KO) MEFs [13, 14] were applied. As compared to the wild-type (WT) MEFs, Akt activation (Figure 3G) and cell growth (Figure 3H) were significantly downregulated in *Gai3* KO MEFs. These results together suggest that *Gai3* is required for Akt activation and glioma cell growth.

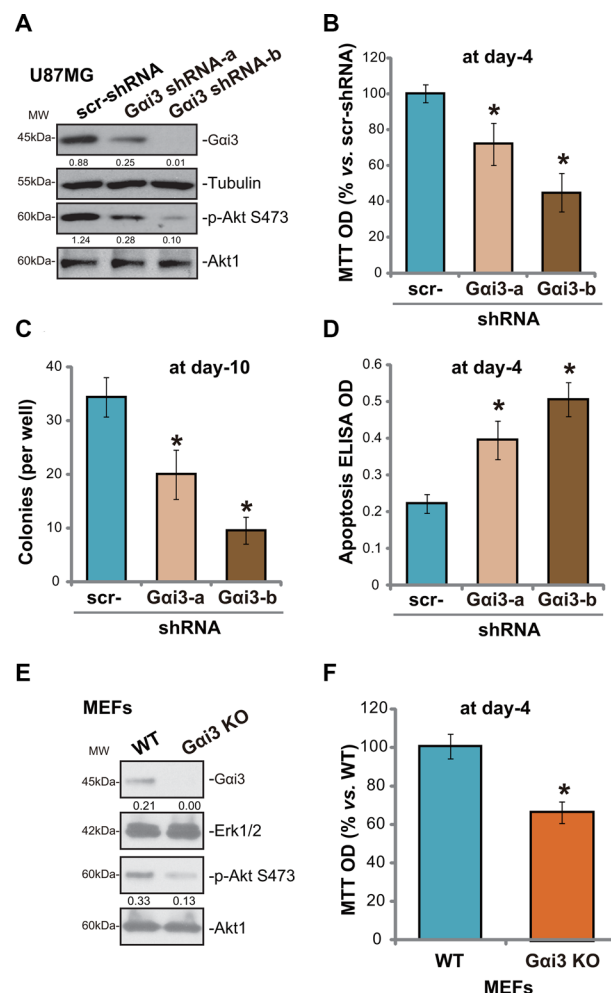


Figure 3: In glioma cells, *Gai3* shRNA knockdown inhibits Akt activation and cell growth. Western blotting analysis showed expression of *Gai3* and other listed proteins in stable U87MG cells (A) with *Gai3* shRNA (“-a/-b”) or scramble control shRNA (“scr-shRNA”); Growth of these cells was tested by MTT assay (B, MTT OD at day-4) or colony formation assay (C, colony number at day-10). Basal apoptosis activation in the U87MG cells was tested by Histone DNA ELISA assay (D, apoptosis OD at day-4). Expression of *Gai3* and other listed proteins in wild-type (WT) and *Gai3* knockout (KO) MEFs was shown (E); Growth of the MEFs was tested by MTT assay (F, MTT OD at day-4). For all these assays, the exact same number of cells of different background were initially plated into each well. Same set of lysate samples were run in sister gels (A and E). Erk1/2 was tested as equal loading in (E). Experiments in this figure were repeated three times, with similar results obtained. Bars stand for mean \pm SD. * $p < 0.05$ vs. “scr-shRNA” group (B–D, $n = 6$). * $p < 0.05$ vs. “WT MEFs” (F, $n = 6$).

Gai3 mutation affects Akt-mTOR activation and glioma cell growth

To further confirm the requirement of Gai3 in Akt-mTOR activation and glioma cell growth, a dominant negative interference strategy was applied. We replaced the conserved Gly (G) residue with Thr (T) in the G3 box of Gai3 [13, 14]. The dominant negative Gai3 (G202T, DN-Gai3) will compete with WT Gai3 for binding to other proteins [16, 17]. In stable U87MG cells expressing DN-Gai3, we noticed substantially decreased phosphorylations of Akt and S6K1, as compared to that in vector control cells (Figure 4A). U87MG cell growth, tested by MTT assay and clonogenicity assay, was also inhibited in DN-Gai3 expressing cells (Figure 4B and 4C). While the cell apoptosis level was increased (Figure 4D).

On the hand, a constitutively active Gai3 (Q204L, CA-Gai3) [13] was introduced into U87MG cells. We showed that overexpression of CA-Gai3 in U87 MG cells led to increased phosphorylations of Akt and S6K1 (vs. vector control U87 cells) (Figure 4A). As a result, U87MG cell growth was increased (Figure 4B and 4C). Yet apoptosis of the CA-Gai3 cells was inhibited (Figure 4D). Collectively, these results provided more evidence to support that Gai3 is required for Akt-mTOR activation and glioma cell growth.

Gai3 shRNA knockdown inhibits U87MG tumor growth in nude mice

At last, we evaluated the potential requirement of Gai3 on U87MG cell growth *in vivo*. As described, same amount of stable U87MG cells expressing scramble control shRNA (“scr-shRNA”) or Gai3 shRNA (-b) were *s.c.* inoculated into the nude mice. After 10–15 days, the U87MG tumors were established. Tumor growth curve in Figure 5A demonstrated that Gai3 shRNA-expressing U87MG tumors grew significantly slower than the scr-shRNA-bearing U87MG tumors. The estimated daily tumor growth results further confirmed the inhibitory effect of Gai3 shRNA on U87MG tumor growth (Figure 5B). Notably, the mice body weights were not significantly different between the two groups (Figure 5C).

We also analyzed Gai3 expression and Akt-mTOR activation in the U87MG tumors. As expected, Gai3 was dramatically downregulated in U87MG tumors bearing Gai3 shRNA (Figure 5D). In line with the *in vitro* findings, p-Akt and p-S6K1 were both inhibited in Gai3 shRNA-expressing U87MG tumors (Figure 5D). IHC staining results (Figure 5E) further confirmed p-Akt inhibition in the U87MG tumor with Gai3 shRNA. Together, these results demonstrated that Gai3 shRNA inhibited Akt-mTOR activation and U87MG tumor growth *in vivo*.

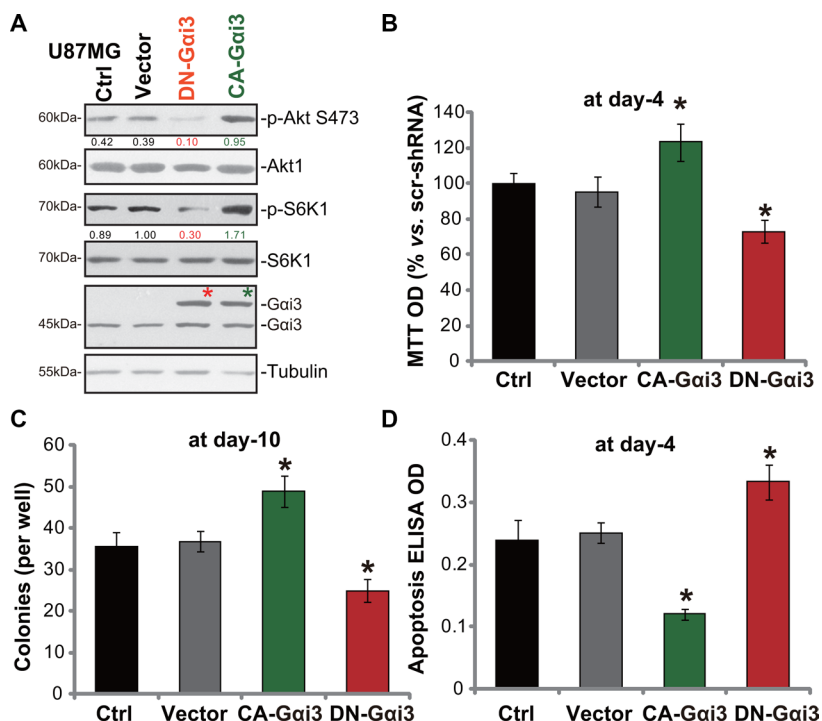


Figure 4: Gai3 mutation affects Akt-mTOR activation and glioma cell growth. Western blotting analysis tested expression of Gai3 and other listed proteins in stable U87MG cells with the dominant negative Gai3 (G202T, DN-Gai3), the constitutively active Gai3 (Q204L, CA-Gai3) or the empty vector (pGCL-GFP-puro) (A). Growth of these cells was tested by MTT assay (B, MTT OD at day-4) or colony formation assay (C, colony number at day-10). Basal apoptosis activation was tested by Histone DNA ELISA assay (D, apoptosis OD at day-4). For all these assays, the exact same number of cells of different background were initially plated into each well. For Western blotting assay, same set of lysate samples were run in sister gels (A). “Ctrl” stands for the un-transfected parental cells. Experiments in this figure were repeated three times, with similar results obtained. Bars stand for mean \pm SD. * $p < 0.05$ vs. “Vector” cells (B–D, $n = 6$).

DISCUSSIONS

Our previous studies [13, 14] have revealed a unique mechanism of Gai3 protein in transducing Akt-mTOR signaling by several RTKs. Upon RTK ligand (i.e. EGF) stimulation, Gai3 protein was shown to associate with the RTKs and to transduce signaling to the adaptor protein Gab1, causing Gab1 and downstream Akt-mTOR activation [13, 14]. shRNA knockdown, dominant negative mutation or complete knockout of Gai3 protein thus inhibited RTK signaling to Gab1, and significantly attenuated downstream Akt-mTOR activation [13, 14].

Here, we showed that Gai3 was over-expressed in multiple human glioma tissues and cells, which was associated with RTK (EGFR, FGFR and PDGFR α) upregulation and Akt-mTOR hyperactivity. Intriguingly, over-expressed Gai3 formed a complex with above RTKs and the adaptor protein Gab1 in glioma tissues and cells, which was also required for downstream Akt-mTOR activation. shRNA knockdown or dominant negative mutation of Gai3 potentially inhibited Akt-mTOR activation and glioma cell growth. Meanwhile, Gai3-depleted MEFs demonstrated reduced Akt-mTOR activity and cell growth. On the other hand, introduction of a constitutively active

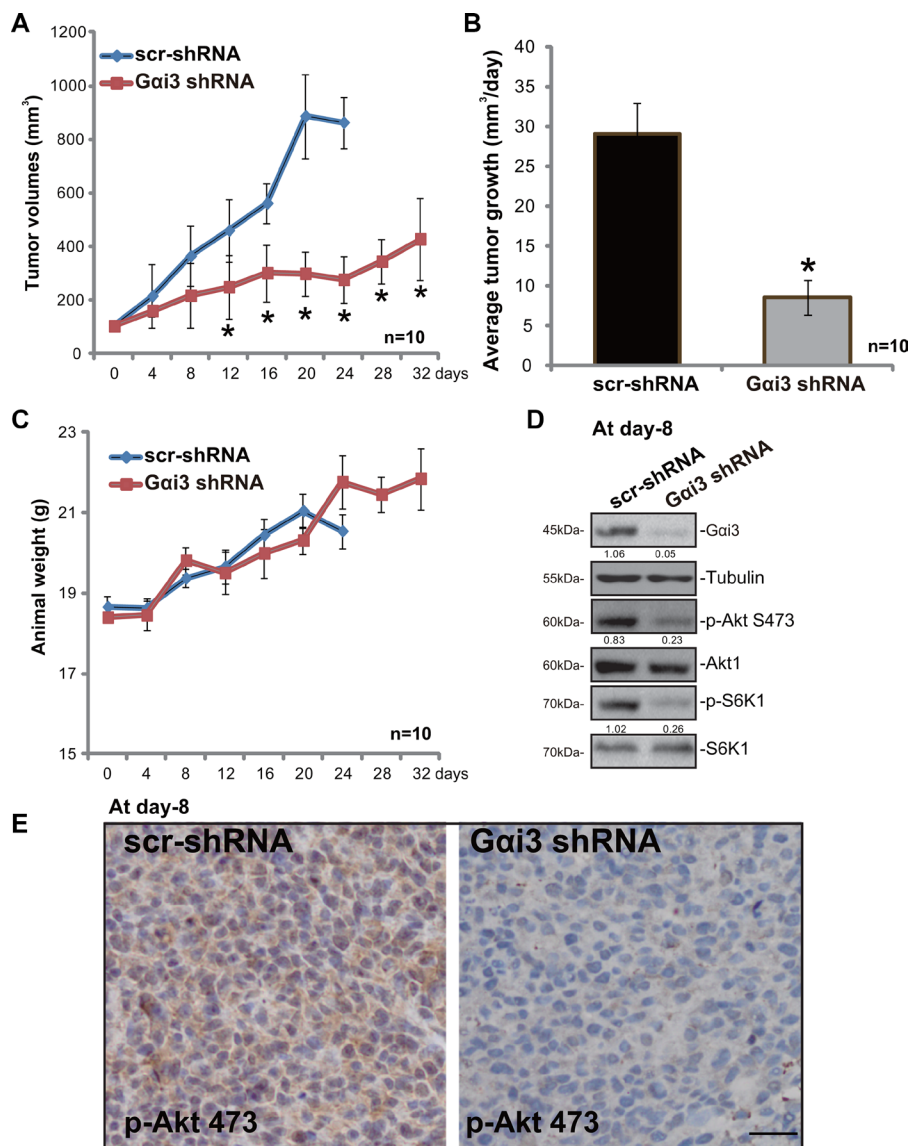


Figure 5: Gai3 shRNA knockdown inhibits U87MG tumor growth in nude mice. Same amount (five millions cells per mouse) of Gai3 shRNA-expressing stable U87MG cells (“Gai3 shRNA”) or scramble control shRNA-expressing stable U87MG cells (“scr-shRNA”) were inoculated *s.c.* into the nude mice (10 mice per group), tumor volumes (A) and mice body weights (C) were recorded every four days; Estimated average daily tumor growth was calculated (B); At day-8, one U87MG tumor per group was isolated, expression of listed proteins in the fresh tumor tissue lysates was tested by Western blotting assay (D). p-Akt Ser473 (E) was also tested by IHC staining, representative images were presented. For Western blotting assay, same set of lysate samples were run in sister gels (D). Bars stand for mean \pm SD (A–C). * $p < 0.05$ vs. “scr-shRNA” tumor group (A and B). Bar = 50 μ m (E).

Gai3 enhanced Akt-mTOR activation and glioma cell growth. These results suggest that over-expressed Gai3 is required for Akt-mTOR activation and glioma cell growth.

It is known that multiple RTKs are amplified and/or hyper-activated simultaneously in human glioma, which have important clinical implications for tumor progress and resistance to targeted therapies [18, 19]. The efficiency of a single targeted therapy (*i.e.* EGFR inhibitors) could therefore be compromised due to co-existence other RTKs activation [10, 11]. Indeed, recent studies have shown that glioma patients often respond better to a combination of inhibitors of different RTKs [18, 19]. Our previous and current findings implied that Gai protein could be the common adaptor protein for several RTKs, which participates in downstream Akt-mTOR activation and tumor cell progression. Significantly, our *in vivo* studies showed that Gai3 shRNA inhibited Akt-mTOR activation and U87MG tumor growth in nude mice. These results, together with the findings of Gai3 over-expression in human gliomas, imply that Gai3 might be a valuable oncotarget for glioma.

MATERIALS AND METHODS

Reagents

The antibodies utilized in this study were described previously [13, 14, 20, 21]. Cell culture reagents were obtained from Gibco (Shanghai, China).

Cell lines

Wild-type (WT) and Gai3 knockout (KO) mouse embryonic fibroblasts (MEFs) were described early [13, 14]. Human U87MG glioma cell line was purchased from the Cell Bank of Chinese Academy of Science (Shanghai, China). Cells were maintained in DMEM medium, supplemented with 8% fetal bovine serum (FBS) and necessary antibiotics, and in the CO₂ incubator at 37°C.

Human glioma tissues

All studies involving human specimens were conducted according to the principles expressed in the Declaration of Helsinki, and to the national and international guidelines. The protocol was approved by the Ethics Review Board (ERB) of Soochow University. A total of twelve informed-consent glioma patients were enrolled (All hospitalized in the Affiliated Hospitals of Soochow University). The patients' basic parameters were as following: Male: 8/Female: 4; 43–62 years old; Grade I–II: 5 and Grade III–IV: 7. Fresh human glioma tissues along with the surrounding normal brain tissues were obtained at the time of surgery. Fresh tissues were minced, homogenized and dissolved in the tissue lysis buffer (Biyuntian, Wuxi, China). Samples were then subjected to real-time PCR assay or Western blotting assay.

Primary culture of human glioma cells

Similar to our previous protocol [17], fresh glioma tissues were thoroughly washed, and were minced into small pieces. Single-cell suspensions were achieved by re-suspending tissues in 0.10% (w/v) collagenase I (Sigma, Shanghai, China). The resulting cell suspensions were then washed, filtered through a 70- μ m cell strainer. Afterwards, the primary glioma cells were pelleted and rinsed twice with DMEM. Cells were then cultured in primary cell culture medium as previously described [21].

Primary culture of human astrocytes

Human primary astrocyte cultures were purchased from the Cell Bank of Fudan University (Shanghai, China). The astrocytes were derived from the cerebral cortices of a single trauma patient. Virtually all the astrocytes were positive of glial fibrillary acidic protein (GFAP). The astrocytes were maintained in astrocyte media (Science Cell, Carlsbad, CA) containing 10% FBS, 1% astrocyte growth supplement and 1% Penicillin/Streptomycin.

Real-time reverse transcriptase polymerase chain reaction

As described in our previous study [18], total RNA was prepared via the standard TRIzol reagents (Invitrogen, Shanghai, China). The PCR reaction mixture contained 1 \times SYBR Master Mix (Applied Biosystem, Foster City, CA), 500 ng RNA and 200 nM primers. An ABI Prism 7300 Fast Real-Time PCR system (Foster City, CA) was applied for PCR reactions. mRNA expression was quantified via the $\Delta\Delta$ Ct method. GAPDH served as the internal control. The following primers were applied: Gai3, Forward: 5'-AAACGGTTATGGCGAGATGGT-3'. Reverse: 5'-TGTCTTCACTCTCGTCCGAA-3'. The GAPDH primers were described previously [22]. The primers were purchased from Genechem (Shanghai, China).

Western blotting analysis

Cells or glioma tissues were lysed with lysis buffer described previously [13, 14, 20]. Aliquots of 40 μ g of protein from each treatment were separated by 10% SDS-PAGE and transferred onto polyvinylidene difluoride (PVDF) membranes (Millipore, Bedford, MA). The membranes were then incubated with specific primary antibody and corresponding second antibody. Antibody-antigen binding was detected with the enhanced chemiluminescence (ECL) detection system (Amersham Biosciences, Piscataway, NJ). Each band was quantified through Image J software (NIH). For the Western blot assay, each lane was loaded with exact same amount of quantified protein lysates (30 μ g per sample). Same set of lysate samples were run in sister gels to test different proteins if necessary.

Co-immunoprecipitation (Co-IP)

The detailed protocol was described in our previous studies [13, 20]. Briefly, aliquots of 600 µg of protein lysates from each sample were pre-cleared, followed by incubation with anti-Gai3 antibody overnight. Thirty µl of protein A/G beads (Sigma) were then added, and the lysates were incubated for 2 hours at 4°C. The beads were washed, and Gai3-associated proteins were then detected by Western blotting.

Generation of Gai3 stable knockdown glioma cells

Two lentiviral Gai3 shRNAs (“-a/-b”, with non-overlapping sequences) were purchased from Genechem (Shanghai, China). The target sequence for Gai3 shRNA-a and Gai3 shRNA-b were 5'-TCAATCATTCTCTTCCTTA-3' and 5'-CCTCAGTG ATTATGACCTT-3', respectively. The detailed protocol was described in our previous studies [14, 21, 22]. Briefly, glioma cells were seeded onto six-well plate with 50% confluence. Twenty µL/mL of lentiviral Gai3 shRNA was added to the cells for 24 hours. Afterward, shRNA-containing medium was replaced by the culture medium for additional 48 hours. The stable glioma cells expressing Gai3 shRNA were selected by puromycin (0.5 µg/mL, Sigma) for a total of 6–8 days. Gai3 expression in stable cells was detected by Western blotting. Same amount of lentiviral scramble shRNA (“scr-shRNA”, Santa Cruz, sc-108080) was added to the control cells.

Gai3 mutation and stable cell selection

The plasmid (0.25 µg per well) encoding a constitutively-active-Gai3 (CA-Gai3-GFP-puro, Q204L) [13], a dominant negative Gai3 (DN-Gai3-GFP-puro, G202T) [13, 14], or the empty vector (pGCL-GFP-puro, GeneChem) was transfected to U87MG cells via the Lipofectamine 2000 protocol as described [14]. Twenty four hours after transfection, cells were cultured in complete medium for additional 48 hours. Puromycin (0.5 µg/mL, Sigma) was then applied to select stable clones expressing target construct. The target protein (Gai-GFP) in stable cells was tested by Western blotting.

Cell growth and apoptosis assay

MTT assay of cell growth, clonogenicity assay of cell growth and histone DNA apoptosis ELISA assay were described in detail in our previous studies [13, 20, 21, 23, 24].

Nude mice xenograft assay

As described [25], Gai3 shRNA(-b)-expressing stable U87MG cells or scr-shRNA-expressing stable

U87MG cells (five millions cells in 200 µl of Matrigel gel per mouse) were subcutaneously (*s.c.*) injected into the right flanks of 4–5 week-old female nude mice (ten mice per group, at Soochow University Animal Facility, Soochow, China). When the tumor volume reached approximately 100 mm³, the recording was started. The size of the U87MG tumors and mice body weights were measured every four days, and tumor volumes were calculated using the following formula: $\pi/6 \times \text{width}^2 \times \text{length}$ [25]. Estimated average daily tumor growth was also calculated [25]. All animal procedures were approved by Soochow University Ethics Review Board and IACUC.

Immunohistochemistry (IHC) staining

As described in our previous study [14], the IHC staining was performed on cryostat sections (3 µm) of U87 xenograft tumors according to standard methods. We incubated slides in the appropriate dilution of primary antibody (anti-Akt Ser 473, 1: 25, Cell Signaling Tech), which were subsequently stained with corresponding secondary antibodies (Santa Cruz). The peroxidase activity was visualized via the 3-amino-9-ethyl-carbazol (AEC) method (Merck) [14].

Statistical analysis

All experiments were performed in triplicate and were repeated at least three times, similar results were obtained in each case. The data presented were means \pm standard deviation (SD). Statistical differences were analyzed by one-way ANOVA followed by multiple comparisons performed with post hoc Bonferroni test (SPSS version 18.0). Values of $p < 0.05$ were considered as statistically significant.

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CONFLICTS OF INTEREST

The authors declare no competing financial interests.

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