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ORIGINAL RESEARCH

Synthetic 1,3,6-Tri-O-Galloyl-α-D-Glucose Mimics the Hippo Pathway Inhibitor VT107 in Suppressing Concanavalin A-Induced Inflammation in Human Glioblastoma Cells

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Background: Glioblastoma (GBM) is the most aggressive primary tumor of the adult central nervous system, not only characterized by rapid proliferation and diffuse brain infiltration but also by a pronounced pro-inflammatory microenvironment that fuels tumor progression and therapeutic resistance. Current standard-of-care, surgical resection followed by radiotherapy and chemotherapy, offers limited survival benefit, partly due to inflammation-driven invasion and immune evasion. The Hippo signaling pathway, a critical regulator of cell proliferation, apoptosis, and tissue homeostasis, has recently been implicated in inflammatory signaling, making it an attractive therapeutic target.

Purpose: In this study, we investigated the anti-inflammatory and anti-invasive properties of 1,3,6-tri-O-galloyl-α-D-glucose (αTGG), the α-anomer of βTGG from *Terminalia chebula*, in comparison with pharmacological Hippo pathway inhibitors IAG933, VT107, and GNE7883.

Results: To mimic the inflammatory milieu associated with GBM, U87 cells were treated with Concanavalin A (ConA), which induced phosphorylation of ERK and IκB, key mediators of MAPK and NF-κB inflammatory pathways. Both αTGG and Hippo pathway inhibitors effectively suppressed these phosphorylation events, with VT107 showing the strongest effect. ConA exposure downregulated Hippo pathway downstream effectors (*AXL, CTGF, CYR61*) in a TEAD-dependent manner, highlighting the interplay between Hippo signaling and inflammatory transcriptional control. Importantly, αTGG and VT107 also significantly attenuated ConA-induced activation of proMMP-2 to MMP-2 and reduced the expression of multiple pro-inflammatory mediators, including *COX2, CCL22, CCR2, CCR4, CXCL10, CXCL12, CXCR1, FASLG, IFNG, IL13*, and *IL17A*.

Conclusion: These findings underscore the dual anti-inflammatory and anti-invasive actions of αTGG, positioning it as a promising candidate for targeting inflammation-driven GBM progression through modulation of Hippo pathway activity.

Keywords: Concanavalin A, glioblastoma, hippo pathway inhibitors, inflammation, 1,3,6-tri-O-galloyl-α-D-glucose

Introduction

Neuroinflammation is a central driver of glioblastoma (GBM) progression and aggressiveness,[1,2] shaping a chronically inflamed tumor microenvironment (TME) that promotes growth, angiogenesis, invasion, and therapy resistance.[3] Persistent release of pro-inflammatory cytokines (for example, IL-1β, IL-6, IL-8, TNF-α) from tumor and infiltrating immune cells disrupts the blood-brain barrier, enhances immune evasion, and fuels tumor cell proliferation and invasion.[4] Key inflammatory signaling cascades, including NF-κB, MAPK, STAT3, and Hippo, sustain this pro-tumorigenic milieu and blunt responses to immunotherapy and conventional treatments.[5–7] Targeting inflammation therefore offers a twofold

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opportunity: to directly suppress tumor-promoting signals, reducing invasiveness and matrix remodeling, and to reprogram the immune microenvironment toward anti-tumor activity.[8,9]

Pharmacological approaches are increasingly directed at these inflammatory axes: small-molecule inhibitors of NF-κB/STAT3 and Hippo pathway modulators (eg, GNE7883, IAG933, verteporfin and related TEAD inhibitors) show anti-proliferative, anti-vasculogenic mimicry, and anti-inflammatory effects in preclinical GBM models;[10–13] repurposed anti-inflammatory drugs including minocycline, celecoxib and CSF-1R-mediated blockade of tumor-associated macrophage activity are also under evaluation to reprogram tumor-associated inflammation.[14–16] Nowadays, immunomodulatory therapies, such as checkpoint inhibitors, are also being combined with anti-inflammatory agents to overcome immune suppression. Natural compounds like curcumin are gaining attention for their dual anti-inflammatory and anti-invasive properties.[17,18] Collectively, they may represent a shift toward integrated, inflammation-targeted GBM therapy.

The Hippo pathway, through its effectors YAP and TAZ, is a key regulator of proliferation, apoptosis, and tissue homeostasis whose dysregulation promotes GBM progression.[19] Dephosphorylated YAP/TAZ translocate to the nucleus and drive genes that enhance invasion and inflammatory signaling, including upregulation of MMPs and pro-inflammatory cytokines.[6,20,21] This activity accelerates extracellular matrix degradation, immune cell recruitment, and a tumor-supportive, immune-suppressive microenvironment, with YAP/TAZ functionally interacting with NF-κB and STAT3 to amplify inflammation.[22] Hippo dysregulation also fosters apoptosis resistance and immune evasion,[23] while pharmacological YAP/TAZ or YAP/TEAD inhibition reduces inflammatory/invasive marker expression in GBM models.[24,25] Targeting Hippo signaling therefore offers a focused strategy to blunt tumor-promoting inflammation and invasion.

Here, we tested the anti-inflammatory activity of 1,3,6-tri-O-galloyl-α-D-glucose (αTGG), the α-anomer of βTGG from *Terminalia chebula*, and compared its effects with Hippo pathway inhibitors IAG933, VT107 and GNE7883 in a human GBM-derived cell line, focusing on inflammatory readouts and invasive phenotypes.

Methods

Reagents and Cells

Sodium dodecyl sulfate (SDS), Concanavalin A (ConA) and bovine serum albumin (BSA) were obtained from Sigma-Aldrich Corp. (St. Louis, MO, USA). The Hippo pathway inhibitors, IAG933, VT107, and GNE7883, were sourced from Chemietek (Indianapolis, IN, USA). αTGG was generously provided by Dr. Yann Pauvert.[26] Eagle's Minimum Essential Medium (EMEM) for cell culture was purchased from Wisent (320–005 CL). Electrophoresis reagents were acquired from Bio-Rad Laboratories (Hercules, CA, USA). The HyGLO™ Chemiluminescent HRP Antibody Detection Reagents were supplied by Denville Scientific Inc. (Metuchen, NJ, USA). Protein quantification was performed using the Micro BCA™ Protein Assay Kit from Pierce (Thermo Fisher Scientific, Waltham, MA, USA). Primary antibodies targeting GAPDH (D4C6R – CAT# 97166 S), IκBα (4814S), phospho-IκBα Ser32/36 (9246S), p44/42 MAPK (ERK1/2), and phospho-p44/42 MAPK (ERK1/2) were purchased from Cell Signaling Technology (Danvers, MA, USA). Secondary HRP-conjugated donkey anti-rabbit and anti-mouse IgG antibodies were obtained from Jackson ImmunoResearch Laboratories (West Grove, PA, USA). Human U87 glioblastoma (GBM)-derived cells were sourced from the American Type Culture Collection (ATCC; Manassas, VA, USA). Cells were cultured under subconfluent conditions and passaged twice weekly at a 1:2 ratio. Incubation and treatments were carried out at 37°C in a humidified atmosphere containing 5% CO_2 as previously described.[27]

Transfection Method and RNA Interference

For gene silencing experiments, U87 cells were transiently transfected with small interfering RNA (siRNA) using Lipofectamine 2000 (Thermo Fisher Scientific, Waltham, MA, USA) as the transfection reagent. Silencing was carried out using 20 nM siRNA targeting *YAP1* (Hs_YAP1_5 siRNA, SI02662954), *TEAD1* (Hs_TEAD1_5 siRNA, SI04181261), or a non-targeting scrambled control (AllStar Negative Control siRNA, 1027281). All siRNA sequences, including the mismatch controls, were synthesized by QIAGEN and annealed to form duplexes prior to transfection. The efficiency of gene knockdown was evaluated by RT-qPCR.

Total RNA Extraction, cDNA Synthesis, and Real-Time Quantitative PCR

Total RNA was extracted from U87 GBM cell monolayers using TRIzol reagent, following the manufacturer's protocol (Life Technologies, Gaithersburg, MD, USA). RNA concentration was determined using a NanoPhotometer P330 (Implen), and 2 µg of RNA were reverse-transcribed into complementary DNA (cDNA) using the High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems, Foster City, CA, USA). Quantitative PCR reactions were prepared using gene-specific primer sets and SsoFast EvaGreen Supermix (Bio-Rad; 1725204). All primers were obtained from QIAGEN as QuantiTect Primer Assays for the following genes: *YAP1* (Hs_YAP1_1_SG, QT00080822), *TEAD1* (Hs_TEAD1_1_SG, QT00000721), *CTGF* (Hs_CTGF_1_SG, QT00052899), *CYR61* (Hs_CYR61_1_SG, QT00003451), *AXL* (Hs_AXL_1_SG, QT00067725), *NF2* (Hs_NF2_va.1_SG, QT01004934), *COX-2* (Hs_PTGS2_1_SG, QT00040586), *IL6* (Hs_IL6_1_SG, QT00083720), *GAPDH* (Hs_GAPDH_1_SG, QT00079247), and *PPIA* (Hs_PPIA_4_SG, QT01866137). Gene expression levels were quantified RT-qPCR using the CFX Connect system (Bio-Rad) and analyzed with Bio-Rad CFX Manager Software version 3.0. Relative expression of target genes was normalized to the housekeeping genes *GAPDH* and *PPIA* using the $2^{-\Delta\Delta Cq}$ method.

PCR Arrays

Preconfigured RT^2 Profiler PCR Arrays for Human Inflammatory Cytokines and Receptors (PAHS-011ZD) and Human Cancer Inflammation and Immunity Crosstalk (PAHS-181Z) were purchased from QIAGEN and used according to the manufacturer's instructions. Prior to reverse transcription, genomic DNA was removed from the RNA samples, total RNA converted into cDNA and relative expression levels of 141 genes and internal controls quantified and analysed as previously described.[27] For data visualization, genes were considered upregulated when fold regulation exceeded +2, and downregulated when fold regulation was below −2, based on the overall expression profile.

Protein-to-Protein Interactions

Protein-protein interaction (PPI) networks were constructed using the STRING database (version 11; https://www.string-db.org), applying a minimum confidence score threshold of 0.4.[28] To enhance the readability of the network visualizations, the maximum number of displayed interactions per protein was limited to 10.

Western Blot

Protein samples (10–20 µg) from total cell lysis were separated by SDS-polyacrylamide gel electrophoresis (SDS-PAGE) , followed by electrotransfer onto low-fluorescence polyvinylidene difluoride (PVDF) membranes, and immunodetection were performed as previously described.[27]

Zymography

Gelatin zymography of the collected conditioned culture media was employed to evaluate the extracellular gelatinolytic activity of pro-MMP-9, pro-MMP-2, and active MMP-2 as previously described.[29]

Statistical Data Analysis

All statistical analyses were performed using GraphPad Prism 7 (GraphPad Software, San Diego, CA; https://www.graphpad.com). Data are presented as mean ± standard error of the mean (SEM) from at least three independent experiments, unless otherwise indicated. Comparisons between two groups were assessed using the Mann–Whitney *U*-test followed by Dunn Tukey's post hoc test (for data with more than three groups). For Figure 1B, statistical significance was determined using two-way ANOVA. A *p*-value less than 0.05 (*) was considered statistically significant.

Results

Time-Dependent Inhibition of Concanavalin A-Induced Phosphorylation of ERK and IκB by αTGG in Human U87 Glioblastoma Cells

Concanavalin A (ConA) is widely used in experimental immunology and cell biology as a pro-inflammatory pharmacological tool.[30–32] Here, we first wished to assess and optimize U87 GBM cell responsiveness to ConA. Serum-starved

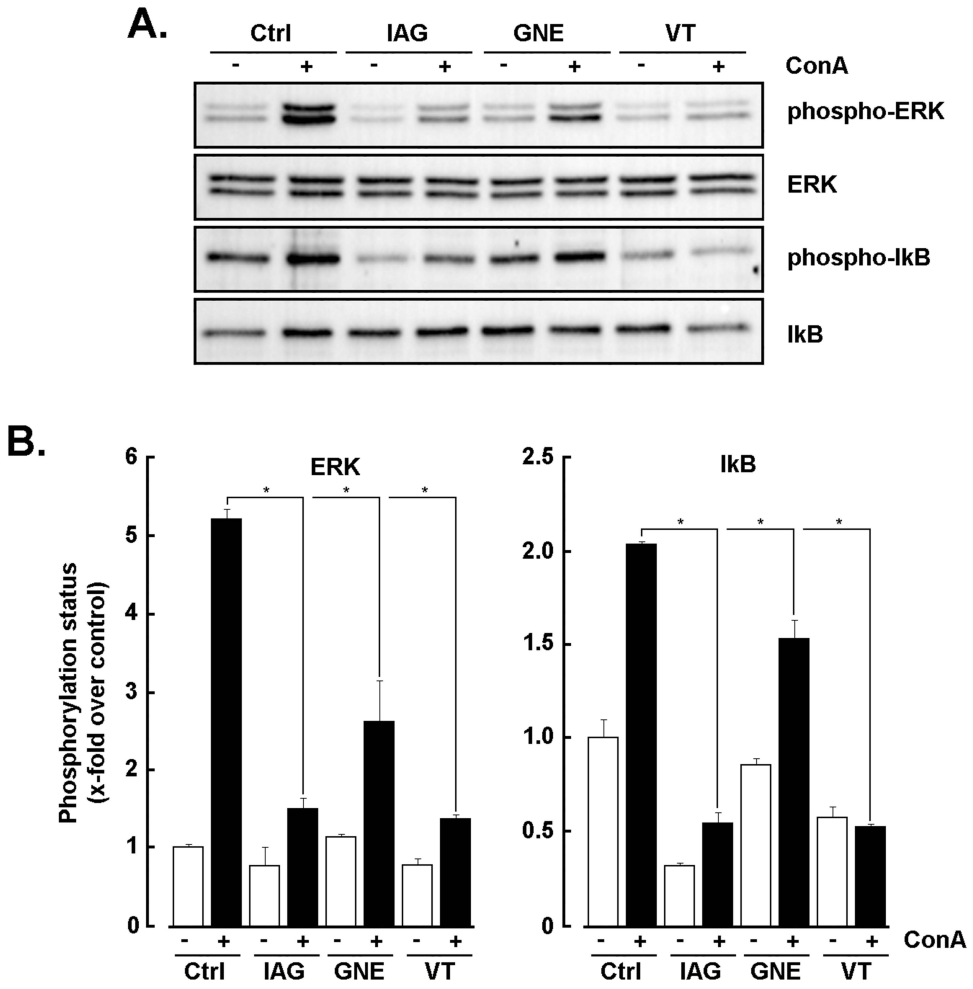

Figure 1 *Hippo pathway inhibitors alter the Concanavalin A-induced phosphorylation of ERK and IκB in human U87 glioblastoma cells*. Serum-starved human U87 glioblastoma cells were treated with 30 μg/mL Concanavalin A (ConA) for 5 min in the absence or presence of 3 μM IAG933 (IAG), GNE7883 (GNE), or VT107 (VT). (**A**) Protein cell lysates were harvested and processed for immunoblotting as described in the Methods section, to detect the phosphorylation status of ERK and of IκB. (**B**) Densitometric analysis was performed and phosphorylation status expressed as the extent of phospho-ERK/ERK or phosphor-IκB/IκB ratios over untreated control cells. Data points are the means ± SEM of 3 independent experiments.

cells were treated with 30 μg/mL ConA in the absence or presence of 30 μM αTGG, and phosphorylation of ERK and of IκB found to be triggered (Figure 2A). Densitometric analysis shows that phosphorylation of ERK peaked at 5 minutes, whereas that of IκB did at 2 minutes (Figure 2B). In both conditions, αTGG treatment prevented these increases.

Dose-Dependent Inhibition of Concanavalin A-Induced Phosphorylation of ERK and IκB by αTGG in Human U87 Glioblastoma Cells

We next screened for the optimal αTGG-to-ConA capacity of cell signaling inhibition (Figure 3A). Serum-starved human U87 GBM cells were therefore treated with increasing concentrations of ConA for 5 min in the absence or presence of 30 μM αTGG and found to significantly inhibit ERK phosphorylation starting at 3 μg/mL ConA (Figure 3B, left panel). Similarly, IκB phosphorylation was also tested at 2 minutes stimulation with ConA, and αTGG found to prevent phosphorylation starting at 1 μg/mL ConA (Figure 3B, right panel).

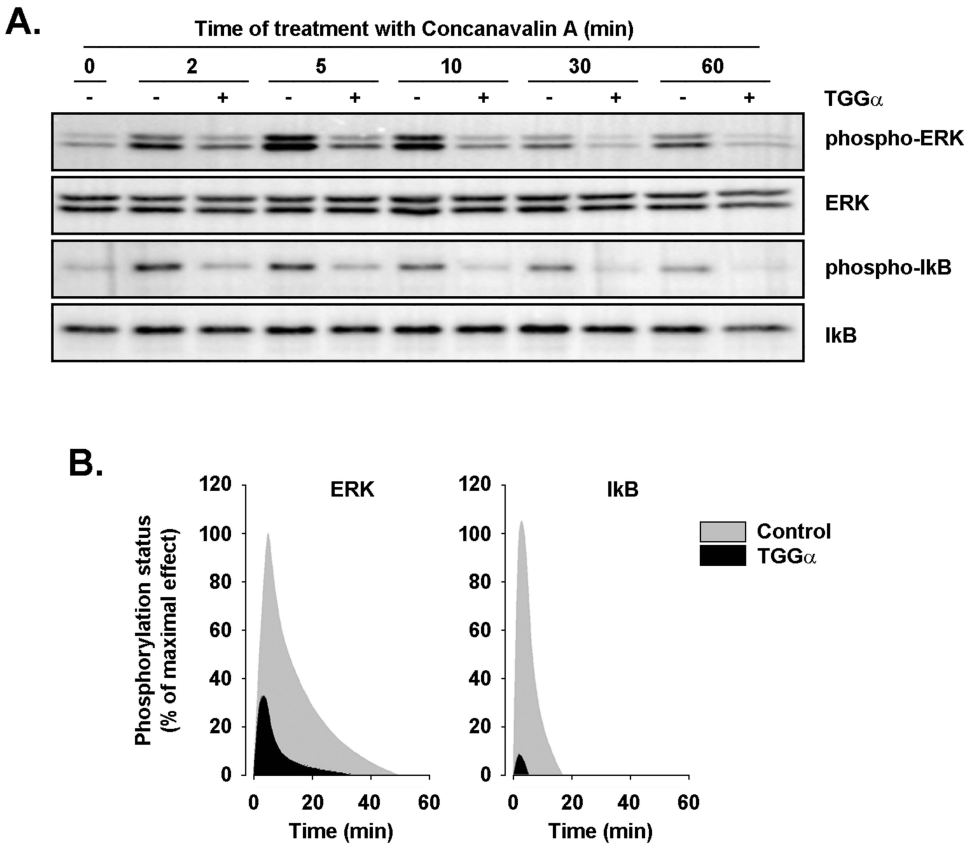

Figure 2 *Time-dependent inhibition of Concanavalin A-induced phosphorylation of ERK and IκB by αTGG in human U87 glioblastoma cells.* Serum-starved human U87 glioblastoma cells were treated with 30 µg/mL Concanavalin A (ConA) for the indicated time in the absence or presence of 30 µM αTGG. (**A**) Protein cell lysates were harvested and processed for immunoblotting as described in the Methods section, to detect the phosphorylation status of ERK and of IκB. (**B**) Densitometric analysis was performed and phosphorylation status expressed as the maximal value of phospho-ERK/ERK or phosphor-IκB/IκB ratios for control (grey shades) vs αTGG (black shades). Western blot and densitometric analysis are representative of 3 independent experiments.

Dose-Dependent Inhibition of Concanavalin A-Induced Snail, COX2, and Activation of proMMP-2 by αTGG in Human U87 Glioblastoma Cells

Downstream induction by ConA of inflammatory and EMT biomarkers expression of respectively COX2 and Snail, and impact of αTGG, was next assessed. Serum-starved human U87 GBM cells were treated with increasing concentrations of αTGG in the absence or presence of ConA for 24 hours. The expression of both Snail and COX2 was effectively triggered by ConA and found to be prevented by αTGG (Figure 4A). Expression of GAPDH in the cell lysates, which served as a loading control, remained unaltered. Along with the above inhibitions of downstream inflammatory biomarkers in ConA-primed U87 cells, αTGG capacity to further inhibit proMMP-2 activation by ConA was examined as previously reported.[33,34] Conditioned media was isolated from the respective conditions and αTGG found to dose-dependently alter the extent of ConA-induced proMMP-2 activation as assessed by gelatin zymography (Figure 4B). Given the long-term treatment, cell viability was assessed and found unaltered upon increasing αTGG treatment concentrations (Figure 4C).

Differential YAP/TEAD Control of Concanavalin A-Mediated Regulation of Hippo Pathway Downstream Effectors

We next wished to address the signaling crosstalk that would inter-relate the Hippo pathway to the pharmacological effects of ConA. Serum-starved human U87 GBM cells were treated with the indicated concentrations of ConA for 24 hours, total RNA was extracted and RT-qPCR performed as described in the Methods section. ConA dose-dependently triggered the expression of *COX2* and *IL6* as previously reported (Figure 5A, left top and bottom panels).[35] Interestingly,

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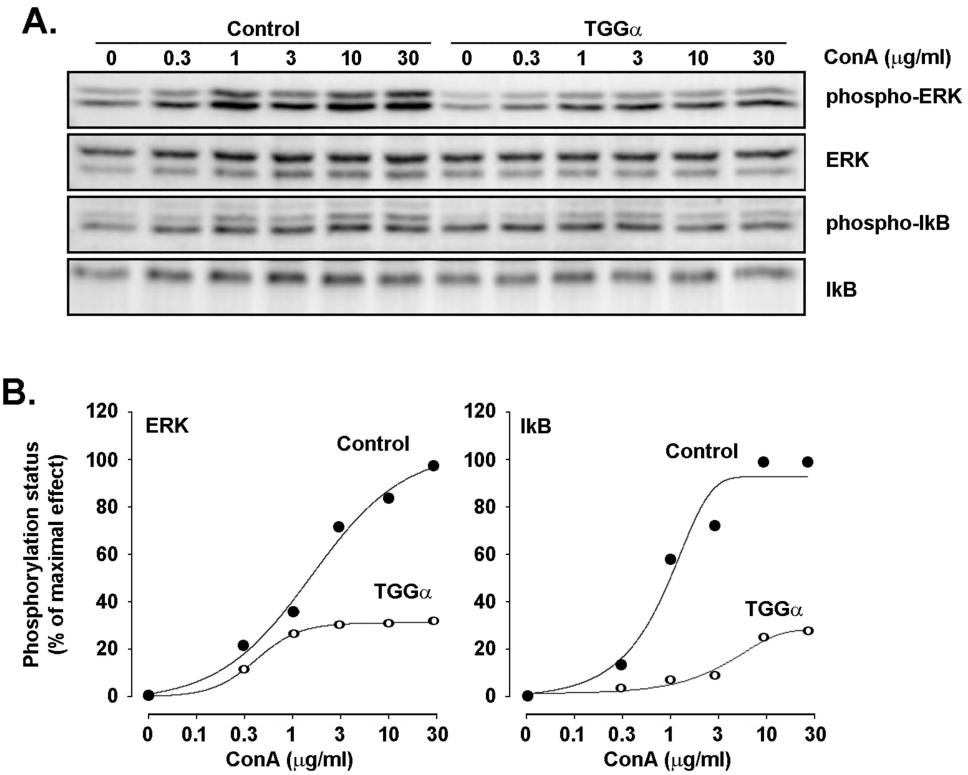

Figure 3 *Dose-dependent inhibition of Concanavalin A-induced phosphorylation of ERK and IκB by αTGG in human U87 glioblastoma cells.* Serum-starved human U87 glioblastoma cells were treated with the indicated concentrations of Concanavalin A (ConA) for 5 min in the absence or presence of 30 μM αTGG. (**A**) Protein cell lysates were harvested and processed for immunoblotting as described in the Methods section, to detect the phosphorylation status of ERK and of IκB. (**B**) A representative densitometric analysis was performed and phosphorylation status expressed as the maximal value of phospho-ERK/ERK or phosphor-IκB/IκB ratios for control (closed circles) vs αTGG (open circles). Western blot and densitometric analysis are representative of 3 independent experiments.

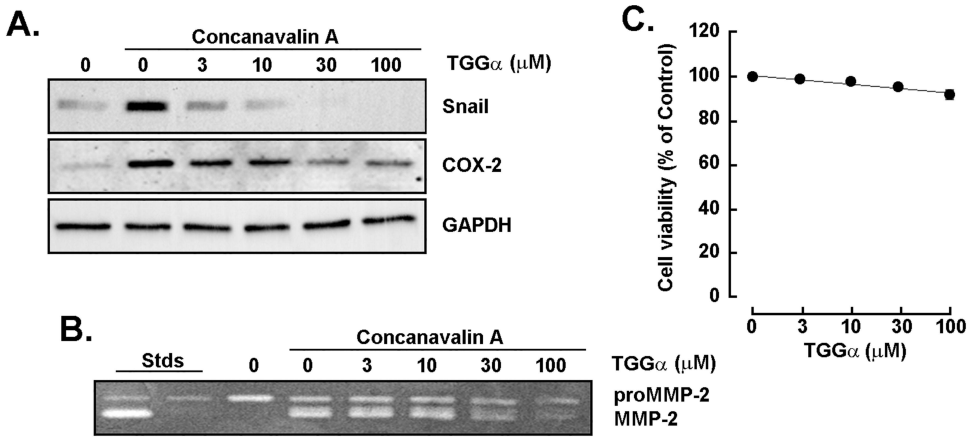

Figure 4 *Dose-dependent inhibition of Concanavalin A-induced Snail, COX2, and activation of proMMP-2 by αTGG in human U87 glioblastoma cells.* Serum-starved human U87 glioblastoma cells were treated with the indicated concentrations of αTGG in the absence or presence of 30 μg/mL Concanavalin A (ConA) for 24 hours. (**A**) Protein cell lysates were harvested and processed for immunoblotting as described in the Methods section, to detect the expression levels of Snail and COX2. GAPDH served as a loading control. (**B**) A gelatin zymography was performed using the conditioned media isolated from the respective conditions as described in the Methods section to assess the effect of αTGG on the extent of ConA-induced proMMP-2 activation. (**C**) U87 glioblastoma cells were treated with the indicated concentrations of αTGG for 24 hours. Cell viability was evaluated for each concentration using the Trypan Blue exclusion assay and a TC20 Automated Cell Counter (Biorad). Data are representative of two independent experiments.

it also decreased the expression of downstream Hippo pathway effectors *AXL, CTGF*, and *CYR61* gene expression, while inducing that of *NF2* (Figure 5A). In order to next assess the involvement of the upstream control exerted by YAP1 and TEAD, transient gene silencing was performed and extent and specificity of gene repression confirmed (Figure 5B).

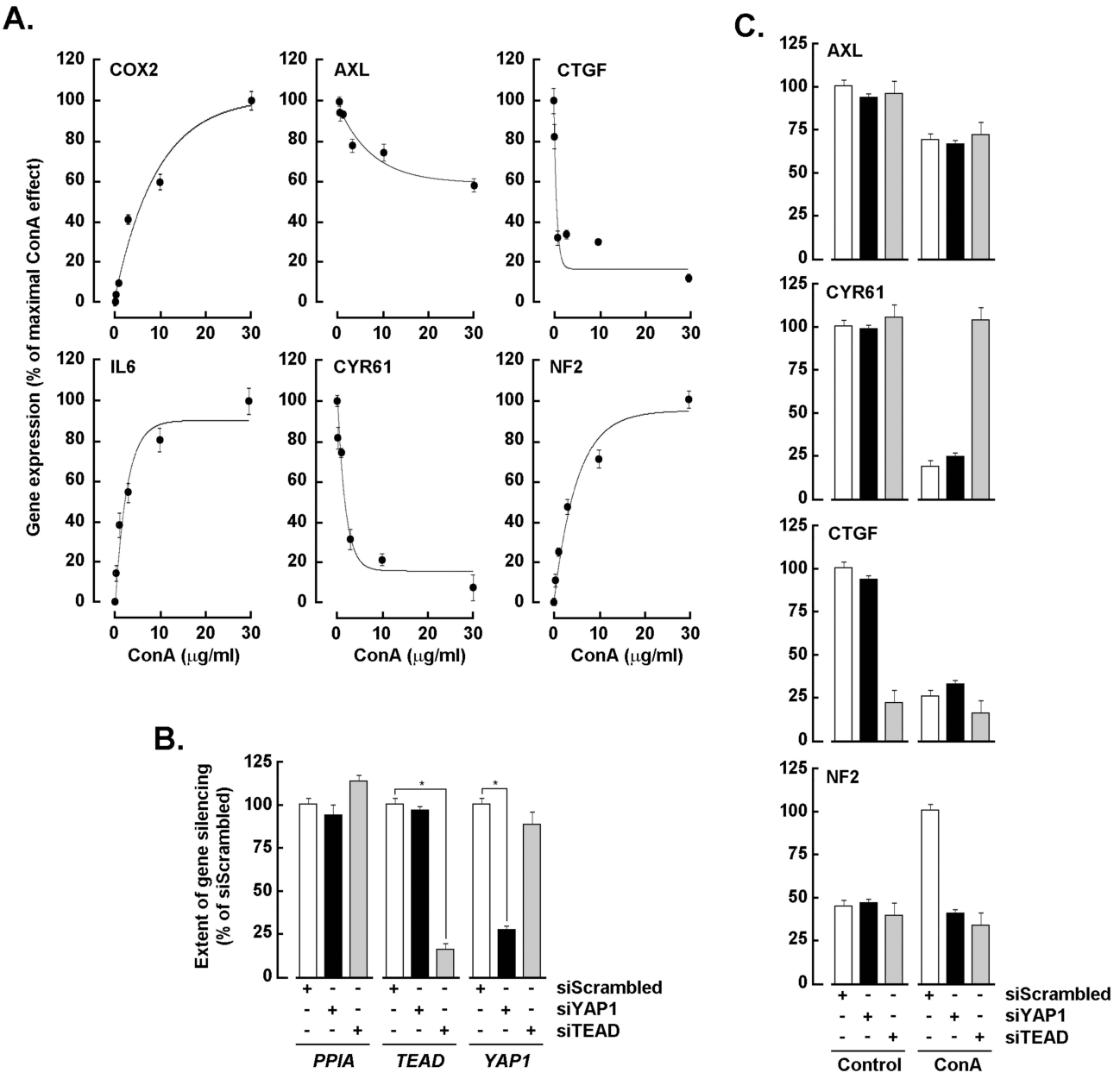

Figure 5 *Differential YAP/TEAD control of Concanavalin A-mediated regulation of Hippo pathway downstream effectors.* Serum-starved human U87 glioblastoma cells were treated with the indicated concentrations of ConA for 24 hours, total RNA was extracted and RT-qPCR performed as described in the Methods section. (**A**) Gene expression of inflammatory (*COX2, IL6*) and downstream Hippo pathway effectors (*AXL, CRGF, CYR61*, and *NF2*). (**B**) Transient gene silencing of YAP1 and TEAD was performed and extent and specificity of gene repression compared to *PPIA*. (**C**) Impact of YAP1 and TEAD silencing on ConA-mediated effects on downstream Hippo pathway effectors. Data points are the means ± SEM of triplicates from independent experiments.

Interestingly, YAP1 and TEAD silencing prevented the effects of ConA on *NF2*, while neither reversed the effects on *AXL* or *CTGF* (Figure 5C). On the other hand, only TEAD appeared to control ConA-mediated *CYR61* gene expression, while basal levels of CTGF in untreated cells also appeared to be decreased (Figure 5C). ConA-mediated downregulation of *CTGF, CYR61*, and *AXL* gene expression is consistent with activation of the Hippo signaling pathway.[36,37] Hippo pathway pharmacological targeting was next assessed. Knockdown efficiency was assessed here by qPCR and is reported as mRNA reduction. We did not obtain protein-level confirmation for the targeted gene and therefore cannot assume complete loss of protein function.

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Hippo Pathway Inhibitors Alter the Concanavalin A-Induced Phosphorylation of ERK and IκB in Human U87 Glioblastoma Cells

Capacity of Hippo pathway inhibitors IAG933, GNE7883, and VT107 was next tested to assess their impact on signal transducing events triggered by ConA. Serum-starved human U87 GBM cells were treated with ConA for 5 min in the absence or presence of 3 μM IAG933 (IAG), GNE7883 (GNE), or VT107 (VT) respectively (Figure 1A). It was found that the phosphorylation status of ERK (Figure 1B, left panel, black bars) and of IκB (Figure 1B, right panel, black bars) in ConA-primed cells was significantly reduced by all three inhibitors, similarly to the impact of αTGG (Figures 2 and 3). VT107 was found to be the most effective inhibitors and was next further characterized.

The Hippo Pathway Inhibitor VT107 Alters Dose-Dependently the Concanavalin A-Induced Phosphorylation of ERK and IκB in Human U87 Glioblastoma Cells

In order to further assess the cell signaling impact of VT107, serum-starved U87 GBM cells were treated with ConA for 5 min (ERK) or 2 min (IκB) in the absence or presence of increasing concentrations of VT107 (Figure 6A, VT). Phosphorylation status of ERK (Figure 6B, left panel) and of IκB (Figure 6B, right panel) was both inhibited by VT107 with an IC_{50} of 0.72 and 0.51 μM respectively against ERK and IκB phosphorylation. Conditioned media was further collected and impact of VT107 against ConA-mediated proMMP-2 activation as assessed by gelatin zymography as described in the Methods section. Along with the above demonstrated cell signaling inhibitory impact, VT107 was further found to prevent proMMP-2 activation into MMP-2 (Figure 6C).

The Hippo Pathway Inhibitor VT107 and αTGG Share a Common Anti-Inflammatory Molecular Signature in Concanavalin A-Primed Human U87 Glioblastoma Cells

Given the evident cell signaling inhibitory profiles and shared capacity to alter downstream events from ConA-primed cells between αTGG and the three Hippo pathway inhibitors tested herein, we next proceeded with a transcriptomic gene array screen of inflammatory-associated biomarkers using panels of 141 genes as described in the Methods section. Serum-starved human U87 GBM cells were treated for 24 hours with ConA, total RNA extracted and gene expression assessed by RT-qPCR. ConA was effectively found to trigger, among the genes investigated, the expression of 41 genes (Figure 7A, green). These included members of the CXCL (*CXCL2, CXCL9, CXCL10, CXCL11, CXCL12, CXCL13*), CXCR (*CXCR1, CXCR2*, and *CXCR4*), CCL (*CCL16, CCL17, CCL22, CCL28*, and *CCL3*), CCR (*CCR2, CCR3, CCR4*, and *CCR6*), and some interleukins/interleukin receptor (*IL9, IL10, IL13, IL17A, IL17C, IL17F, IL23A, IL33, IL1R1, IL1RN*) (Supplemental Table 1). Altogether, this highlights activation of immune-related pathways, cytokine signaling, and chemokine receptor expression, and suggests that ConA treatment triggers a robust immunomodulatory response in U87 cells, potentially involving inflammatory signaling and tumor microenvironment remodeling. In addition, 17 genes were concomitantly downregulated upon ConA treatment (Supplemental Table 1). Among those genes included *TLR3, IL5, CCL2, CXCL1*, and *GBP1*, reflecting a shift in immune response and reduced inflammatory signaling following ConA treatment. Next, the 10 commonly shared genes which expression was triggered by ConA, and that was altered by treatment with all three Hippo pathway inhibitors tested, were compared to the inhibitory effects of αTGG. It was found that the best correlation existed when αTGG was compared to VT107 ($r^2 = 0.87$), while no correlation was found when αTGG effects were compared to those of either GNE7883 or IAG933 (Figure 7B). Protein-to-protein interaction network of the 10 commonly shared and downregulated genes between all the inhibitors tested in ConA-treated cells was determined with STRING and confirms the predicted inter-relationship they have between them.

Discussion

In this study, we sought to validate and optimize the responsiveness of U87 GBM cells to ConA, with the goal of characterizing inflammation-related molecular events that may contribute to the TME. ConA indeed reliably modeled inflammatory signaling in U87 GBM cells by activating diverse signaling pathways across multiple cell types[30–32] including ERK and NF-κB/IκB pathways and inducing downstream inflammatory and invasion-associated markers such as Snail, COX2, proMMP-2. Furthermore, transcriptomic profiling revealed induction of cytokine transcripts (*IFNG,*

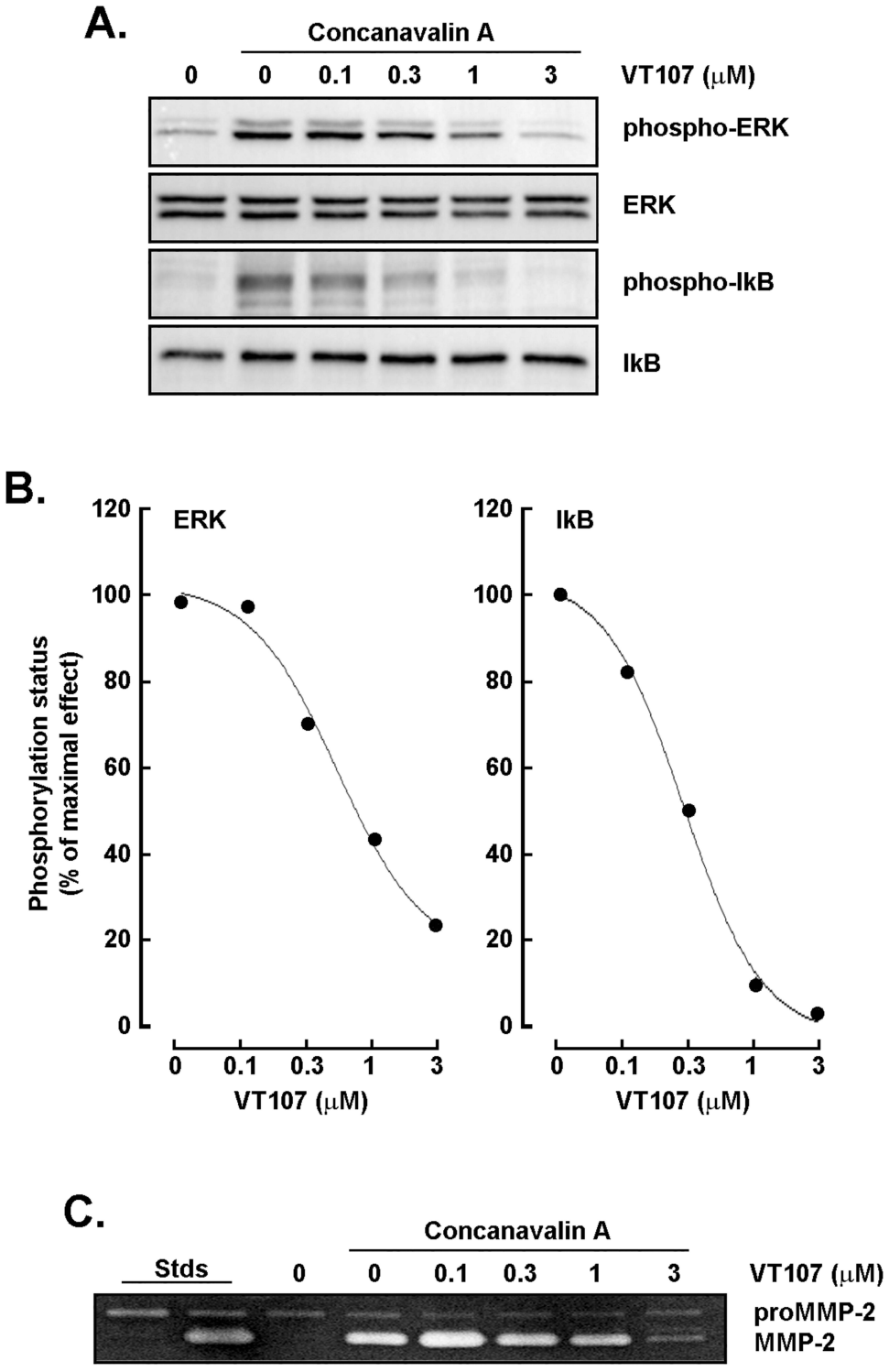

Figure 6 *The Hippo pathway inhibitor VT107 alters dose-dependently the Concanavalin A-induced phosphorylation of ERK and IκB in human U87 glioblastoma cells*. Serum-starved human U87 glioblastoma cells were treated with 30 μg/mL Concanavalin A (ConA) for 5 min in the absence or presence of the indicated concentrations of VT107 (VT). (**A**) Protein cell lysates were harvested and processed for immunoblotting as described in the Methods section, to detect the phosphorylation status of ERK and of IκB. (**B**) A representative densitometric analysis was performed and phosphorylation status expressed as the percent of phospho-ERK/ERK or phospho-IκB/IκB ratios of ConA-treated cells. Western blot and densitometric analysis are representative of 3 independent experiments. (**C**) Conditioned media was collected and gelatin zymography performed as described in the Methods section to monitor the impact of VT107 on proMMP-2 activation.

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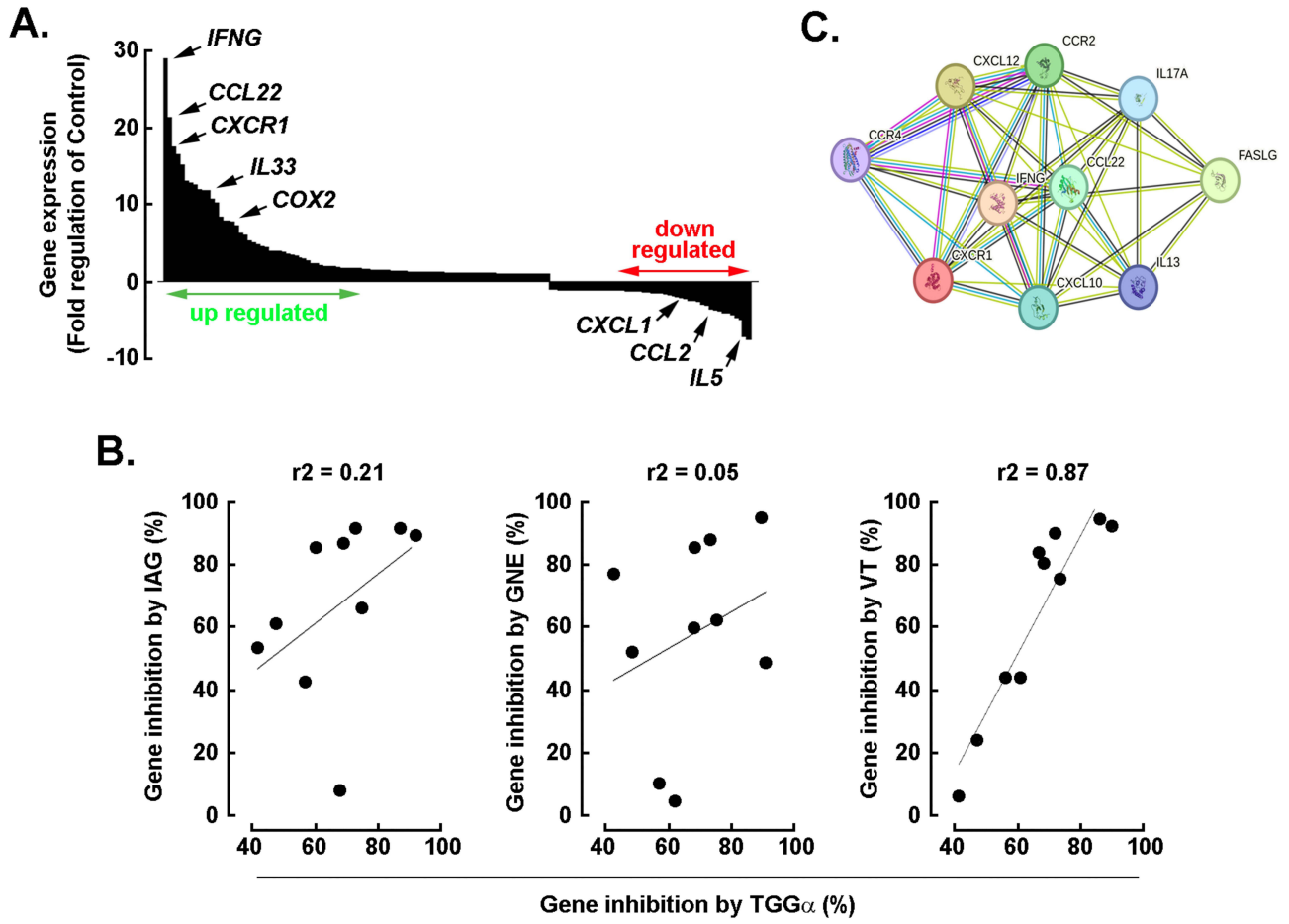

Figure 7 *The Hippo pathway inhibitor VT107 and αTGG share a common anti-inflammatory molecular signature in Concanavalin A-primed human U87 glioblastoma cells.* (**A**) Serum-starved human U87 glioblastoma cells were treated for 24 hours with 30 μg/mL Concanavalin A (ConA), total RNA extracted and processed for a gene array screen of 141 inflammatory-associated genes as described in the Methods section by RT-qPCR. (**B**) Serum starved cells were similarly treated with ConA in the presence of 1 μM of either IAG933 (IAG), GNE7883 (GNE) or VT107 (VT) for 24 hours and extent of inhibition of the 10 most induced common genes assessed and correlated to that of 30 μM αTGG. (**C**) Protein-to-protein interaction network of the 10 commonly shared and downregulated genes between all the inhibitors tested in ConA-treated cells as determined with STRING.

IL-17A/F, IL-9), indicating an inducible inflammation-like program in tumor cells that may modulate the TME, although protein secretion remains to be confirmed. αTGG robustly suppressed ConA-driven ERK and IκB phosphorylation, reduced expression of inflammatory and EMT markers, and prevented proMMP-2 activation, consistent with attenuation of inflammation-linked invasion. VT107 produced highly similar effects (transcriptomic $r^2 = 0.87$ with αTGG), similarly inhibiting ERK/IκB phosphorylation and proMMP-2 activation and suggesting a shared anti-inflammatory signature linked to Hippo/YAP modulation. These findings support the notion that GBM cells can engage in inflammation-like signaling, which may play a pivotal role in shaping tumor behavior and interactions with immune components.

ConA-stimulated induction of the transcription of key cytokine genes in U87 GBM cells, suggests that these cells may possess a latent or inducible inflammatory signaling capacity. Although these cytokines are traditionally associated with immune cells, particularly T helper subsets, emerging evidence indicates that tumor cells can aberrantly express immune-related genes under specific stimuli, contributing to the modulation of the TME. The upregulation of these transcripts may reflect an intrinsic ability of GBM cells to engage in inflammatory crosstalk, potentially influencing immune cell recruitment, angiogenesis, or tumor progression. While protein expression and secretion remain to be confirmed, these transcriptional changes open new avenues for exploring non-canonical inflammatory pathways in GBM. Future studies should investigate whether these cytokines are translated and functionally active, which could reveal novel mechanisms of tumor-immune interaction and identify new therapeutic targets.

Inflammation and immune cell infiltration in GBM are usually described as tumor-promoting, but an alternative, controversial hypothesis argues that certain inflammatory states and immune infiltrates can act as limitans that constrain tumor growth. This perspective highlights that inflammatory signaling is context dependent: the same mediators and cells that foster proliferation, invasion, and immune suppression under chronic, low-grade inflammation can, under different timing, magnitude, or cellular composition, trigger anti-tumor effects such as cytotoxicity, senescence, or growth restriction. Reconciling the pro- and anti-tumor roles of inflammation therefore requires high-resolution, time-dependent, and cell-type-specific studies that explicitly measure functional immune activity and Hippo pathway status. Therapeutic strategies should therefore be precision-guided: selectively amplify inflammation components that restrain growth while suppressing those that facilitate invasion, immune evasion, and possibly YAP/TAZ-driven tumorigenesis.

Interestingly, ConA decreased transcripts of canonical YAP/TEAD targets (AXL, CTGF, CYR61), implying activation of upstream Hippo kinases and functional suppression of YAP output in this context; both VT107, a direct YAP/TEAD inhibitor, and αTGG converged on suppressing inflammatory gene programs and invasion, supporting a model in which modulation of YAP activity can blunt inflammation-driven pro-tumor signaling. Recently, combining temozolomide (TMZ) with a YAP inhibitor enhanced anti-tumor efficacy in GBM models,[38,39] suggesting that targeting the Hippo/YAP axis helps overcome TMZ resistance, a major clinical challenge in GBM.[40] Thus, the high degree of molecular signature overlap between VT107 and αTGG in terms of inflammatory gene suppression suggests that modulation of YAP activity, whether through upstream Hippo activation or direct inhibition of YAP/TEAD, can attenuate inflammation-associated signaling. These findings reinforce the relevance of the Hippo-YAP axis in regulating GBM inflammation and support the therapeutic potential of targeting this pathway to reshape the TME.

However, key unresolved points include protein-level confirmation of induced cytokines and identification of the direct molecular targets of αTGG and VT107 within the ERK/IκB and upstream lectin/glycoprotein receptor networks. Recommended next steps would be validation of cytokine secretion and protein changes, mapping drug targets in the ERK/IκB–Hippo axis, and testing efficacy and bioavailability in orthotopic GBM models. Taken together, these results indicate that targeting inflammation via αTGG or Hippo inhibitors may both reduce invasion and help reprogram the microenvironment to improve responses to conventional therapies and immunotherapy, warranting mechanism-driven combination studies and biomarker development to stratify likely responders.

Conclusion

This study shows that ConA triggers a robust pro-inflammatory program in U87 GBM cells and that αTGG potently suppresses these responses in a time- and dose-dependent manner, identifying αTGG as a strong anti-inflammatory candidate extendable beyond GBM models. Hippo pathway inhibitors, especially VT107, produced comparable inhibition of ConA-induced ERK/NF-κB signaling, downstream inflammatory markers, and pro-invasive readouts, and yielded a transcriptomic anti-inflammatory signature closely matching that of αTGG. Together, these results reveal a convergence between αTGG activity and Hippo/YAP pathway modulation in dampening inflammation-driven oncogenic signaling, supporting further preclinical evaluation of αTGG and Hippo inhibitors as inflammation-targeted therapies for GBM.

Abbreviations

ATCC, American type culture collection; BSA, bovine serum albumin; ConA, Concanavalin A; EMT, epithelial-to-mesenchymal transition; ERK, extracellular signal-regulated kinases; GBM, glioblastoma; IkB, inhibitor of kappa B; MAPK, mitogen-activated protein kinase; MMP, matrix metalloproteinase; SDS, sodium dodecyl sulfate; STAT3, signal transducer and activator of transcription 3; TAZ, transcriptional coactivator with a PDZ-binding domain; TME, tumor microenvironment; TMZ, temozolomide; YAP, yes-associated protein.

Data Sharing Statement

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

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Disclosure

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