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The functional role of p38 MAPK pathway in malignant brain tumors

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Gliomas are extremely debilitating malignant brain tumors with very limited response to therapies. The initiation and progression of gliomas can be attributed to several molecular abnormalities, such as mutations in important regulatory networks. In this regard, the mitogen-activated protein kinases (MAPKs) arise as key signaling pathways involved in cell proliferation, survival, and differentiation. MAPK pathway has been altered in most glial tumors. In glioma cells, the activation of p38 MAPK contributes to tumor invasion and metastasis and is positively correlated with tumor grade, being considered a potential oncogenic factor contributing to brain tumorigenesis and chemotherapy resistance. Hence, a better understanding of glioma pathogenesis is essential to the advancement of therapies that provide extended life expectancy for glioma patients. This review aims to explore the role of the p38 MAPK pathway in the genesis and progression of malignant brain tumors.

KEYWORDS

glioma, mitogen-activated protein kinases, p38 MAPK inhibitors, small molecules, brain tumors

Introduction

Malignant brain tumors are rapidly growing cancer with high invasion potential to surrounding healthy brain structures, which include gliomas and neuronal or mixed neuronal-glial tumors (Lapointe et al., 2018). Gliomas are the most common central nervous system (CNS) cancers, comprising approximately 80% of all brain malignancies in adults (Hanif et al., 2017; Morrone et al., 2021). The heterogeneity and high invasiveness are hallmarks implicated in the poor prognosis of these tumors (Colquhoun, 2017; Reni et al., 2017).

The initiation and progression of gliomas can be attributed to several molecular abnormalities, such as mutations in important regulatory networks (Morrone et al., 2016; Pandey et al., 2016). The mitogen-activated protein kinases (MAPKs) are key signaling pathways involved in the regulation of cell proliferation, survival, and differentiation (Gao et al., 2005). In this regard, the MAPK pathway has been widely studied and is altered in most glial tumors. In gliomas, this pathway has been associated with poor prognosis, and resistance to radiotherapy, and appears to regulate, directly and indirectly, its genesis and progression through crucial signaling mediators (Patil et al., 2013; Pandey et al., 2016).

Among the MAPK pathways, p38 mitogen-activated protein kinase (p38 MAPK) signaling was identified as a mediator of stress and inflammation responses (Ono and Han, 2000). This pathway is involved in the biology of different types of cancer, and plays an extremely significant role in cancer progression, such as proliferation, invasion, and survival, and has been widely studied as a potential pharmacological target (Wagner and Nebreda, 2009; Roche et al., 2020). Originally described as a tumor suppressor kinase, p38 has a dual role in tumorigenesis, also acting as a tumor promoter (Koul et al., 2013; Martínez-Limón et al., 2020). In gliomas, phosphorylated p38 MAPK has been considered a potential biomarker of progression once its activation contributes to tumor invasion and metastasis and is positively correlated with the tumor grade (Glassmann et al., 2011; Pandey et al., 2016).

Considering the importance of the signaling pathways involved in the genetic and molecular alterations in the onset of cancer, describing the role of the p38 MAPK pathway in tumor microenvironment and in the progression of gliomas becomes a key strategy to comprehend and propose new treatments for malignant brain tumors.

The glioma microenvironment

Malignant brain tumors are aggressive and impact directly patients' life quality (Omuro, 2013). Gliomas are representative of around 25% of CNS cancers and are classified according to their similarities with glial cells from which arise, and astrocytomas are the most frequent type. Their classification includes both molecular and histological parameters and encompasses two principal subgroups: diffuse and non-diffuse gliomas. Diffuse gliomas reveal a massive infiltrative growth in the surrounding parenchyma and are more genetically heterogenic in their composition and difficult to treat when compared to non-diffuse gliomas (Omuro, 2013; Perry and Wesseling, 2016; Ostrom et al., 2018).

Glioblastoma (GBM) is the highest grade of diffuse astrocytoma and is considered incurable (DeAngelis, 2001;

Omuro, 2013; Perry and Wesseling, 2016; Ostrom et al., 2018). Despite the improvements in therapeutic research, maximal surgical resection followed by radiotherapy and chemotherapy remains the main standard of treatment. Tumor recurrence and therapeutic resistance are frequent, so the median survival rate is around 15 months. Hence, treatments of malignant brain tumors remain challenging (Lin et al., 2017).

It is well known that molecular characteristics inside the tumor microenvironment (TME) indicate the sensitivity of tumors to therapy. Initially, tumorigenesis is related to the gain of numerous genetic mutations, which provide malignant cells resistant to the growth-inhibitory and apoptotic signals (Hanahan and Weinberg, 2011; Kelly and Strasser, 2011). All GBM have common oncogenes likely to carry a growth advantage, which are considered driver mutations for their pathogenesis. As pointed in the literature, well characterized oncogenes and tumor suppressor genes perform critical roles in several signaling pathways, being great influencers in biological behaviors and in glioma heterogeneity (Eder and Kalman, 2014).

In general, tumors are complex tissues composed of distinct cell types that interact with each other forming an intense signaling network (Hanahan and Weinberg, 2011). The glioma microenvironment includes non-neoplastic cells, GBM stem cells (GSCs), fibroblasts, immune cells, tumor-associated macrophages (TAMs), endothelial cells, and vascular pericytes. In addition, TME also includes proteins and non-protein biomolecules produced by all of these distinct cell types, supporting the various processes of tumor promotion (Schiffer et al., 2018). Numerous interrelated pathways are frequently mutated in the glioma microenvironment, typically those controlling cell-cycle, cellular survival, invasion, and angiogenesis. These alterations result in tumor self-sufficiency with growth signals, cell death resistance, growth suppressors evasion, sustained angiogenesis, and tissue invasion (Pojo and Marques, 2011; Nørøxe et al., 2017).

Hypoxia is considered a hallmark of GBM, and a critical factor associated with mutations in multiple signaling pathways that affect the tumor landscape (Oliver et al., 2009; Schiffer et al., 2018). Solid tumors grow fast, surpassing vascular supply and consequently, inhibiting oxygen diffusion. Several hypoxia-mediated signaling pathways play a role in angiogenesis, tumor proliferation, and immunosuppression (Mohan et al., 2021; Scheffel et al., 2021). Glioma cells, under hypoxic conditions, secrete interleukins and chemokines, which provide proliferative signals and have been implicated in the stimulation of angiogenesis. Likewise, extracellular adenosine increases in hypoxic conditions and is associated with tumor cell proliferation through a variety of pathways including MAPK signaling and the upregulation of cyclin proteins (Zhou et al., 2017; Scheffel et al., 2021).

The mitogen-activated protein kinases pathway

Protein kinases are enzymes that have the property to catalyze protein phosphorylation through the transfer of a phosphoryl group from ATP and GTP to threonine, serine (Ser-/Thr-specific protein kinases; S/T PKs), tyrosine (Tyr-specific protein kinases; T PKs), both serine/threonine and tyrosine (dual-specificity protein kinases) (Cohen, 2002; Baier and Szyszka, 2020). The phosphorylation of these amino acids residues triggers extra and intracellular stimuli, orchestrating a highly efficient mechanism for the control of protein activity (Bononi et al., 2011). About 30% of all human proteins can be altered by kinases activity, which can regulate most cellular pathways, particularly those related to signal transduction (Ardito et al., 2017).

MAPKs are Ser/Thr kinases ubiquitously expressed, that regulate cellular mechanisms in response to a wide range of stimuli including cytokines, growth factors, antigens, toxins, drugs, osmolarity, temperature, oxygen radicals, ultraviolet light, changes in cell shape, adherence, and cell-cell interactions (Pearson et al., 2001; Cuevas et al., 2007; Lee et al., 2020). In mammals, 14 MAPKs have been described so far, characterized in seven groups. The conventional MAPKs include the extracellular signal-regulated kinases 1/2 (ERK1/2), c-Jun amino (N)-terminal kinases 1/2/3 (JNK1/2/3), p38 isoforms (α , β , γ , and δ), and ERK5. Atypical MAPKs have nonconforming particularities and consist of ERK3/4, ERK7, and Nemo-like kinase (NLK) (Cargnello and Roux, 2011).

The activation of MAPKs and their downstream targets plays a pivotal role in different signaling cascades involved in transcription, development, differentiation, migration, cell death, and many other critical cellular functions (Geest and Coffer, 2009; Yue and Lopez, 2020). Detriment in MAPKs signaling due to mutation or altered expression of proteins regulating MAPKs cascades can lead to pathological conditions such as cancer, neurodegeneration, inflammation, and developmental defects (Johnson et al., 2005; Kim and Choi, 2015).

MAPKs signaling cascades present recurrent contributions to oncogenesis, tumor progression, and drug resistance, which suggests that its pharmacological modulation can be a promising strategy in the development of cancer therapies (Chaikuad et al., 2018; Braicu et al., 2019; Wittlinger and Laufer, 2021). It is well known that MAPKs can regulate cellular events directly related to tumor development, such as proliferation, apoptosis, inflammation, and immunity (Kim and Choi, 2015). JNK, ERK1/2, and p38 have been described as the most involved in the carcinogenesis processes (Sebolt-Leopold and Herrera, 2004; Lei et al., 2014; Kim and Choi, 2015; Peluso et al., 2019).

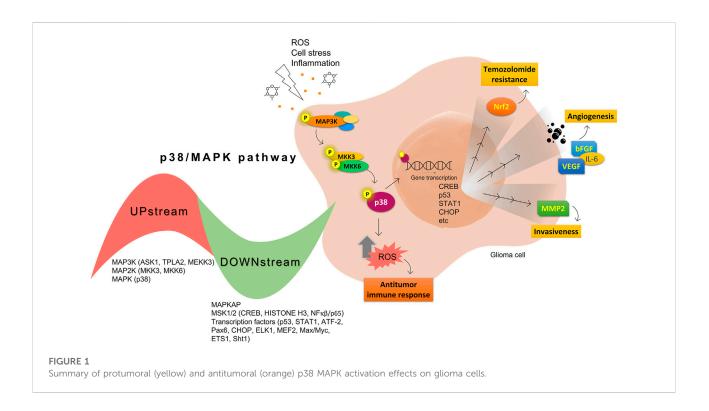
The p38 MAPK pathway and cancer

Discovered on a pharmacological screen in 1994, p38 MAPK is a signal transduction pathway that plays a key role in cellular adaptation to extracellular stimuli (Han et al., 1994; Yong et al., 2009; Zou and Blank, 2017). Its activation is often in response to various environmental and cellular stresses, inflammation, and other signals such as UV irradiation, oxidative stress, and exposure to DNA damaging agents, as well as growth factors and cytokines (Loesch and Chen, 2008; Keshet and Seger, 2010).

After extracellular signals, activation of the p38 pathway usually proceeds through a classical phosphorylation cascade, where a MAPKKK (ASK1, TPL2, MEKK3) phosphorylates and activates the MAPKKs specifics of p38 MAPK, MKK3, and 6, which in turn, mediate the activation of the different p38 MAPK isoforms (Cuadrado and Nebreda, 2010; Stramucci et al., 2018). The p38 sometimes can also be phosphorylated by MKK4, a kinase well known as a JNK activator (Brancho et al., 2003). Once activated, p38 can phosphorylate many cytosolic proteins as Bcl-2 family and tau proteins. Besides the phosphorylation of cytosolic proteins, p38 can be translocated from the cytosol to the nucleus, where it phosphorylates, among other, the MSK 1 and 2, which in turn can phosphorylate histone H3 and the related transcription factors CREB and ATF1. This p38 phosphorylation cascade regulates cellular responses ranging from apoptosis to cell division, cell invasion, and inflammatory response (Deacon et al., 2003; Cuadrado and Nebreda, 2010; Reyskens and Arthur, 2016).

The p38 MAPK family compromises four isoforms: p38a (also known as MAPK14 or SAPK2a), p38 β (MAPK11, SAPK2b), p38 γ (MAPK12, SAPK3, ERK6), and p38 δ (MAPK13, SAPK4) (Zou and Blank, 2017). The four isoforms share more than 60% homology and are widely expressed; however, each isoform has different tissue-specific expression patterns (Cuenda and Sanz-Ezquerro, 2017; Mai et al., 2020). The isoform p38a is expressed in most cell types and is widely cited (Wagner and Nebreda, 2009). In contrast, p38 β is expressed at very low levels, being restricted to the brain and lung. The p38 γ and p38 δ have more limited expression and are likely to have specialized functions. While p38 γ is mostly detected in skeletal muscle and nervous system, the p38 δ is enriched in uterus and pancreas (Ono and Han, 2000; Cuenda and Rousseau, 2007).

In recent years, the involvement of p38 MAPK in cancer has been widely described (Zou and Blank, 2017; Martínez-Limón et al., 2020; Lee et al., 2020; Anton et al., 2021). This pathway, as well as several other signaling cascades, regulates the balance between cell survival and death in response to stress, which impacts directly on tumorigenesis (Hanahan and Weinberg, 2011; Grossi et al., 2014). This regulation, depending on the type and strength of stress, cell type, and the interference among other signaling pathways can lead to opposite cell fates of survival or death (Dhillon et al., 2007; Wagner and Nebreda, 2009).



Some studies have suggested a role for p38 MAPK in mediating pathways that lead to cell apoptosis and growth inhibitory signals, particularly in promoting cell cycle arrest and differentiation, which supports the idea that the stressactivated kinase is a tumor suppressor (Bulavin and Fornace, 2004; Olson and Hallahan, 2004; Koul et al., 2013). However, other studies have shown that activation of this signaling pathway can produce exactly the opposite effect such as antiapoptotic and proliferative effects, enhancing cell survival migration, or resistance to stress pathways, and chemotherapeutic agents in tumor cells (Wada and Penninger, 2004; Wagner and Nebreda, 2009; Martínez-Limón et al., 2020). The p38 MAPK has also been related to cell death by apoptosis, which led us to consider this pathway as a key factor in the response to chemotherapy (O'Callaghan et al., 2015; García-Cano et al., 2016).

Malignant brain tumors and p38 MAPK signaling

MAPKs are expressed in various types of malignant brain tumors (Jones, et al., 2012; Soeda et al., 2017). Besides, p38 is upregulated GBM cell lines as well as in GBM patients (Demuth et al., 2007; Pandey et al., 2016). This protein is shown to be involved in the response of diverse molecules, it is mainly implicated in inflammation, proliferation, migration, invasion, and ROS signaling been involved in GBM initiation, progression, metastasis, and chemotherapy response (Yeung et al., 2013; Pandey et al., 2016).

Among diverse brain tumor types, glioma presents one of the worst patients' prognostics. GBMs are hard to treat and avoid recurrence due to its infiltrative pattern. The involvement of p38 MAPK in the GBM migration and invasion has been extensively described (Park et al., 2006; Yoshino et al., 2006; Demuth et al., 2007; Chen et al., 2020). Demuth et al. (2007) have identified the MKK3 as a key activator of GBM invasiveness through p38 activation, both *in vitro* and *in vivo*. Irradiation is often part of the GBM treatment scheme, although, in cells that present mutant PTEN it was described that irradiation can activate p38/Akt and PI3K/Akt signaling pathways, increasing MMP-2 expression and intensifying invasiveness (Park et al., 2006).

Long noncoding RNAs (lncRNAs) are transcripts with more than 200 nucleotides that commonly do not encode proteins, many of them have been characterized as oncogenes or tumor suppressors in cancer (Ma et al., 2018). The MRCCAT1 is an oncogenic lncRNA that promotes proliferation and migration of GBM cells *via* p38 MAPK signaling activation. Moreover, lncRNA-ATB promotes invasiveness mediated by tumor growth factor- β (TGF- β) which activates the p38 MAPK pathway (Tang et al., 2019).

Nowadays it is known that, in tumor progression, gliomas orchestrate the immune system to a protumoral phenotype. The p38 MAPK is also correlated with immune and inflammation signaling, being responsible for the

Agent/p38 MAPK inhibitor structure	Cell line	Outcome	Reference
BIRB796	U87	Autophagy reduction: lower fluorescence intensity and the lower number of autophagic vacuoles per cell treated.	Xu et al. (2020)
	U87 e U251	Blocked the G1 phase cell cycle and decreased S and G2 phases; And inhibited the proliferation, migration, and invasion of GBM cell lines.	Zhao et al. (2021)
SB203580	F98	Decreased ROS production and the cell number in early apoptosis.	Li et al. (2018)
SB203580 (and TMZ)	U87 and U251	Increased the sensitivity of glioma cells to TMZ.	Ma et al. (2015)
SB203580 (plus Anisomycin and TMZ)	U87 and U251	SB203580 reduced anisomycin and TMZ antitumoral effects promoting migration and invasion.	Chen et al. (2017)
SB203580 (and Vandetanib)	SF767 and U251	Synergism on antitumoral effect against glioblastoma cells.	Sooman et al. (2013)
SB203580 (and Anisomycin)	GBM: X01, X02, X04, X05, X06, 08–322, 08–387; X07 Gliosarcoma; and X03Anaplastic oligoastrocytoma	Decreased proliferation. Increased the undifferentiated GSC population and apoptotic events.	Soeda et al. (2017)
SB203580 (plus Arenobufagin and Hellebrigenin)	U87 and primary mouse glial cells	SB203580 decreased cell viability and enhanced the cytotoxicity of arenobufagin and of hellebrigenin.	Han et al. (2018)
LY2228820/Ralimetinibe (and PD-L1 antibody) \downarrow \downarrow \downarrow \downarrow \downarrow \downarrow \downarrow \downarrow \downarrow \downarrow	GL261-C57BL/6 mice	Enhanced survival of mice with temozolomide-resistant glioma-bearing with reduction of the accumulation of macrophages/microglia.	Dang et al. (2021)
	U251	Inhibited migration, invasion and the antitumoral inflammatory response.	Yeung et al. (2012)

TABLE 1 Use of p38 MAPK inhibitors in pre-clinical studies on glioma cell lines.

Abbreviations: GBM, glioblastoma; MK2, kinase MAPK-activated protein kinase 2; TMZ, temozolomide.

production of cytokines in the TME (Choi et al., 2001; Schieven, 2009; Kühnöl et al., 2013; Wang et al., 2019). Wang et al. (2019) have been shown that MXB (also named MX2) protein, a component of the innate immune response, is downregulated in GBM cells. This fact corroborates to tumor progression once MXB overexpression decrease the cell proliferation, invasion, and migration due to the decrease in ERK1/2 and p38 phosphorylation/activation, and Nf- κ B levels (Wang et al., 2019). In this context, it is well known that angiogenesis is essential for tumor progression, T98G, U373, and U87 glioma cell lines have been revealed the p38 MAPK and JNK constitutively activated contributing angiogenesis induced by the vascular endothelial growth factor (VEGF) release (Yoshino et al., 2006). Other studies have shown that MAPKs and hypoxia can control VEGF expression in cell model (Berra et al., 2000). Besides, VEGF, p38 still contributes to the basic fibroblast growth factor (bFGF), epidermal growth factor (EGF), IL-6, and another proangiogenic cytokine secretion (Tate et al., 2013). The p38 MAPK inhibition on glioma cells showed decreased VEGF secretion (Yoshino et al., 2006) and enhanced immune responses *in vitro* (Kühnöl et al., 2013). Figure 1 summarizes the p38 activation effects on glioma cells.

The p38 MAPK inhibitors in gliomas

Several small-molecule protein kinase inhibitors have been tested for cancer treatment, demonstrating interesting effects on the immune system. Among these, there is the EGFR tyrosine kinase inhibitor gefitinib, and other inhibitors focusing on multiple targets, like imatinib, sorafenib, and sunitinib (Ott and Adams, 2011). Regardless of p38 MAPK dual role as a possible oncogene or tumor suppressor, this signaling pathway has attracted much attention as a promising drug target for cancer therapy based on small inhibitory compounds (Borst et al., 2013; Koul et al., 2013; Haller et al., 2020). Since its first inhibitor, a pyridinylimidazole compound, described in 1994, numerous inhibitors against p38 MAPKs have been reported with diverse chemical structures (Han et al., 1994; Zhang et al., 2007; Yong et al., 2009; Borst et al., 2013; Haller et al., 2020). These inhibitors are divided into two groups, depending on their mode of binding: the direct inhibitors, such as SB203580, and the majority of the p38 inhibitors, which binds competitively to the ATP-binding site; and the indirect inhibitors such as BIRB-796, which inhibits p38 MAPK activity by conformational change (Zhang et al., 2007; Yong et al., 2009; Haller et al., 2020). Regarding GBM proliferation, a study has shown that the p38y is correlated with the grade of glioma malignancy and promotes proliferation and progression (Yang et al., 2013). Cycloartenal is an important triterpenoid prevalently found in plants. This compound inhibits p38 MAPK activation and demonstrated antiproliferative effects in U87 human glioma cells (Niu et al., 2018).

Once p38 MAPK is involved in glioma proliferation, researchers have investigated the potential of p38 MAPK inhibitors in inducing cell death in GBM by itself or in association with other treatments (Table 1). The LY479754 p38 inhibitor increased temozolomide antiglioma effects in U87 and SNB19 spheroids when used in combination for 5 days (Demuth et al., 2007). The SB203580 p38 MAPK inhibitor potentialized the antiproliferative effects of temozolomide when U87 and U251 cells were treated for 24 h *via* Nrf2 signaling inhibition, indicating that p38 MAPK/ Nrf2 activation is a network involved in temozolomide glioma cells resistance (Ma et al., 2015). Curiously, a study has shown that the circadian clock has an important role in the activation of the p38 MAPK pathway, which means that the treatment with p38 MAPK inhibitors may be more effective and less toxic depending on the time the therapy is administered (Goldsmith et al., 2018).

Glioma cells undergo metabolism reprogramming due to high proliferation rates and elevated consumption of glucose in this process. TGF- β participates in this mechanism, and an interesting study showed that TGF- β activated PFKFB3 expression and activity *via* activation of the transcript factor Smad, p38 MAPK e PI3K/Akt signaling pathways while p38 MAPK inhibition reversed TGF- β stimulatory effects (Rodríguez-García et al., 2017).

Since p38 is a ubiquitous protein, treatment of gliomas with p38 MAPK inhibitors may be successful, however, the involvement of this pathway in multiple cellular processes may result in ambiguous effects. An interesting study showed that temozolomide inhibited proliferation, migration, and invasion in U87 and U251 cell lines, and these effects were associated with a decrease in the levels of AQP4 dependent on p38 MAPK activation. When the p38 MAPK inhibitor (SB203580) was used in combination with temozolomide, it reduced temozolomide antitumoral effects (Chen et al., 2017). Besides, treatment with SB203580 reduced proliferation but enhanced EGFR expression and cancer stem-like cells self-renewal enhancing undifferentiated state which could confer treatment resistance (Soeda et al., 2017). Furthermore, the predominant association among p38 MAPK activation (p-p38) with malignancy and progression in gliomas could be explained, in part, because high p38 or p-p38 levels are linked to increasing ROS, which is harmful to cancer cells and confers antitumor responses (Liu et al., 2015; Thiyagarajan et al., 2016; Liu et al., 2020).

Clinical studies targeting p38 MAPK in cancer

Several clinical trials targeting p38 MAPK in cancer are currently underway. Ralimetinib (LY2228820), for example, is a potent and selective inhibitor of p38 α and p38 β and has been tested as a single agent and in combination with chemotherapeutic agents for the treatment of ovarian cancer, GBM, and metastatic breast cancer (Campbell et al., 2014; Vergote et al., 2020). An important clinical trial NCT02364206, including the ralimetinib, has been conducting to determine the recommended dose of the p38 inhibitor in combination with temozolomide and radiotherapy during chemoradiotherapy period (phase I) in patients with newly diagnosed GBM and to estimate the 6-month progression free survival (PFS) rate of patients when administered at the recommended dose in combination with radiotherapy and concomitant temozolomide (phase II).

Because of the wide-ranging controlling role of p38 in different cellular processes, the possibility of side effects resulting from an undesired pharmacological activity is a relevant concern for the p38 inhibitors. There are many discontinued p38 inhibitors that failed due to safety concerns, presenting adverse effects directed mostly to the hepatic system and skin (Xu et al., 2008; Karcher and Laufer, 2009; Yong et al., 2009). Other interesting approaches using CRISPR/Cas9 can allow the comparison of the altered gene expression profiles of the MAPK pathway members and the response to specific cancer treatments (Braicu et al., 2019). It is relevant to note that small molecules targeting p38 can cause a significant delay in cancer growth through multiple mechanisms, which becomes the development of p38 MAPK inhibitors with therapeutic benefits and reduced side effects a promising opportunity for future clinical studies to treat cancer.

Conclusion

Malignant brain tumors are debilitating diseases with a dismal prognosis and extremely limited response to therapies. The aggressiveness of GBM has been marked by several signaling pathway dysregulations that are implicated in cell proliferation, survival, migration, and angiogenesis. Tumor cells are heterogeneous, so it is also important to note that targeting a mediator involved in multiple pathways would constitute a more efficient therapy. MAPKs are shown to support numerous processes of cell survival. The p38 MAPK pathway is a key route capable to influence different frameworks of cellular survival mechanisms such as inflammation, proliferation, migration, invasion, and ROS signaling. Briefly, the p38 MAPK is likely to be an oncogenic factor contributing to GBM initiation, progression, and chemotherapy resistance. Hence, a better understanding of the GBM tumor microenvironment is essential to the advancement of therapies that provide extended life expectancy for patients. Thus, targeting key components of these signaling pathways using smallmolecule inhibitors, such as p38 inhibitors and antibodies, could provide progress in the treatment of gliomas.

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NG, TS, FFC, LR, MG, and SL wrote and critically appraised the literature. FM wrote, reviewed, and approved final version of the manuscript.

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