Translational Oncology 64 (2026) 102645

Contents lists available at ScienceDirect

Translational Oncology

journal homepage: www.elsevier.com/locate/tranon

Review Article

Radial glial cells and glioblastoma: how developmental neurobiology can inform our understanding of brain cancer initiation, treatment resistance, and resilience

Caitland A Love [a], John W Figg [b], Mia Engelbart [b], Illeana West [b], Catherine Flores [a,b,*]

[a] University of Florida, Department of Neuroscience, 1149 Newell Drive, Room L1-100 Gainesville, FL 32610, USA
[b] University of Florida, Lillian S. Wells Department of Neurological Surgery, PO Box 100265, Gainesville, FL 32610, USA

ARTICLE INFO

Keywords:
Glioma stem cells
Radial glial cells
Glioblastoma
Neurodevelopment

ABSTRACT

Glioblastoma (GBM) remains one of the most lethal brain malignancies, with an abysmal five-year survival rate near 6 %. Despite advances in tumor biology, clinical outcomes have not improved, partially due to glioma stem cells (GSCs) that drive treatment resistance. Radial glial cells (RGCs), recognized as key progenitors in neurodevelopment, have recently gained attention in GBM research due to RGC-like populations being identified in GBM. RGCs have striking similarities with GSCs, including their mechanisms of self-renewal, pluripotency, and migration. This review highlights those parallels between as well as recent studies on their critical intersections to expand our comprehension of neurodevelopmental paradigms in GBM. Understanding these parallels may uncover developmental pathways that can be exploited to improve therapeutic strategies for GBM.

Significance

This review takes a prospective approach to GBM research by examining how developmental programs in RGCs mirror GSCs, and further how RGC-like cells in GBM mimic aspects of neurodevelopment. Through a neuroscience perspective, we explore new insights into tumor initiation, progression, and therapeutic resistance.

Introduction

Brain tumors are among the most complex and fatal cancers in the world [1]. Their significant morbidity and mortality in the United States have largely been unchanged despite advancements in the treatment of other solid tumors [2]. Specifically, glioblastomas, the most common primary brain malignancy in adults, present with a 5-year survival rate of only 5.5 % [3]. Though progress has been made in the field of glioblastoma (GBM) research to address issues such as tumoral heterogeneity, the blood-brain barrier and drug delivery, and the immunosuppressive microenvironment, clinical translation of these discoveries has not improved outcomes for patients [2]. This valley in translatability emphasizes the importance of understanding GBM inception so that researchers may better capture disease progression and seek solutions that curtail its worsening over time.

The similarity between developmental biology and cancer formation was first postulated over a century ago with the "embryonic rest" theory [4]. Julius Cohnheim and Rudolf Virchow found shared pathological features between tissue in early development and tumor tissue, leading to the hypothesis that dormant embryonic cells left over from development could be reactivated into cancer [5]. Decades later, many groups have demonstrated the ability of stem-like populations in cancer to initiate premalignant lesions, establish functional heterogeneity, contribute to metastasis, and maintain the tumor bulk [6,7]. In GBM, glioma stem cells (GSCs) share overlapping characteristics with neural stem cells (NSCs) including the capacity for self-renewal, the ability to differentiate into multiple lineages, and the maintenance of a proliferative state [8–10]. In xenograft experiments of human tumor cells into immunocompetent nude mice, GSCs show greater tumorigenic potential than non-stem matched tumor cells [11]. They further exhibit malignant behaviors such as expressing elevated levels of VEGF, leading to tumor angiogenesis, and possessing an enhanced capacity for DNA repair, leading to radiation and chemotherapy resistance [12,13]. These discoveries emphasize the intimate relationship between developmental

* Corresponding author at: Lillian S. Wells Department of Neurological Surgery, University of Florida, PO Box 100265, Gainesville, FL 32610, USA.
E-mail address: catherine.flores@neurosurgery.ufl.edu (C. Flores).

https://doi.org/10.1016/j.tranon.2025.102645
Received 9 September 2025; Received in revised form 11 November 2025; Accepted 8 December 2025
Available online 13 December 2025

biology and some of the more complicated aspects of GBM initiation, invasion, and recurrence. However, the specific developmental cell types, signaling pathways, and functions remain to be fully elucidated.

Most studies and reviews on developmental biology and GBM have used a top-down, retrospective approach to engage with the intersection of the two fields [14]. In contrast, a bottom-up, prospective framework begins with specific neurodevelopmental cell types, such as radial glia, and extrapolates how their intrinsic programs of proliferation, migration, and self-renewal may be aberrantly reactivated or hijacked during gliomagenesis. Whereas top-down models infer developmental parallels from end-stage tumor heterogeneity, a prospective approach leverages developmental neurobiology to predict which cellular programs or progenitor identities could give rise to tumor behavior, allowing new hypotheses for therapeutic targeting that may not emerge from retrospective transcriptomic clustering alone. In this review, we would like to present a bottom-up, prospective approach to our understanding of this intersection. In particular, we will exhibit the body of research on one neurodevelopmental cell type, the radial glial cell, and its attributions to various GBM features. Further, this review will convey how such contributions can be as valuable to our understanding of brain cancer as they can to our comprehension of neurodevelopment and resilience.

For clarity throughout this review, the term radial glial cell (RGC) will refer to the developmentally normal, embryonic progenitor responsible for neurogenesis, gliogenesis, and cortical organization during brain development. In contrast, the term “RGC-like” will be used to denote tumor or progenitor cells that re-express, mimic, or functionally adopt programs unique to RGCs, such as interkinetic nuclear migration, Pax6/Nestin co-expression, or mitotic somal translocation, outside of the embryonic context [15]. This distinction underscores how developmental paradigms can be aberrantly leveraged in glioma to blur the boundary between neurogenesis and oncogenesis.

Radial glia cells

RGCs were first identified in the fetal spinal cord in the late 19th century by Camillo Golgi [16]. Since then, they have been identified throughout the entirety of the human central nervous system (CNS) and in some peripheral structures such as the retina [17]. Much interest primarily revolved around their morphological polarity, in which the soma of the cell lies near the developing brain’s ventricle, called the subventricular zone (SVZ), and a radial process extends from the soma to the pial surface of the brain, named the cortical plate (CP) [18]. Their unique morphology and strategic positioning enable them to orchestrate complex processes of proliferation, self-renewal, and differentiation, which are essential for the proper formation and functionality of the CNS.

During early neurodevelopment, RGCs undergo rapid proliferation to expand the progenitor cell pool. This expansion is crucial for generating a vast number of progenitor cells, as well as neurons and glial cells, required for the developing brain. RGCs possess the ability to divide symmetrically or asymmetrically [19]. Symmetric divisions result in two identical progenitor cells, thereby amplifying the RGC population [20]. Asymmetric cell division (ACD) results in two different daughter cells, one which retains the RGC identity and the other which is more committed towards a neuronal or glial progenitor type, expanding these respective progenitor pools [17]. This proliferative capacity is tightly regulated by intrinsic genetic programs and extrinsic signaling cues within the neural microenvironment [21]. For instance, signaling pathways such as Notch and fibroblast growth factors (FGFs) play significant roles in modulating the rate of RGC proliferation as well as the transition between quiescent and proliferative states, influencing the overall size, structure, and generative capacity of the developing cortex [22,21].

A defining feature of RGCs is their ability to self-renew and maintain a stem cell pool throughout neurodevelopment. Though there is debate around the timing by which they possess this faculty, ranging around gestational week 7 (GW7) to a few months post-natal in humans and embryonic day 10 to postnatal day 14 in murine models, this feature also centralizes on symmetric and asymmetric division [23,24]. However, it relies further on the length of the cortical neurogenic period. The self-renewal capacity depends on the maintenance of the RGC identity internally via expression of intermediate filaments proteins (Nestin) and transcription factors (Pax6, Sox2), to promote stemness. It is further maintained through cell-extrinsic factors that prevent differentiation into a more committed lineage [25]. This balance is achieved through another limited repertoire of molecules known as morphogens, including Notch and FGFs but also bone morphogenic proteins (BMPs), Sonic Hedgehog (SHH), and WNT [25,26]. Corroborated in both human and murine system, these factors work in harmony to maintain the RGC pool and its stemness. To demonstrate just one intricate example of how RGCs can retain self-renewal in humans, external FGF8 induces the ERK cascade which initiates *BMP7* expression. This ultimately promotes formation of GLI3R, that then antagonizes SHH signaling and thus prevents differentiation into glial progenitors [26]. This exemplifies the complexity of interactions between influential external inhibitory factors and internal malleability.

RGCs are multipotent, giving rise to various lineages including neurons, astrocytes, and oligodendrocytes. The differentiation process is influenced by temporal and spatial cues that guide RGC populations to produce specific cell types within the appropriate developmental stage [23]. The initial differentiation process predominately generates neurons (neurogenesis) and, as development progresses, differentiation shifts towards generation of astrocytes and oligodendrocytes (gliogenesis) [25,27]. This shift has been studied in murine models, where the alternation from neurogenesis to gliogenesis requires the transcription of *Olig2* within cortical progenitors and is controlled by several enhancers that regulate the neural stem cell lineage [28].

A final feature of importance to RGCs is their role as a scaffold for migrating neurons and glia. Their elongated radial fibers which traverse the coronal plane of the cortex serve as pathways to guide nascent cells to their destined positions within the expanding cortical plate [29]. This guidance is essential to the laminar architecture of the CNS, in which distinct layers house subpopulations of neurons and glia that will ultimately ensure proper formation of functional neural circuits [29]. This is known as the “radial unit” hypothesis, proposed by Pasko Rakic in 1978 to describe the way in which an assembly of RGCs leads to migration of vertically oriented cohorts of neurons outwards to the expanding marginal zone (MZ) [30]. This intricate fidelity of cytoarchitecture between the ventricular zone (VZ) and the distant CP is achieved in murine models via transcriptional activators such as YAP/TAZ, Pax6, and Emz2, amongst others [31]. Further, the imprint of these patterns leads radial glial themselves to their final resting place as astrocytes in the cortex. In human fetal tissue experiments, this process has been found to depend on the microtubule actomyosin motor system, and the necessity of its modulation via the Rho/Rho kinase (ROCK) pathway [32]. It is further supported by the topography of interactions between neighboring cells and the extracellular matrix [31].

RGCs are indispensable architects whose propensities for proliferation, self-renewal, and multipotency underpin the complexity of neurodevelopment. These functions make RGCs foundational in brain development, and of course, this central role in the maturation of the CNS can lead to profound implications when RGCs are dysfunctional. They are keystones of research around various developmental disorders, including autism spectrum disorder (ASD), schizophrenia, and epilepsy, and curiosities for innovation in potential therapeutics which harness their multipotency [33,34]. However, their role in the generation, maintenance, and invasiveness of tumors is a relatively new area of interest in brain cancer biology. We will use the primary attributes outlined above to underscore recent findings about the involvement of RGCs in brain malignancies.

Radial glia and differentiation in glioblastoma

Radial glia guide the laminar development and respective differentiation of subpopulations of neurons, astrocytes, and oligodendrocytes with fidelity in a healthy nervous system [17,35]. In GBM, it was previously believed that unlike RGCs, GSCs had a restricted differentiation potential to cells of a neural lineage [36]. However, recent studies have highlighted how human GSCs can differentiate into or influence the differentiation towards an expanded repertoire of cell types: astrocytes, endothelium, mesenchyme, neurons, and oligodendrocytes [37–39]. Further, both RGCs and GSCs can perform asymmetric cellular division (ACD) [39]. However, classic RGCs are typically not present in the adult brain, which is the primary tissue that glioma affects [15]. The similarity of these multipotent properties has implicated an RGC-like cell as part of the GSC cohort that contributes to the heterogeneity of glioblastoma tumors (Fig. 1).

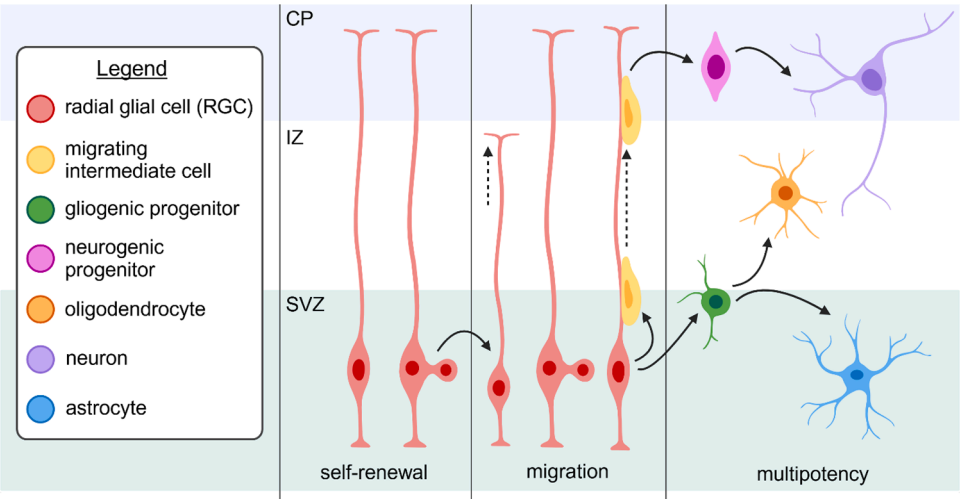
An important recent study published by Bhaduri et al. in 2020 highlighted the ways in which RGC-like populations within GBM human tumor samples are multipotent, and how this ability to differentiate into many different lineages contributed to the diversity of subsets of cells within the tumor sample [15]. First, single-cell RNA sequencing analysis characterized RGC-like populations in GBM that expressed markers such as SOX2, NES, and FABP7 [15]. Further, radial glia network markers, or those which license RGCs to key molecular processes such as ACD and mitotic somal translocation (MST) and are normally only expressed in neurodevelopment, were replicated in these RGC-like GBM cells [15]. Phylogenetic reconstruction based on copy number variants (CNV) demonstrated that RG-like cells were some of the earliest progenitor populations, appeared at multiple points throughout the phylogenetic tree, and persisted in driving tumor heterogeneity [15]. Other groups have recapitulated these findings [40–42]. In summary, RGC-like tumor-associated cells either reactivate or retain developmental programs to express stemness markers that allow them to serve as progenitors for a diverse population of tumor cells.

The malignant implications of RGCs should not minimize from their implications in neuro-resilience as well. Preclinical models for therapeutics harnessed neural stem cells, including RGC subpopulations, for the treatment of GBM to help heal the brain via repopulation of healthy, non-tumorous subtypes [43,44]. Further, the set of genes which maintain RGC pluripotency, various basally transcribed RNAs among other molecules, give the cell type a high “entropic state”, allowing the cells to adapt and respond to changes in its environment that impact cell differentiation [45]. However, research into GSCs has identified this same degree of entropy as a characteristic, and this dynamic state is one of the primary hypotheses underpinning treatment resistant and tumor recurrence in GBM [46].

The central role RGCs play in neurodevelopment, orchestrating various progenitors, neurons, and glia, speaks to the impact of their ability to differentiate and guide differentiation. This same feature of RGC-like cells within human and murine glioma models implicates the way that pluripotency can promote tumor heterogeneity, treatment response, and resistance. However, much remains to be explored around the ways that this potent cell type could be useful in healing patients in brain cancer recovery, or whether the ability to differentiate into multiple cell types comes as a function of reactivation, or retention, of developmental programs in GSCs.

Radial glia and proliferation and self-renewal in glioblastoma

Radial glia are pivotal progenitor cells in the early development of the central nervous system, serving as scaffolds for neuronal and later glial migration and differentiation. At earlier stages of development, RGCs undergo primarily symmetric divisions in which both daughter cells retain the RGC identity, and a progenitor pool is expanded; later stages shift towards asymmetric proliferation which results in a self-renewed RGC and an intermediate progenitor cell (IPC) or another more terminally differentiated cell (neuron, glia) [31]. In malignant gliomas, CD133+ GSCs dissociated from human tissue have demonstrated a similar mechanism by which to maintain a self-renewing stem cell pool (symmetric division) and diversely differentiated progeny (asymmetric division) [39]. Further, recent studies in immunocompetent xenografts have emphasized the ways in which ACD contributes to



	self-renewal	migration	multipotency
Developmental Context	Replenish the RGC pool and maintain stemness capacity.	Expand the cortical plate with integrity of laminar structure.	Generate diverse progenitors with capacity to become neurons or glia and increase respective pools.
Cancer Context	Sustain a population of malignant cells with stem-like potency.	Allow invasion into surrounding healthy tissue by abnormally proliferating cells	Increase entropy of aberrant cell, leading to treatment resilience. Contribute various heterogenous cell types to tumor bulk.

Fig. 1. The role of RGCs and RGC-like cells is context dependent. In development, key functions such as self-renewal and proliferation, migration, and multipotency are essential to the expansion and fidelity of the central nervous system [20]. However, these same behaviors may become potent drivers of tumor formation, heterogeneity, and invasion when co-opted by cancerous populations [15,40]. SVZ = subventricular zone, IZ = intermediate zone, and CP = cortical plate. These zones are only relevant to the developing cortex and are not transferable to regions of RGC-like cells within tumors.

treatment resistance in GBM, as therapeutic stress promotes ACD to form daughter cells which are resistant to that therapy [38]. This has centered NSC-like populations that possess the ACD capacity as potent in contributing to tumor bulk expansion and treatment resistance [38]. More importantly, however, the specific morphological retention of a projection fiber within some of these GSC populations, and the RGC-like behavioral profile of tumor-generating GSCs, has further indicated the relevance of RGCs in glioma research [32,40].

The implication of RGC behaviors like ACD in GBM was recently highlighted by a study which characterized adult human GBM samples via their mitotic behaviors [40]. Aside from ACD, other classic functions such as MST, interkinetic nuclear migration (INM), and retention of radial fiber were used to increase the specific identification of RGC-like cells [40]. They utilized immunofluorescence and real-time imaging of GBM tumor explants to quantify dividing cells and found that around 27 % of dividing cells had RGC-like behaviors and co-expression of characteristic proteins [40]. These cells were capable of self-renewal via symmetric division and tumor formation via ACD. Further, these cells had a tropism for the SVZ, where RGCs normally reside during embryogenesis [40]. Finally, inflammation was found to activate quiescent RGC-like populations into a proliferative state [40].

Other research has drawn parallels between the proliferation and self-renewing capacities of RGCs and RGC-like glioma cells. For example, stem cells like RGCs delicately maintain their stemness through tight regulation of a quiescent state [47]. Proper internal regulation and external signals can trigger the cell into a more active proliferative state [47]. This has value in several pathological paradigms, such as aging, neurodegeneration, and ASD, and external and internal cues have been identified as causing this transition towards proliferation including *Ascl1, Olig2*, and Notch signaling [22]. In transgenic murine models that overexpressed *Ascl1* or *Olig2*, heterogenous tumors reliably formed and contained all molecular subtypes of GBM, including proneural, classical, and mesenchymal [28]. Similar regulatory pathways containing these proteins can maintain RGC-like cells in glioma and thus maintain potent stem cell pools, or they can force RGC-like populations and other SVZ cells towards generating tumor bulk [48]. This exemplifies the context-dependent parallel of RGCs—self-renewable to continue cortical expansion in neurodevelopment, or immortal and generating heterogeneity in GBM (Fig. 1).

RGCs' capacity for neurogenesis and the identification of RGC-like populations in glioma raise a central question: does GBM arise from the abnormal persistence of embryonic radial glia into adulthood, or from the reactivation of RGC-like developmental programs within dormant adult NSCs? Both mechanisms would represent aberrant re-engagement of developmental states that are normally silenced in the mature brain.

In healthy adults, only NSCs persist within neurogenic niches such as the SVZ and subgranular zone (SGZ) of the hippocampal dentate gyrus; bona fide embryonic RGCs are no longer present [49]. These adult NSCs share some transcriptional and morphological features with RGCs, including elongated processes and expression of brain lipid binding protein (BLBP), Sox2, and Nestin, but are not equivalent [47,49]. Adult NSCs represent a more restricted, astrocyte-like lineage with limited neurogenic potential, whereas embryonic RGCs possess broader multipotency and serve as scaffolds for cortical organization [50]. Within these adult niches, type I quiescent NSCs (qNSCs) can be activated into type II proliferative NSCs (aNSCs), and re-express select genes associated with RGC self-renewal and proliferation, though their differentiation potential remains largely astrocytic [50,51].

In the context of gliomagenesis, it remains unresolved whether RGC-like populations arise from reactivation of developmental programs in normal NSCs or glia, or from the pathological persistence of embryonic RGCs that failed to undergo normal maturation and silencing [38]. Distinguishing between these possibilities is critical for understanding lineage relationships and for developing therapeutics that selectively target reactivated developmental pathways without disrupting normal neurogenic niches.

Radial glia, migration, and motility in glioblastoma

During cortical development, RGCs are indispensable scaffolds guiding neuronal migration through coordinated cycles of INM and MST. INM synchronizes nuclear position with the cell cycle as RGC nuclei move basally during S-phase and apically for mitosis [52]. This is driven by microtubule motors, actomyosin tension, and adhesion-dependent polarity [52,53]. MST, characteristic of outer radial glia (oRG), enables a basal "jump" of the RGC soma preceding division, powered by actomyosin contractility and RhoA–ROCK signaling [32,54]. Adhesion proteins such as N-cadherin stabilize the RG scaffold and activate Rho-family GTPases to coordinate MST, while Cdk5 modulates cytoskeletal organization and detachment to coordinate INM and MST [55]. Together, these pathways orchestrate precise positioning of progenitors and neurons, ensuring cortical lamination and structural fidelity.

Remarkably, before the recognition of RGC-like cells within GBM, these same molecular pathways had already been identified as key regulators of glioma cell motility. Inhibition of ROCK or Cdk5 in GBM cultures and xenografts reduced migration, invasion, and tumor spread [56,57]. This parallel convergence suggests that the RGC-like invasion phenotype of GBM was functionally evident even before it was transcriptionally defined. RGC-like GBM cells later identified by single-cell sequencing recapitulate the migratory and motility phenotype of radial glia, and this has been behaviorally identified in ex vivo tumoroid models [15]. Many GBM cells (now called RGC-like) exhibit elongated basal fibers, MST-like nuclear translocation, and dependence on RhoA/ROCK and Cdk5 signaling for motility [15,40,58]. In essence, GBM invasion may be supported through maintenance of RGC-like cells that would typically not persist in healthy adult brains, or through reactivation of their developmental migration toolkit. This includes adhesive polarity via N-cadherin, contractile machinery through RhoA–ROCK, and cell-cycle-linked motility via Cdk5. These mechanistic echoes of radial glial migration guidance and motility are now taken advantage of in GBM to drive diffuse infiltration. Further, these paradigms are vital for therapeutic exploration, as the majority of GBM patients die from recurrence, driven by GBM invasion, rather than primary tumor impact [59].

Alternative models and limitations in exploring RGCs in GBM

Although RGC-like transcriptional states have been identified in several datasets, not all studies agree that GBM contains discrete developmental hierarchies [15,40]. Single-cell multi-omic analyses by Neftel et al [60] and Garofano et al [61] instead contend that there is a continuum of plastic transcriptional states in which nearly all tumor cells retain the capacity for self-renewal, migration, and multipotency [62]. In this alternative model, GBM cells contain developmental cell "states" and not cell "types" [60]. This challenges the idea of a consistent RGC-like compartment, that acts as GSCs or invaders into surrounding healthy tissue; it raises the possibility that RGC-like programs are transiently and dynamically engaged under pressure, either imposed by the microenvironment or therapeutics. Moreover, many RGC markers (SOX2, NES, FABP7) and some distinct features are shared across various progenitor populations, limiting their specificity and requiring multiple techniques to verify RGC-like populations in GBM [20]. Finally, whether GBM reactivates or maintains bona fide embryonic RGC programs versus merely converging on similar gene networks remains unresolved, and this is an important distinction for potential therapeutic targeting.

Despite these contradictions and limitations, there is still value in examining GBM through a developmental lens. It provides a mechanistic framework to trace how neural progenitor programs are co-opted, reactivated, or distorted in malignancy, offering insight into both

tumor origin and invasion, and further potential therapeutic vulnerabilities.

Therapeutic and translational implications

The developmental parallels between RGC and GBM offer more than a conceptual framework; they define a mechanistic roadmap for therapy. The same signaling pathways that sustain RGC proliferation and self-renewal during neurodevelopment, including Notch, FGF/ERK, BMP, SHH, and WNT, also maintain stemness and therapeutic resistance in GBM [63,64]. Modulating these pathways has shown promise in preclinical models: inhibition of Notch or SHH signaling can reduce tumor propagation, while selective targeting of downstream effectors such as ERK-mediated BMP7 or YAP/TAZ may more precisely disrupt RGC-like programs without impairing normal adult NSC niches [31,65,66]. Similarly, blockade of RhoA–ROCK or Cdk5, long known to regulate RGC motility and INM, limits GBM invasion in vitro and ex vivo, demonstrating how developmental migration machinery can be therapeutically exploited [15,58].

At a broader translational level, developmental frameworks guide new therapeutic design strategies that move beyond single-mutation targeting toward cell-state-directed interventions. Understanding how RGC-like transcriptional and behavioral states arise will allow researchers to define vulnerabilities that may be shared across GBM's intraheterogeneity and intertumoral plasticity. For example, targeting the molecular programs that govern ACD or quiescence-to-proliferation transitions could prevent the emergence of therapy-resistant clones [40].

Moreover, identifying RGC-derived or RGC-restricted gene products offers an opportunity for antigen discovery, informing immunotherapeutic approaches that selectively recognize malignant cells maintaining or reactivating developmental programs. Our laboratory is pursuing this concept directly by exploring the potential of RGCs as source antigen for polyclonal T cell therapy in GBM [67]. Rather than using tumor neoantigens, this approach aims to expand immune recognition to the developmental programs often driving generation of tumor bulk and invasive seeding in GBM. In this way, the developmental biology of RGCs not only illuminates the origins of GBM but also provides a renewable source of targets for next-generation immunotherapy.

Future directions: value of highlighting radial glia in brain cancer

Much remains to be elucidated about the role of neurodevelopmental cell types, such as radial glia, in malignant brain tumors. Analyses of late-stage tumor samples provide multiple lines of evidence implicating RGC-like populations in glioma biology, yet questions regarding their cellular origins and tumorigenic potential remain unanswered. Specifically, it is still unclear whether GBM arises from the abnormal persistence of embryonic RGCs or the reactivation of RGC-like programs within adult progenitor cells, each of which represents a distinct and therapeutically relevant path to malignancy.

Traditional retrospective studies beginning at the time of biopsy provide limited insight into disease initiation, as they are inherently biased toward aggressive phenotypes and confounded by treatment history and microenvironmental effects [68]. A prospective and inductive approach, beginning with defined developmental cell types and tracing their potential oncogenic trajectories, is therefore essential to uncover how neurodevelopmental programs are co-opted in GBM. Future work should examine how RGCs and RGC-like states contribute to tumor formation, lineage plasticity, and invasion in vitro and in vivo, integrating single-cell transcriptomics, organoid/tumoroid models, and 3D bioprinted microenvironments that more accurately model the tumor niche.

Equally important is translating these developmental insights into therapeutic design. The developmental pathways that sustain RGC identity, such as Notch, SHH, and WNT signaling, may serve as tractable therapeutic targets when aberrantly reactivated in GBM [63]. Moreover, identifying RGC-like subpopulations lays the foundation for antigen discovery and immunotherapeutic targeting, as exemplified by our laboratory's work investigating RGCs as antigenic sources for ACT in GBM [67]. Such approaches move beyond the static notion of "stemness" toward targeting transient developmental states that may be conserved across intratumoral heterogeneity and fuel tumor recurrence and resistance.

Ultimately, revisiting GBM through a developmental lens offers not only mechanistic clarity but also translational promise. The resemblance between neurodevelopment and tumor biology has long been recognized, yet defining how specific cell types like RGCs are repurposed in malignancy can uncover novel therapeutic vulnerabilities. In recognizing that the same cellular logic that builds the brain has the potential to also unmake it, we gain a powerful vantage point to imagine how we might redirect those programs toward regeneration instead of malignancy.

Generative AI disclosure

Generative AI was not used in the process of writing, editing, or submitting this manuscript.

CRediT authorship contribution statement

Caitland A Love: Writing – review & editing, Writing – original draft, Visualization, Data curation, Conceptualization. **John W Figg:** Writing – review & editing, Writing – original draft, Formal analysis. **Mia Engelbart:** Visualization. **Illeana West:** Writing – original draft. **Catherine Flores:** Writing – review & editing.

Declaration of competing interest

Catherine Flores is a founder of iOncologi. Other authors declare no conflicts of interest.

References

[1] A. Lam, The Masters of Medicine: Our Greatest Triumphs in the Race to Cure Humanity's Deadliest Diseases, BenBella Books, 2023.
[2] R.S. Angom, N.M.R. Nakka, S. Bhattacharya, Advances in glioblastoma therapy: an update on current approaches, Brain Sci. 13 (11) (2023), https://doi.org/10.3390/brainsci13111536. Article 11.
[3] J.N. Cantrell, M.R. Waddle, M. Rotman, J.L. Peterson, H. Ruiz-Garcia, M. G. Heckman, A. Quiñones-Hinojosa, S.S. Rosenfeld, P.D. Brown, D.M. Trifiletti, Progress toward long-term survivors of glioblastoma, Mayo Clin. Proc. 94 (7) (2019) 1278–1286, https://doi.org/10.1016/j.mayocp.2018.11.031.
[4] J.-P. Capp, Cancer stem cells: from historical roots to a new perspective, J. Oncol. 2019 (1) (2019) 5189232, https://doi.org/10.1155/2019/5189232.
[5] Ratajczak M.Z., Tarnowski M., Borkowska S., Serwin K. The Embryonic Rest Hypothesis of Cancer Development: 150 Years Later. In: Resende RR, Ulrich H, editors. Trends in Stem Cell Prolif. and Cancer Res. [Internet]. Dordrecht: Springer Netherlands; 2013 [cited 2025 Dec 12]. p. 51–63. 10.1007/978-94-007-6211-4_3.
[6] T. Zhang, L. Zhuang, M. Muaibati, D. Wang, A. Abasi, Q. Tong, D. Ma, L. Jin, X. Huang, Identification of cervical cancer stem cells using single-cell transcriptomes of normal cervix, cervical premalignant lesions, and cervical cancer, EBioMedicine 92 (2023), https://doi.org/10.1016/j.ebiom.2023.104612.
[7] Frank M.H., Wilson B.J., Gold J.S., Frank N.Y. Clinical Implications of Colorectal Cancer Stem Cells in the Age of Single-Cell Omics and Targeted Therapies. Gastroenterology. 2021 May 1;160(6):1947–60.
[8] G. Lee, B. Auffinger, D. Guo, T. Hasan, M. Deheeger, A.L. Tobias, J.Y. Kim, F. Atashi, L. Zhang, M.S. Lesniak, C.D. James, A.U. Ahmed, Dedifferentiation of glioma cells to glioma stem-like cells by therapeutic stress-induced HIF signaling in the recurrent GBM model, Mol. Cancer Ther. 15 (12) (2016) 3064–3076, https://doi.org/10.1158/1535-7163.MCT-15-0675.
[9] L. Ryskalin, F. Biagioni, P. Lenzi, A. Frati, F. Fornai, mTOR modulates intercellular signals for enlargement and infiltration in glioblastoma multiforme, Cancers 12 (9) (2020), https://doi.org/10.3390/cancers12092486. Article 9.
[10] A.R. Safa, M.R. Saadatzadeh, A.A. Cohen-Gadol, K.E. Pollok, K. Bijangi-Vishehsaraei, Glioblastoma stem cells (GSCs) epigenetic plasticity and interconversion between differentiated non-GSCs and GSCs, Genes. Dis. 2 (2) (2015) 152–163, https://doi.org/10.1016/j.gendis.2015.02.001.

[11] X. Wang, B.C. Prager, Q. Wu, L.J.Y. Kim, R.C. Gimple, Y. Shi, K. Yang, A.R. Morton, W. Zhou, Z. Zhu, E.A.A. Obara, T.E. Miller, A. Song, S. Lai, C.G. Hubert, X. Jin, Z. Huang, X. Fang, D. Dixit, J.N. Rich, Reciprocal signaling between glioblastoma stem cells and differentiated tumor cells promotes malignant progression, Cell Stem Cell 22 (4) (2018) 514–528, https://doi.org/10.1016/j.stem.2018.03.011, e5.

[12] S. Bao, Q. Wu, R.E. McLendon, Y. Hao, Q. Shi, A.B. Hjelmeland, M.W. Dewhirst, D. D. Bigner, J.N. Rich, Glioma stem cells promote radioresistance by preferential activation of the DNA damage response, Nature 444 (7120) (2006) 756–760, https://doi.org/10.1038/nature05236.

[13] S. Bao, Q. Wu, S. Sathornsumetee, Y. Hao, Z. Li, A.B. Hjelmeland, Q. Shi, R. E. McLendon, D.D. Bigner, J.N. Rich, Stem cell–like glioma cells promote tumor angiogenesis through vascular endothelial growth factor, Cancer Res. 66 (16) (2006) 7843–7848, https://doi.org/10.1158/0008-5472.CAN-06-1010.

[14] J.P. Savaryn, A.D. Catherman, P.M. Thomas, M.M. Abecassis, N.L. Kelleher, The emergence of top-down proteomics in clinical research, Genome Med. 5 (6) (2013) 53, https://doi.org/10.1186/gm457.

[15] A. Bhaduri, E.D. Lullo, D. Jung, S. Müller, E.E. Crouch, C.S. Espinosa, T. Ozawa, B. Alvarado, J. Spatazza, C.R. Cadwell, G. Wilkins, D. Velmeshev, S.J. Liu, M. Malatesta, M.G. Andrews, M.A. Mostajo-Radji, E.J. Huang, T.J. Nowakowski, D. A. Lim, A.R. Kriegstein, Outer radial glia-like cancer stem cells contribute to heterogeneity of glioblastoma, Cell Stem. Cell 26 (1) (2020) 48–63, https://doi.org/10.1016/j.stem.2019.11.015, e6.

[16] M. Bentivoglio, P. Mazzarello, The history of radial glia, Brain Res. Bull. 49 (5) (1999) 305–315, https://doi.org/10.1016/S0361-9230(99)00065-9.

[17] L. Pinto, M. Götz, Radial glial cell heterogeneity—The source of diverse progeny in the CNS, Prog. Neurobiol. 83 (1) (2007) 2–23, https://doi.org/10.1016/j.pneurobio.2007.02.010.

[18] R.S. Cameron, P. Rakic, Glial cell lineage in the cerebral cortex: a review and synthesis, Glia 4 (2) (1991) 124–137, https://doi.org/10.1002/glia.440040204.

[19] Y. Miranda-Negrón, J.E. García-Arrarás, Radial glia and radial glia-like cells: their role in neurogenesis and regeneration, Front. Neurosci. 16 (2022), https://doi.org/10.3389/fnins.2022.1006037.

[20] D.S. Barry, J.M.P. Pakan, K.W. McDermott, Radial glial cells: key organisers in CNS development, Int. J. Biochem. Cell Biol. 46 (2014) 76–79, https://doi.org/10.1016/j.biocel.2013.11.013.

[21] E. Than-Trong, S. Ortica-Gatti, S. Mella, C. Nepal, A. Alunni, L. Bally-Cuif, Neural stem cell quiescence and stemness are molecularly distinct outputs of the Notch3 signalling cascade in the vertebrate adult brain, Development 145 (10) (2018) dev161034, https://doi.org/10.1242/dev.161034.

[22] L. Harris, P. Rigo, T. Stiehl, Z.B. Gaber, S.H.L. Austin, M. Masdeu, M. del, A. Edwards, N. Urbán, A. Marciniak-Czochra, F. Guillemot, Coordinated changes in cellular behavior ensure the lifelong maintenance of the hippocampal stem cell population, Cell Stem. Cell 28 (5) (2021) 863–876, https://doi.org/10.1016/j.stem.2021.01.003, e6.

[23] R. Chakraborty, M.J. Vijay Kumar, J.P. Clement, Critical aspects of neurodevelopment, Neurobiol. Learn. Mem. 180 (2021) 107415, https://doi.org/10.1016/j.nlm.2021.107415.

[24] L. Duan, C.-Y. Peng, L. Pan, J.A. Kessler, Human pluripotent stem cell-derived radial glia recapitulate developmental events and provide real-time access to cortical neurons and astrocytes, Stem Cells Transl. Med. 4 (5) (2015) 437–447, https://doi.org/10.5966/sctm.2014-0137.

[25] J. Ferent, D. Zaidi, F. Francis, Extracellular control of radial glia proliferation and scaffolding during cortical development and pathology, Front. Cell Dev. Biol. 8 (2020), https://doi.org/10.3389/fcell.2020.578341.

[26] M. Sun, Y. Gao, Z. Li, L. Yang, G. Liu, Z. Xu, R. Guo, Y. You, Z. Yang, ERK signaling expands mammalian cortical radial glial cells and extends the neurogenic period, Proc. Natl. Acad. Sci. 121 (13) (2024) e2314802121, https://doi.org/10.1073/pnas.2314802121.

[27] X. Wang, R. Zhou, Y. Xiong, L. Zhou, X. Yan, M. Wang, et al., Sequential fate-switches in stem-like cells drive the tumorigenic trajectory from human neural stem cells to malignant glioma, Cell Res. 31 (6) (2021 June) 684–702.

[28] B.L. Myers, K.J. Brayer, L.E. Paez-Beltran, E. Villicana, M.S. Keith, H. Suzuki, J. Newville, R.H. Anderson, Y. Lo, C.M. Mertz, R.K. Kollipara, M.D. Borromeo, Q. R. Lu, R.M. Bachoo, J.E. Johnson, T.Y. Vue, Transcription factors ASCL1 and OLIG2 drive glioblastoma initiation and co-regulate tumor cell types and migration, Nat. Commun. 15 (2024) 10363, https://doi.org/10.1038/s41467-024-54750-9.

[29] M.G. Andrews, L. Subramanian, J. Salma, A.R. Kriegstein, How mechanisms of stem cell polarity shape the human cerebral cortex, Nat. Rev. Neurosci. 23 (12) (2022) 711–724, https://doi.org/10.1038/s41583-022-00631-3.

[30] P. Rakic, The radial edifice of cortical architecture: from neuronal silhouettes to genetic engineering, Brain Res. Rev. 55 (2) (2007) 204–219, https://doi.org/10.1016/j.brainresrev.2007.02.010.

[31] A. Lavado, R. Gangwar, J. Paré, S. Wan, Y. Fan, X. Cao, YAP/TAZ maintain the proliferative capacity and structural organization of radial glial cells during brain development, Dev. Biol. 480 (2021) 39–49, https://doi.org/10.1016/j.ydbio.2021.08.010.

[32] B.E.L. Ostrem, J.H. Lui, C.C. Gertz, A.R. Kriegstein, Control of outer radial glial stem cell mitosis in the Human brain, Cell Rep. 8 (3) (2014) 656–664, https://doi.org/10.1016/j.celrep.2014.06.058.

[33] C. Falcone, N.-Y. Mevises, T. Hong, B. Dufour, X. Chen, S.C. Noctor, V. Martínez Cerdeño, Neuronal and glial cell number is altered in a cortical layer-specific manner in autism, Autism. 25 (8) (2021) 2238–2253, https://doi.org/10.1177/13623613211014408.

[34] N. Sasaki-Takahashi, H. Shinohara, S. Shioda, T. Seki, The polarity and properties of radial glia-like neural stem cells are altered by seizures with status epilepticus: study using an improved mouse pilocarpine model of epilepsy, Hippocampus 30 (3) (2020) 250–262, https://doi.org/10.1002/hipo.23153.

[35] N. Saldivia, K. Salazar, M. Cifuentes, F. Espinoza, F.E. Harrison, F. Nualart, Ascorbic acid and its transporter SVCT2, affect radial glia cells differentiation in postnatal stages, Glia 72 (4) (2024) 708–727, https://doi.org/10.1002/glia.24498.

[36] A. Loras, L.G. Gonzalez-Bonet, J.L. Gutierrez-Arroyo, C. Martinez-Cadenas, M. A. Marques-Torrejon, Neural stem cells as potential glioblastoma cells of origin, Life 13 (4) (2023) 905, https://doi.org/10.3390/life13040905.

[37] R. Azzarelli, A. McNally, C. Dell'Amico, M. Onorati, B. Simons, A. Philpott, ASCL1 phosphorylation and ID2 upregulation are roadblocks to glioblastoma stem cell differentiation, Sci. Rep. 12 (1) (2022) 2341, https://doi.org/10.1038/s41598-022-06248-x.

[38] K. Biserova, A. Jakovlevs, R. Uljanovs, I. Strumfa, Cancer stem cells: significance in origin, pathogenesis and treatment of glioblastoma, Cells 10 (3) (2021), https://doi.org/10.3390/cells10030621. Article 3.

[39] M. Stevanovic, N. Kovacevic-Grujicic, M. Mojsin, M. Milivojevic, D. Drakulic, SOX transcription factors and glioma stem cells: choosing between stemness and differentiation, World J. Stem Cells 13 (10) (2021) 1417–1445, https://doi.org/10.4252/wjsc.v13.i10.1417.

[40] R. Wang, R. Sharma, X. Shen, A.M. Laughney, K. Funato, P.J. Clark, M. Shpokayte, P. Morgenstern, M. Navare, Y. Xu, S. Harbi, I. Masilionis, G. Nanjangud, Y. Yang, G. Duran-Rehbein, M. Hemberg, D. Pe'er, V. Tabar, Adult Human glioblastomas harbor radial glia-like cells, Stem Cell Rep. 14 (2) (2020) 338–350, https://doi.org/10.1016/j.stemcr.2020.01.007.

[41] Y. Hu, Y. Jiang, J. Behnan, M.M. Ribeiro, C. Kalantzi, M.-D. Zhang, D. Lou, M. Häring, N. Sharma, S. Okawa, A. Del Sol, I. Adameyko, M. Svensson, O. Persson, P. Ernfors, Neural network learning defines glioblastoma features to be of neural crest perivascular or radial glia lineages, Sci. Adv. 8 (23) (2022) eabm6340, https://doi.org/10.1126/sciadv.abm6340.

[42] J.H. Lee, J.E. Lee, J.Y. Kahng, S.H. Kim, J.S. Park, S.J. Yoon, J.-Y. Um, W.K. Kim, J.-K. Lee, J. Park, E.H. Kim, J.-H. Lee, J.-H. Lee, W.-S. Chung, Y.S. Ju, S.-H. Park, J. H. Chang, S.-G. Kang, J.H. Lee, Human glioblastoma arises from subventricular zone cells with low-level driver mutations, Nature 560 (7717) (2018) 243–247, https://doi.org/10.1038/s41586-018-0389-3.

[43] J.R. Bagó, A. Alfonso-Pecchio, O. Okolie, R. Dumitru, A. Rinkenbaugh, A. S. Baldwin, C.R. Miller, S.T. Magness, S.D. Hingtgen, Therapeutically engineered induced neural stem cells are tumour-homing and inhibit progression of glioblastoma, Nat. Commun. 7 (1) (2016) 10593, https://doi.org/10.1038/ncomms10593.

[44] P. Lu, S. Ceto, Y. Wang, L. Graham, D. Wu, H. Kumamaru, E. Staufenberg, M. H. Tuszynski, Prolonged human neural stem cell maturation supports recovery in injured rodent CNS, J. Clin. Invest. 127 (9) (2017) 3287–3299, https://doi.org/10.1172/JCI92955.

[45] Gupta, R., & Claassen, M. (2023). Factorial state-space modelling for kinetic clustering and lineage inference (p. 2023.08.21.554135). bioRxiv. https://doi.org/10.1101/2023.08.21.554135.

[46] B.C. Prager, S. Bhargava, V. Mahadev, C.G. Hubert, J.N. Rich, Glioblastoma stem cells: driving resilience through chaos, Trends. Cancer 6 (3) (2020) 223–235, https://doi.org/10.1016/j.trecan.2020.01.009.

[47] J.I. Arellano, Y.M. Morozov, N. Micali, P. Rakic, Radial glial cells: new views on old questions, Neurochem. Res. 46 (10) (2021) 2512–2524, https://doi.org/10.1007/s11064-021-03296-z.

[48] T.Y. Vue, R.K. Kollipara, M.D. Borromeo, T. Smith, T. Mashimo, D.K. Burns, R. M. Bachoo, J.E. Johnson, ASCL1 regulates neurodevelopmental transcription factors and cell cycle genes in brain tumors of glioma mouse models, Glia 68 (12) (2020) 2613–2630, https://doi.org/10.1002/glia.23873.

[49] V. Llorente, P. Velarde, M. Desco, M.V. Gómez-Gaviro, Current understanding of the neural stem cell niches, Cells 11 (19) (2022), https://doi.org/10.3390/cells11193002. Article 19.

[50] J.M. Morante-Redolat, E. Porlan, Neural stem cell regulation by adhesion molecules within the subependymal niche, Front. Cell Dev. Biol. 7 (2019), https://doi.org/10.3389/fcell.2019.00102.

[51] P. Malatesta, I. Appolloni, F. Calzolari, Radial glia and neural stem cells, Cell Tissue Res. 331 (1) (2008) 165–178, https://doi.org/10.1007/s00441-007-0481-8.

[52] P.C. Spear, C.A. Erickson, Interkinetic nuclear migration: a mysterious process in search of a function, Dev. Growth Differ. 54 (3) (2012) 306–316, https://doi.org/10.1111/j.1440-169X.2012.01342.x.

[53] Y. Kosodo, T. Suetsugu, M. Suda, Y. Mimori-Kiyosue, K. Toida, S.A. Baba, A. Kimura, F. Matsuzaki, Regulation of interkinetic nuclear migration by cell cycle-coupled active and passive mechanisms in the developing brain, EMBO J. 30 (9) (2011) 1690–1704, https://doi.org/10.1038/emboj.2011.81.

[54] B.L. Meyerink, N.K. Tiwari, L.-J. Pilaz, Ariadne's thread in the developing cerebral cortex: mechanisms enabling the guiding role of the radial glia basal process during neuron migration, Cells 10 (1) (2020) 3, https://doi.org/10.3390/cells10010003.

[55] H. Jinnou, M. Sawada, K. Kawase, N. Kaneko, V. Herranz-Pérez, T. Miyamoto, T. Kawaue, T. Miyata, Y. Tabata, T. Akaike, J.M. García-Verdugo, I. Ajioka, S. Saitoh, K. Sawamoto, Radial glial fibers promote neuronal migration and functional recovery after neonatal brain injury, Cell Stem. Cell 22 (1) (2018) 128–137, https://doi.org/10.1016/j.stem.2017.11.005, e9.

[56] R. Liu, B. Tian, M. Gearing, S. Hunter, K. Ye, Z. Mao, Cdk5-mediated regulation of the PIKE-A-Akt pathway and glioblastoma cell invasion, Proc. Natl. Acad. Sci. 105 (21) (2008) 7570–7575, https://doi.org/10.1073/pnas.0712306105.

[57] V.M. Zohrabian, B. Forzani, Z. Chau, R. Murali, M. Jhanwar-Uniyal, Rho/ROCK and MAPK signaling pathways are involved in glioblastoma cell migration and proliferation, Anticancer Res. 29 (1) (2009) 119–123.

[58] L. Ciraku, Z.A. Bacigalupa, J. Ju, R.A. Moeller, G. Le Minh, R.H. Lee, M.D. Smith, C. M. Ferrer, S. Trefely, L.T. Izzo, M.T. Doan, W.A. Gocal, L. D'Agostino, W. Shi, J. G. Jackson, C.D. Katsetos, K.E. Wellen, N.W. Snyder, M.J. Reginato, O-GlcNAc transferase regulates glioblastoma acetate metabolism via regulation of CDK5-dependent ACSS2 phosphorylation, Oncogene 41 (14) (2022) 2122–2136, https://doi.org/10.1038/s41388-022-02237-6.

[59] D.A. Putavet, P.L.J. de Keizer, Residual disease in Glioma recurrence: a dangerous liaison with senescence, Cancers 13 (7) (2021) 1560, https://doi.org/10.3390/cancers13071560.

[60] C. Neftel, J. Laffy, M.G. Filbin, T. Hara, M.E. Shore, G.J. Rahme, A.R. Richman, D. Silverbush, M.L. Shaw, C.M. Hebert, J. Dewitt, S. Gritsch, E.M. Perez, L. N. Gonzalez Castro, X. Lan, N. Druck, C. Rodman, D. Dionne, A. Kaplan, M.L. Suvà, An integrative model of cellular states, plasticity, and genetics for glioblastoma, Cell 178 (4) (2019) 835–849, https://doi.org/10.1016/j.cell.2019.06.024, e21.

[61] L. Garofano, S. Migliozzi, Y.T. Oh, F. D'Angelo, R.D. Najac, A. Ko, B. Frangaj, F. P. Caruso, K. Yu, J. Yuan, W. Zhao, A.L. Di Stefano, F. Bielle, T. Jiang, P. Sims, M. L. Suvà, F. Tang, X.-D. Su, M. Ceccarelli, A. Iavarone, Pathway-based classification of glioblastoma uncovers a mitochondrial subtype with therapeutic vulnerabilities, Nat. Cancer 2 (2) (2021) 141–156, https://doi.org/10.1038/s43018-020-00159-4.

[62] M.L. Suvà, I. Tirosh, The glioma stem cell model in the era of single-cell genomics, Cancer Cell 37 (5) (2020) 630–636, https://doi.org/10.1016/j.ccell.2020.04.001.

[63] N. Rajakulendran, K.J. Rowland, H.J. Selvadurai, M. Ahmadi, N.I. Park, S. Naumenko, S. Dolma, R.J. Ward, M. So, L. Lee, G. MacLeod, C. Pasiliao, C. Brandon, I.D. Clarke, M.D. Cusimano, M. Bernstein, N. Batada, S. Angers, P. B. Dirks, Wnt and Notch signaling govern self-renewal and differentiation in a subset of human glioblastoma stem cells, Genes Dev. 33 (9–10) (2019) 498–510, https://doi.org/10.1101/gad.321968.118.

[64] J.Y. Chai, V. Sugumar, A.F. Alshanon, W.F. Wong, S.Y. Fung, C.Y.. Looi, Defining the role of GLI/Hedgehog signaling in chemoresistance: Implications in therapeutic approaches, Cancers 13 (19) (2021 Jan) 4746.

[65] J. Chen, S. Kesari, C. Rooney, P.R. Strack, J. Chen, H. Shen, L. Wu, J.D. Griffin, Inhibition of notch signaling blocks growth of glioblastoma cell lines and tumor neurospheres, Genes. Cancer 1 (8) (2010) 822–835, https://doi.org/10.1177/1947601910383564.

[66] S.A. Ward, J.B. Rubin, Not so fast: co-requirements for Sonic Hedgehog induced brain tumorigenesis, Cancers 7 (3) (2015) 1484–1498, https://doi.org/10.3390/cancers7030848.

[67] C.A. Love, J.W. Figg, I. West, M. Englebart, A. Reid, D. Jin, D. Mitchell, C. Flores, OS05.5.A radial glial Cells AS source antigen for adoptive cellular therapy in Glioblastoma, Neuro-Oncol. 27 (2025), https://doi.org/10.1093/neuonc/noaf193.053. Supplement_3iii18.

[68] C.S. Chopra, M. Handmacher, D.C. Neubauer, C. Reid, Chapter 94—epidemiology, in: A.E.M. Eltorai, J.A. Bakal, P.C. Newell, A.J. Osband (Eds.), Translational Surgery, Academic Press, 2023, pp. 609–613, https://doi.org/10.1016/B978-0-323-90300-4.00041-0.