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Abstract

Glioblastomas are the most common form of malignant primary brain tumor and an important cause of morbidity and mortality. In recent years there have been important advances in understanding the molecular pathogenesis and biology of these tumors, but this has not translated into significantly improved outcomes for patients. In this consensus review from the Society for Neuro-Oncology (SNO) and the European Association of Neuro-Oncology (EANO), the current management of isocitrate dehydrogenase wildtype (*IDH*wt) glioblastomas will be discussed. In addition, novel therapies such as targeted molecular therapies, agents targeting DNA damage response and metabolism, immunotherapies, and viral therapies will be reviewed, as well as the current challenges and future directions for research.

Keywords

glioblastoma | diagnosis | therapy | clinical trials

Glioblastomas are the most common type of malignant primary brain tumor and account for the majority of deaths among patients with primary brain tumors.[1] Although there has been progress in understanding the biology of these tumors, this has not translated into significant improvements in therapies or outcomes for patients. In this consensus review from SNO and EANO recent advances in the management of glioblastoma are discussed, as well as the current challenges and future directions for research. The focus will be on the 90–95% of glioblastomas that do not harbor *IDH* mutations (*IDH*wt) and have a worse prognosis.[2,3] We concur with the current considerations to regroup *IDH*-mutant glioblastomas with other *IDH*-mutant gliomas in the framework of the revision of the World Health Organization (WHO) classification of brain tumors, and to restrict the term "glioblastoma" to tumors without *IDH* mutations.[4]

Epidemiology

The overall age-adjusted incidence of glioblastoma in the United States is 3.22/100 000 persons, and increases with advanced age at diagnosis and male sex (Fig. 1A; Central Brain Tumor Registry of the United States, 2012–2016).[1] Incidence also varies worldwide.[5] Recent data show no trend toward increased incidence in the US or Canada,[6] although data from England indicate that the incidence is increasing.[7,8] These differences might reflect differing surveillance procedures, coding, and changes in classifications of glioblastoma over time.[2] Glioblastomas contribute disproportionately to morbidity and mortality, with a 5-year overall relative survival of only 6.8%, which varies by age at diagnosis and by sex (Fig. 1B; National Program of Cancer Registries, 2012–2016).[1] Known risk factors for glioblastoma account for only a small proportion of cases.[9] In multiple independent studies, one risk factor, ionizing radiation exposure to the head and neck, and one protective factor, history of atopic diseases (including allergies, asthma, eczema, and hay fever), have been validated for all brain tumors (as reviewed by Ostrom et al[9]). While cell phone use (ie, non-ionizing radiation exposure) has been heavily studied as a potential risk factor for brain tumors, studies have shown no consistent evidence of any association.[9,10] However, the latency period for disease after exposure to non-ionizing radiation is not known, hence continued careful monitoring of the incidence trend is advised.

The vast majority of glioblastoma patients do not have a family history of cancer. Approximately 5% of all gliomas are familial,[11] and there are multiple rare Mendelian

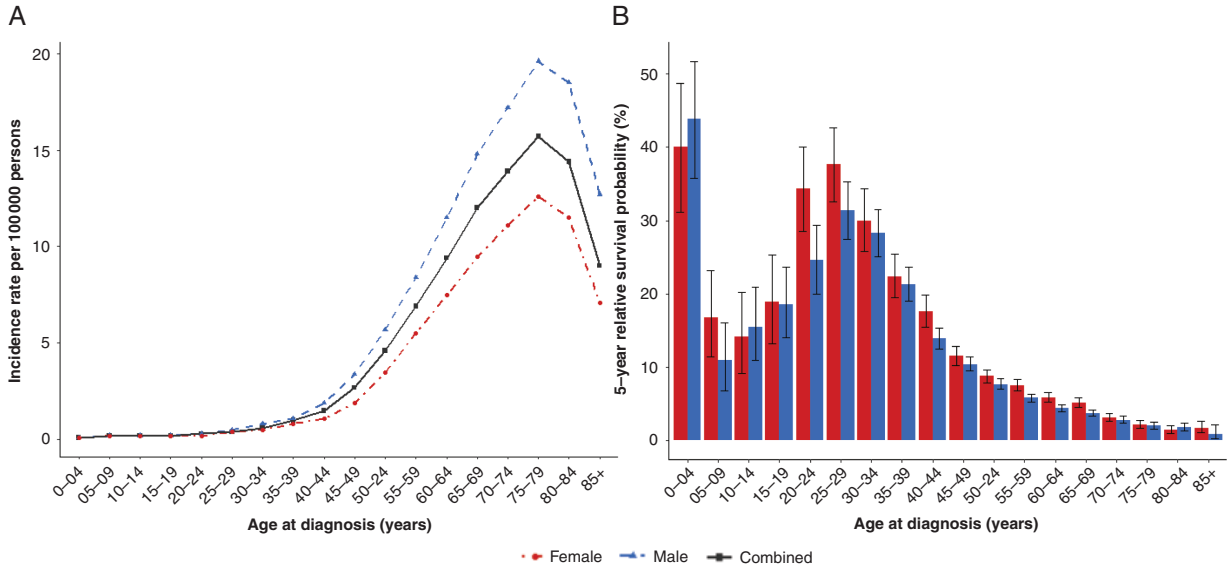


Fig. 1 Glioblastoma. (A) Incidence rate per 100 000 persons by age at diagnosis and sex, Central Brain Tumor Registry of the United States (CBTRUS) 2012–1016 (50 US states and Puerto Rico included) and (B) 5-year relative survival probability (with 95% confidence intervals) by age at diagnosis and sex, National Program of Cancer Registries (NPCR) 2012–2016 (43 US states included). **Glioblastoma defined by International Classification of Disease-Oncology (ICD-O) version 3 codes 9440/3, 9441/3, 9442/3.

inherited syndromes that involve adult glioma and glioblastoma[12] (Table 1 adapted from Ostrom et al[9]). The frequency of germline variants is higher than expected based on family history data with up to 13% of glioma patients harboring at least one deleterious or likely deleterious alteration in the germline.[13] Genome-wide association studies of genetic risk factors have validated 25 single nucleotide polymorphisms associated with increased risk for glioma, where 11 are specific to glioblastoma.[14] While the biological significance of these associations remains to be elucidated, this genome-wide approach identified loci containing critical glioma genes such as telomerase reverse transcriptase (*TERT*), *RTEL1*, epidermal growth factor receptor (*EGFR*), and cyclin-dependent kinase inhibitor 2B (*CDKN2B*).[14] The majority of these loci are associated with molecularly defined glioma subtypes.[15] Continued improvements in accurate measurement of potential risk factors and advances in technology allowing for discovery of additional germline and tumor molecular features will be critical to future understanding of causes and risk factors for glioblastoma.

Biology

Glioblastomas are thought to arise from neuroglial stem or progenitor cells and are characterized by molecular heterogeneity. Detailed discussion of glioblastoma biology is beyond the scope of this paper, but has recently been reviewed.[16–23]

Molecular Pathogenesis and Genomics

Molecular profiling has identified genes and core pathways that are commonly mutated in sporadic glioblastoma (Fig. 2).[24,25,26] Extension of this work to more tumors and additional dimensions (gene expression, DNA methylation) identified 3 main glioblastoma subgroups, each enriched for specific somatic alterations. The proneural gene expression/receptor tyrosine kinase (*RTK*) I/LGm6 DNA methylation group is marked by cyclin-dependent kinase 4 (*CDK4*) and platelet derived growth factor alpha (*PDGFRα*) amplifications and is most common in relatively younger adults. The classical gene expression/classic-like/RTK II DNA methylation group shows a high frequency of *EGFR* amplifications and homozygous loss of *CDKN2A/B*. The mesenchymal/mesenchymal-like subtype is enriched for tumors with neurofibromatosis type 1 (*NF1*) loss and increased tumor infiltration with macrophages. These 3 groups, and mixed entities between them, account for the vast majority of glioblastomas, and are all associated with *TERT* promoter mutations.[27–30] The molecular classification of glioblastoma into distinct subtypes provides a framework for research, but its clinical utility remains unclear. None of the glioblastoma subtypes are predictive for treatment response to current therapies, and assignment of glioblastoma subtype can be challenging in some tumors due to apparent coexistence of multiple subtypes within the same tumor and subtype "switching" through the course of the disease.

One important finding in more recent studies has been the identification of rare glioblastoma entities and their

Table 1 Inherited syndromes associated with adult gliomas (and adult glioblastomas) (adapted from Ostrom et al[9])

Gene Symbol (Chromosome Location)	Disorder/Syndrome (OMIM ID)	Mode of Inheritance	Phenotypic Features	Associated Brain Tumors
APC, MMR (5q21)	Familial adenomatous polyposis (FAP, 175100), Turcots syndrome type 2	Dominant	Development of multiple adenomatous colon polyps (>100), predisposition to colorectal cancer, and brain tumors	Medulloblastoma, glioma
ATM (11q22.3)	Ataxia- telangiectasia (208900)	Autosomal recessive trait	Progressive cerebellar ataxia, susceptibility to infections, predisposition to lymphoma and lymphocytic leukemia.	Astrocytoma and medulloblastoma
CDKN2A (9p21.3)	Melanoma-neural system tumor syndrome (155755)	Dominant	Predisposition to malignant melanoma and malignant brain tumors	Glioma
IDH1/IDH2 (2q33.3/15q26.1)	Ollier disease	Acquired post-zygotic mosaicism, dominant with reduced penetrance	Development of intraosseous benign cartilaginous tumors, cancer predisposition	Glioma
MLH1, PMS2	Turcots syndrome type 1	Autosomal recessive trait	Development of multiple adenomatous colon polyps (<100), predisposition to colorectal cancer, and brain tumors	Medulloblastoma, glioma,
MSH2,MLH1,MSH6,PMS2	Lynch syndrome (120435), biallelic mismatch repair deficiency, constitutional MMR *deficiency*	Dominant	Predisposition to gastrointestinal, endometrial and other cancers	Glioblastoma, other gliomas
MSH2,MLH1,MSH6,PMS2	Mismatch repair deficiency syndrome (276300)	Recessive	Pediatric cancer predisposition; café-au-lait spots; colon polyps	Glioma
NF1 (17q11.2)	Neurofibromatosis 1 (NF1) (162200)	Dominant	Neurofibromas, schwannomas, café-au-lait macules	Astrocytoma, schwannomas, optic nerve glioma
RB1 (13q14)	Retinoblastoma	Dominant	Development of multiple tumors of the eye, increased risk of some brain tumors	Retinoblastoma, pineoblastoma, malignant glioma
TP53 (17p13.1)	Li–Fraumeni syndrome (151623)	Dominant	Predisposition to numerous cancers, especially breast, brain, and soft-tissue sarcoma	Glioblastoma, other gliomas
TSC1,TSC2 (9q34.14,16p13.3)	Tuberous sclerosis (TSC) (191100, 613254)	Dominant	Development of multisystem nonmalignant tumors	Giant cell astrocytoma

Abbreviations used: ATM, ataxia telangiectasia; APC, adenomatous polyposis coli; CDKN2A, cyclin-dependent kinase inhibitor 2A; MLH1, MutL homolog 1, colon cancer, nonpolyposis type 2; MSH2, MutS protein homolog 2; MSH6, MutS protein homolog 6; OMIM, Online Mendelian Inheritance in Man; PMS2, postmeiotic segregation increased homolog 2; RB1, retinoblastoma transcriptional corepressor 1; TP53, tumor protein p53.

properties. For example, the alternative lengthening of telomeres phenotype, defined by alpha thalassemia/mental retardation syndrome X-linked (*ATRX*) mutation associated with *TP53* mutation, is mostly found in glioblastomas with mutations in *IDH1/2*, *H3K27M*, or *H3G34R*. *FGFR3-TACC3* fusion positive glioblastomas have been found to activate oxidative phosphorylation and appear to be metabolically distinct from the more common glycolytic glioblastomas.[31] Epigenetic tumor profiles have been particularly informative in distinguishing tumor entities beyond glioma, as they contain information retained from the cell of origin and acquired tumor associated changes. Characteristic epigenetic patterns are associated with certain presumed driver mutations, including mutant *IDH1* and *IDH2*, mutations in either H3F3A or HIST1H3B genes, specifically *H3K27M* in diffuse midline gliomas, and *H3G34R/H3G34V* mutations in younger patients with glioblastomas.[32,33]

After first-line therapy, which typically includes surgical resection, radiation, and chemotherapy, tumor cell subclones may emerge with distinct features—for example, deficiency in DNA mismatch repair (MMR).[34,35] About 10% of recurrent, post-temozolomide (TMZ) glioblastomas show a markedly higher mutation rate.[36] DNA "hypermutation" is associated with germline defects in MMR genes and can be acquired following therapy with DNA alkylating agents,[37–39] the latter occurring more commonly in O^6-methylguanine-DNA methyltransferase (*MGMT*) methylated gliomas, including those with *IDH* mutations. Oncogene amplification on extrachromosomal DNA, which is common in sporadic adult glioblastoma, likely represents another mechanism for tumor

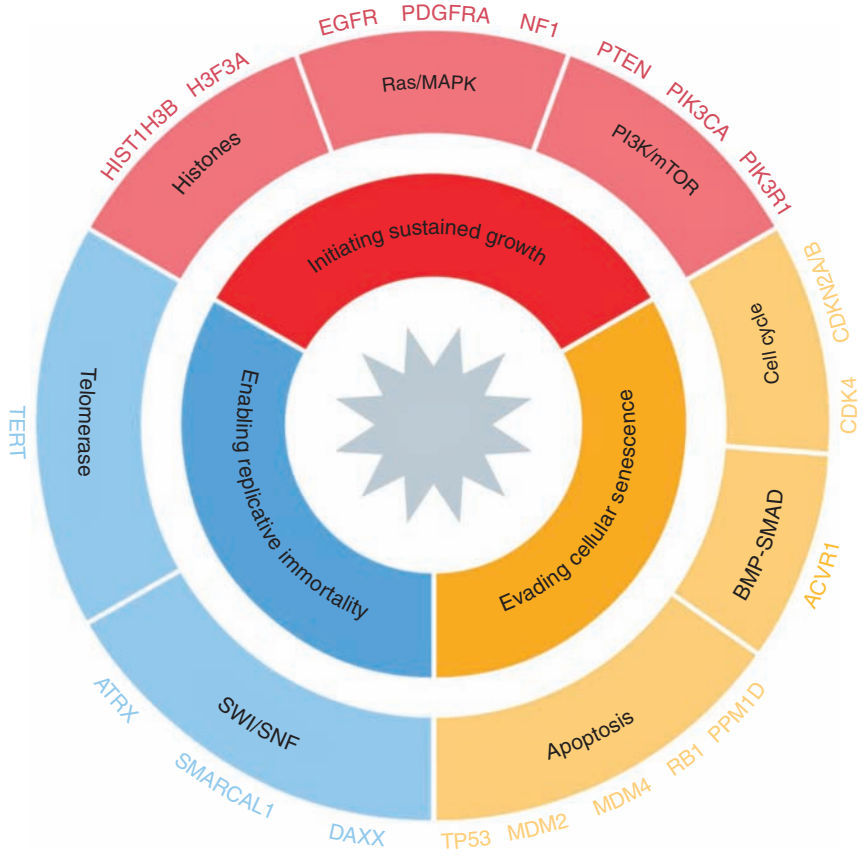


Fig. 2 Glioblastomas are characterized by somatic molecular defects in 3 major processes: initiating tumor growth, evading senescence and enabling immortal growth. Genomic abnormalities in each of the 3 processes appear required for gliomagenesis. The 3 processes are shown here, as are some of the most frequently altered genes and pathways.

cells to overcome scarcity in resources within the tumor microenvironment.[40,41] Comparison of tumor samples obtained at diagnosis and at recurrence show that 80% of mutations and copy-number variants remained unchanged between the primary and recurrent tumors.[36,42] Mutations of *PIK3CA*, *TERT*, and *EGFR* amplification in the primary tumor were usually retained in the recurrent tumor, whereas amplifications of *PDGFRA*, mutations in *EGFR*, and presence of the variant III (*EGFRvIII*) rearrangement were the genetic events most likely to be lost. The most frequent genetic changes acquired in recurrent tumors included *TP53*, *EGFR*, and phosphatase and tensin homolog (*PTEN*) mutations. These molecular changes between initial and recurrent tumors may potentially affect the design of clinical trials for recurrent glioblastomas if the tumor genotype is based on analysis of the initial tumor. For trials targeting genetic changes that are frequently altered at recurrence, re-biopsy may be indicated.

Novel sequencing technologies add another layer of detail to our understanding of intratumoral heterogeneity and tumor evolution in glioblastoma. Single-cell transcriptomics show that glioblastomas are mixtures of cells from each of the 3 gene expression subtypes, not one single category,[43] corroborating previous findings from multisector bulk gene expression profiling.[44] Single-cell DNA profiling confirmed prior fluorescence in situ hybridization findings, showing that many glioblastomas contain admixtures of subclones,[45] each of which has amplification of a different RTK (eg, *EGFR*, *PDGFRA*, *MET*).[46,47] More recently, single-cell analyses of glioblastoma samples revealed 4 cellular states within individual tumor samples that demonstrate plasticity and are influenced by tumor genetics and the microenvironment.[19] Lastly, sequencing of circulating tumor DNA (ctDNA) in cerebrospinal fluid (CSF) can yield a genetically faithful snapshot of the glioma genome in 50% of patients and may eventually obviate the need for tumor re-biopsy in certain instances.[48] As technology improves, evaluation of plasma ctDNA may also be feasible in the future.

Genomic profiling has advanced our understanding of the molecular pathogenesis of glioblastoma and identified opportunities for the development of genotype-directed therapies for subsets of patients. Thus far, however, treatment outcomes for patients with glioblastoma have not improved despite this knowledge. Silencing of MGMT-mediated DNA repair, typically the result of *MGMT* promoter methylation and loss of the second allele of

chromosome 10, currently remains the only predictive biomarker of treatment response to TMZ.[49] It is thus critical to annotate the molecular data with relevant clinical information through cooperative data-sharing efforts such as the Glioma Longitudinal Analysis (GLASS) Consortium,[42] and to incorporate prospective tumor profiling into hypothesis-driven, genotype-directed clinical trials.

Pathology and Classification of Glioblastoma

The pathologic hallmarks of glioblastoma are that of a diffusely infiltrative neoplasm with astroglial appearance (angulated nuclei and irregular chromatin), microvascular proliferation, and/or pseudopalisading necrosis (Fig. 3).[50] Mitoses are usually easy to identify. Some variants include giant cell astrocytoma (which tends to have a high frequency of *TP53* mutations but only rare *EGFR* amplifications) and gliosarcoma. Epithelioid glioblastoma resembles metastatic poorly differentiated carcinoma and is characterized by frequent *BRAFV600E* mutations,[2] although many of these tumors may be difficult to distinguish from pleomorphic xanthoastrocytomas (Fig. 3).[51]

Occasionally, a tumor specimen does not show the classic histopathologic features of a glioblastoma. Before the era of integrated histopathology-molecular classification, such tumors would have been assigned a lower WHO grade. However, numerous studies have consistently shown that if such a tumor contains the molecular signature of a glioblastoma, it will act like one and should be treated as such. This was incorporated into the third update of cIMPACT-NOW (the Consortium to Inform Molecular and Practical Approaches to CNS Tumor Taxonomy), which recommended diagnostic criteria for "diffuse astrocytic gliomas, *IDH*-wildtype, with molecular features of glioblastoma, WHO grade IV."[52] In the absence of *IDH* mutations, either *TERT* promoter mutations, the combination of gain of chromosome 7 and loss of chromosome 10, or *EGFR* amplification are now considered sufficient molecular evidence of glioblastoma with similar clinical outcome, even when histologic examination meets only WHO grade II or III criteria.[52,53] The recently described CNS tumor methylation classifier[33] represents a major advance in the diagnostic armamentarium in the goal of diagnostic accuracy of brain tumors, and specific glioblastoma subclasses are defined. While the clinical utility of these glioblastoma subtypes is not yet shown, use of the classifier to confirm a glioblastoma diagnosis can be helpful in selected cases, especially in unusual clinical situations (for example, unusual histopathology or history of long-term patient survival).

Conversely, mutations in *IDH1/2* in adult diffuse gliomas allow prediction of extended patient survival.[3,54] A fast, inexpensive upfront screen for IDH mutation is mutation-specific immunohistochemistry for the most common variant, *IDH1-R132H*, which comprises well over 90% of all IDH mutations in glioblastoma.[54,55] Reflex sequencing for non-canonical IDH mutations, such as *IDH2* (codon 172), and non-R132H mutations in *IDH1* (for example, *R132C* or *R132S*), is common practice at many institutions, especially when it is part of a larger next-generation sequencing (NGS) panel. However, targeted sequencing

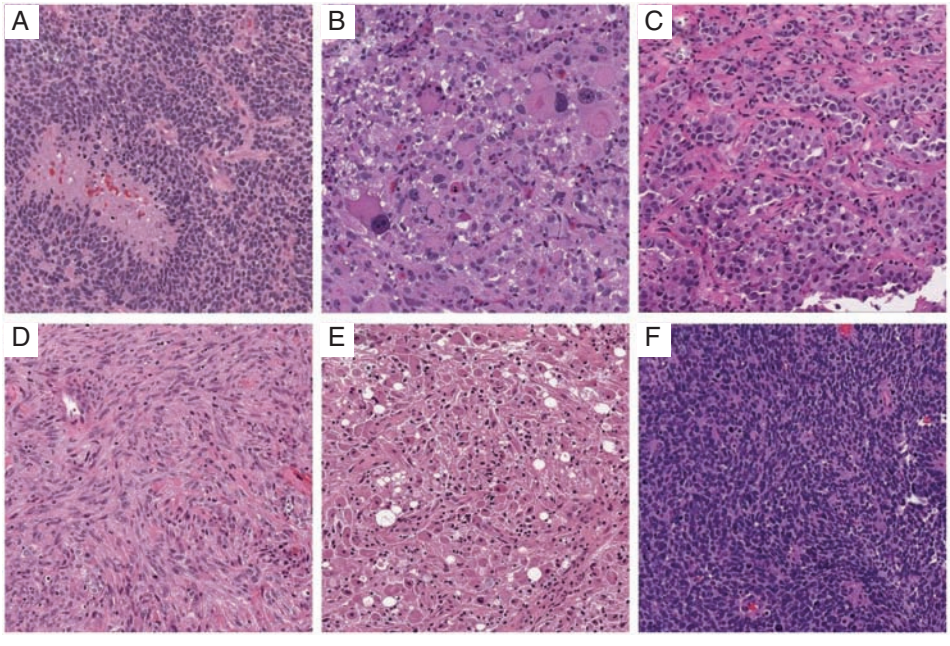


Fig. 3 The many forms of GBM. (A) Classic GBM, with pseudopalisading necrosis and microvascular proliferation. (B) Giant cell GBM. (C) Epithelioid GBM with BRAF V600E. (D) Gliosarcoma. (E) Granular cell GBM. (F) Small cell GBM. All images are from the UPMC Neuropathology Virtual Slide Database, 200x magnification.

for "antibody-negative" glioblastoma (ie, tumors which are not positive on *IDH1 R132H* immunohistochemistry) is considered optional when patients are ≥55 years old, since IDH mutations overall, and especially those that are non-canonical, are very uncommon in older patients.[56] On a practical level, it is also very unusual for a glioblastoma, upon initial diagnosis, to have an IDH mutation when it contains microthrombi and/or unequivocal pseudopalisading necrosis.[57] Finally, the use of *ATRX* immunohistochemistry can be a useful screen, since most cases of *IDH*-mutant glioblastoma show concomitant loss of *ATRX* (although not all cases of histologically defined glioblastoma with *ATRX* loss are *IDH*-mutant). In keeping with the distinct biology and clinical behavior of grade IV gliomas as a function of IDH mutation status, the cIMPACT-NOW consensus group suggests that the term "glioblastoma" no longer apply to *IDH*-mutant tumors, and suggests instead the term "astrocytoma, *IDH*-mutant, WHO grade IV" for such tumors, to distinguish them from *IDH*wt glioblastoma.[4]

Predictive Biomarkers

Genomic profiling has advanced our understanding of the molecular pathogenesis of glioblastoma and identified opportunities for the development of genotype-directed therapies for subsets of patients. Thus far, however, treatment outcomes for glioblastoma patients have not improved despite this knowledge.

Multiple phase III trials have shown that the presence of *MGMT* promoter methylation results in approximately 50% longer median survival for glioblastoma patients treated with TMZ.[49,58,59] In glioblastomas that lack *MGMT* promoter methylation, TMZ has little or no benefit.[49,60] Whether TMZ may be withheld from these patients, especially in the context of clinical trials, remains controversial, although an increasing number of studies are doing so.[61]

There are multiple ways to test for *MGMT* promoter methylation, including methylation-specific polymerase chain reaction (MS-PCR), methylation-specific high-resolution melting, pyrosequencing, and MethyLight, as well as other methodologies.[62] A recent method, STP-27,[63] employing data obtained from the Illumina methylation array (the same methodology in use for the diagnostic brain tumor classifier[33]) has also shown promise. The method with the most prospective clinical trial validation is quantitative MS-PCR. However, one retrospective study employing various methods on the same set ofTMZ-treated glioblastomas suggested that pyrosequencing might actually provide the best stratification in terms of outcomes, although this needs to be validated by other independent studies.[62] Due to the large number of assays available and differences in cutoffs for calling methylation, there is a nontrivial amount of interlaboratory heterogeneity, and better harmonization of *MGMT* promoter methylation testing is critically needed. In addition, approximately 10% of patients fall into a "gray zone" with tumors that are neither truly methylated nor unmethylated but appear to derive some benefit from TMZ.[64] Immunohistochemistry has been proven to be unreliable and should not be used.[65]

Diagnosis and Imaging

Most glioblastomas are diagnosed following symptomatic presentation due to their rapid expansion and displacement, or infiltrative destruction of brain structures. Suggestive symptoms may include new onset epilepsy, progressive headaches, focal neurologic signs, and mental status alterations in combination with signs of increased intracranial pressure.[66] Contrast-enhanced MRI is the diagnostic tool of choice for glioblastoma. These tumors typically manifest as an enhancing, necrotic-appearing mass surrounded by non-enhancing signal abnormalities consisting of edema and infiltrative tumor (Fig. 4). Hemorrhage, cystic changes, or multicentric enhancement is also frequently present.[67] When combined with the clinical history, radiological diagnosis of glioblastoma is often achieved with confidence,

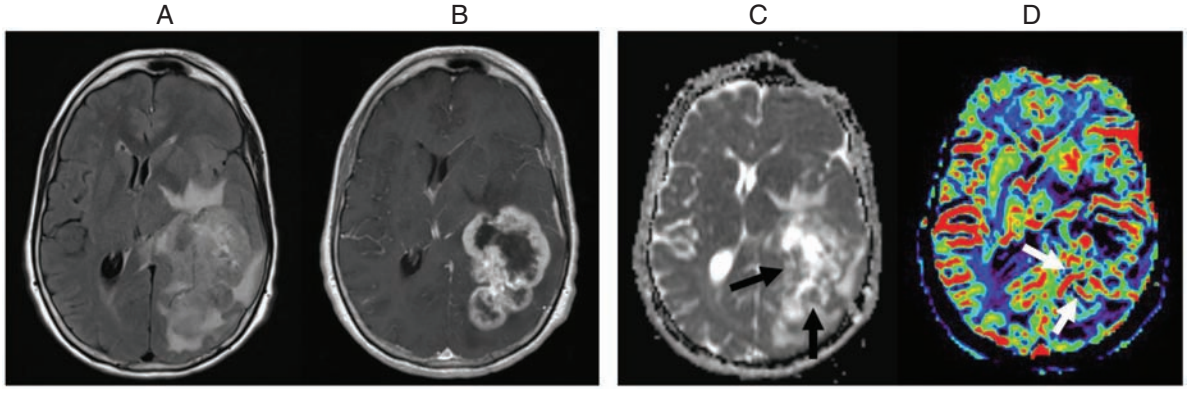


Fig. 4 Sixty-four-year-old with a glioblastoma who presented with word finding difficulty. FLAIR (A) and contrast-enhanced T1W (B) images show a large, necrotic-appearing, enhancing mass with surrounding T2/FLAIR signal abnormality in the periventricular regions. There is evidence of hypercellularity on ADC map (black arrow in C) and elevated blood volume on CBV map (white arrow in D)

although challenges may arise as other intra-axial neoplasms, including metastasis, some lower-grade gliomas, and occasionally lymphoma can share similar imaging findings. Nonneoplastic neurologic conditions, such as abscess or demyelinating lesions, may also have a similar appearance. MRI also provides essential anatomic details of the tumor and its adjacent brain structures for surgical planning. For tumors located close to eloquent locations, functional MRI can help plan optimal surgical trajectory and achieve safe maximal resection of enhancing tumor with the goal to improve patient survival.[68,69] For clinical trials, the standardized brain tumor imaging protocol is recommended to reduce variability and increase reliability.[70] Ideally this protocol would also be incorporated into routine clinical imaging of glioblastoma patients.

Advanced MRI techniques are increasingly available to assist in the diagnosis of glioblastomas by evaluating their physiological or metabolic properties. Perfusion-weighted imaging such as dynamic susceptibility contrast (DSC) MRI measures cerebral blood volume (CBV), an imaging marker that correlates with microvessel density and area (Fig. 4D).[71,72] Since microvascular proliferation due to tumor-induced angiogenesis is a hallmark of glioblastoma,[73] CBV may allow differentiation of glioblastoma from other tumor types[74–76] or histological grades.[77] DSC-MRI may also be useful for differentiation of pseudoprogression in response to radiotherapy (RT) and immunotherapies from true progression, although both false negative and false positive studies may occur.[78,79] Apparent diffusion coefficient (ADC), derived from diffusion weighted MRI, inversely correlates with tumor cell density.[80,81] ADC values for glioblastomas are lower than for lower grade glioma[82] but higher than for lymphoma.[83,84] (Fig. 4C) Magnetic resonance spectroscopy (MRS) can detect alterations of metabolite concentrations within the tumor[85]; glioblastomas typically show markedly elevated choline due to increased cell proliferation and reduced N-acetyl aspartate from neuronal loss. These changes are sensitive but not specific for the diagnosis of glioblastoma, since similar changes can also be observed with other neoplasms or inflammatory disease.[79]

Positron emission tomography (PET) can also provide additional information about biology, differential diagnosis, delineation of tumor extent for surgical and RT

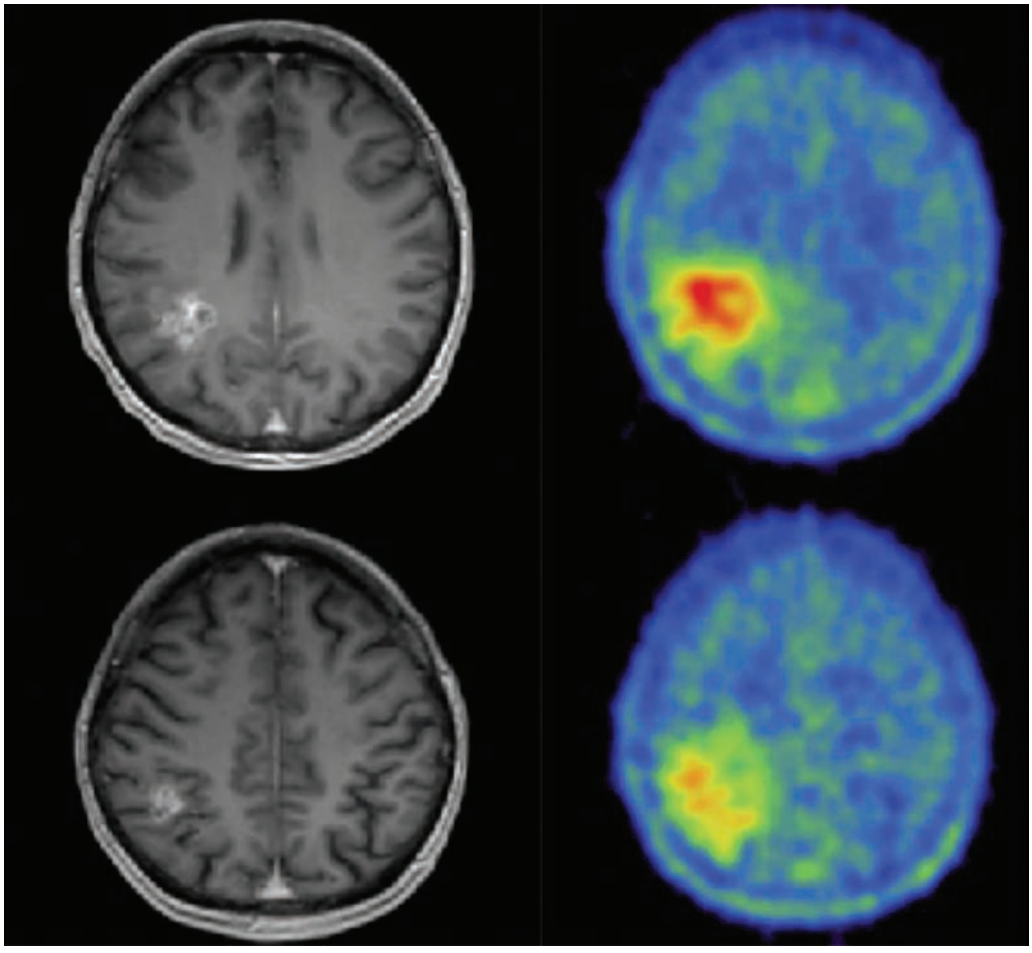


Fig. 5 Contrast-enhanced MRI T1W (left) and ^{18}FET-PET (right) of a 42-year-old patient showing much larger extent of a glioblastoma on the PET images compared with the enhancing tumor evident by MRI. The tumor extent on the PET image was confirmed by histology.

planning, and posttreatment surveillance (progression vs pseudoprogression).[86,87] Amino acids are the preferred PET tracer (^{11}C-MET, ^{18}F-FET, ^{18}F-FDOPA) based on higher specificity and lower signal/noise ratio than glucose (^{18}F-FDG) (Fig. 5).[88] However, the lack of insurance coverage currently limits the widespread incorporation of these studies into standard clinical practice in the United States.

Accurate determination of response and progression remains a challenge. Currently, the Response Assessment in Neuro-Oncology (RANO) criteria for high-grade gliomas is the most widely used standard in clinical trials for glioblastoma.[89,90] These criteria use 2D tumor measurements and provide guidance on evaluating pseudoresponse, non-enhancing progression, and pseudoprogression. More recently, modifications to the RANO criteria have been suggested using a post-RT baseline,[91,92] and confirmation of progression on subsequent scans has been advised, especially for agents associated with pseudoprogression, to ensure that patients are not removed from therapies prematurely. This schema also lowers the possibility that patients with spontaneously improving pseudoprogression would be offered salvage options or placed inappropriately on clinical trials for presumed progressive disease.[91,93] Additional work is needed to improve response assessment for glioblastomas, with first reports on automated volumetric measurements and deep learning algorithms showing that these may improve outcome assessment.[94,95]

Medical Management and Supportive Care

Corticosteroids, preferably dexamethasone (in conjunction with gastric protection if used at high doses), are given to reduce symptomatic peritumoral vasogenic edema.[96] Dexamethasone alleviates neurologic deficits and signs of increased intracranial pressure such as headache and drowsiness. Low doses (eg, 4 mg/day given in 1–2 doses) are effective in most clinically symptomatic patients without signs of herniation.[97,98] There is no need to give dexamethasone 4 times a day.[98] Side effects of dexamethasone worsen with increased dose and duration of treatment.[99,100] There is also growing evidence that corticosteroids may have an adverse effect on patient outcome, so they should be avoided if patients are not symptomatic.[101] Patients on chronic corticosteroids (≥20 mg prednisone equivalents daily for ≥1 month) should be considered for prophylaxis for osteoporosis and *pneumocystis jerovecii* pneumonia.[102]

Seizures affect 23% of glioblastoma patients at presentation[103] and an additional 20% later in the disease course. While patients with seizures require anti-epileptic drugs (AEDs), studies have not clearly shown a benefit of prolonged primary AED prophylaxis in patients who have never had a seizure.[104,105] Current guidelines recommend tapering AEDs 1–2 weeks after surgery and avoiding long-term prophylaxis.[106] There is no role for primary perioperative prophylaxis (ie, in patients who have never had a seizure). A meta-analysis of 6 studies,[107] a Cochrane systematic review,[108] and a subsequent randomized trial of phenytoin versus no prophylaxis[109] have all shown no significant benefit from primary prophylaxis. When AEDs are used, newer agents including levetiracetam and lacosamide are preferred over older drugs because of generally more favorable side effect profiles, reduced laboratory monitoring requirements, and lack of drug-drug interactions.[110] Emerging data suggesting that neurons and glioma cells form synapses via AMPA (α-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid) receptors raises the possibility that AEDs that inhibit these receptors, such as perampanel, may be beneficial not only in controlling seizures, but also through possible antiglioma activity.[111,112] However, a prior trial with another glutamate inhibitor, talampanel, was ultimately interpreted to be negative.[113]

Venous thromboembolism (VTE) risk is high in the perioperative period and persists well beyond, with one-year incidence of approximately 20%,[114,115] mandating a low threshold for pursuing diagnostic studies.[115] Most,[116,117] though not all,[118] studies suggest that the risk of precipitating intratumoral hemorrhage with anticoagulants is acceptably low, even in patients receiving bevacizumab.[119] The preferred anticoagulant is not well studied in brain tumors; in systemic cancer, low molecular weight heparin (LMWH) is preferred over warfarin.[120] Direct oral anticoagulants (DOACs) (factor Xa and thrombin inhibitors) have been reported to be safe in patients with brain tumors.[121] However, no randomized data are available for glioma patients and randomized trials on secondary prophylaxis of VTE with DOACs enrolling cancer patients have generally shown a similar or slightly higher efficacy than LMWH but with a slightly higher risk of bleeding.[122,123]

A high incidence of recurrent VTE with inferior vena cava (IVC) filters limits their use to patients with recent intracranial surgery, intratumoral hemorrhage, or absolute contraindications to anticoagulation.[110] Prophylaxis with anticoagulation outside of the perioperative setting has not been definitively studied, as the only trial addressing this issue was prematurely terminated for slow accrual.[124] A meta-analysis of pooled randomized clinical trial data indicated no survival benefit from anticoagulation in glioblastoma patients, but rather suggested that VTE should be treated more vigorously in this patient population.[125]

Cognitive deficits, personality changes, and mood disturbances are major comorbidities for glioblastoma patients.[96] Before treatment, up to 91% of brain tumor patients have cognitive deficits, with only moderate correlation with cognitive complaints.[126,127] The frequent presence of fatigue and sleep disturbance contributes to cognitive impairment.[128,129] Medical treatments with acetylcholinesterase inhibitors (donepezil) or psychostimulants (methylphenidate, modafinil) to prevent cognitive decline and fatigue after RT in patients with brain tumors (<50% were glioblastoma) have been unsuccessful.[130–133] Although the 6-month prevalence of clinical depression is about 20% in brain tumor patients,[134] randomized studies on medical treatment are lacking.

Regular exercise,[135] adoption of a healthy diet, avoidance of hyperglycemia,[136] early discussion of goals of care, and involvement of palliative care should be considered. Despite extensive interest in ketogenic diets and cannabinoids, there are currently no clinical data supporting their routine use.

Standard Therapy

Despite recent advances in our understanding of glioma biology, the prognosis of patients with glioblastoma remains poor. With standard-of-care consisting of surgery, RT, and TMZ chemotherapy, median overall survival (OS) in well-selected patients in clinical trials is approximately 15–18 months,[58,59,137] and 5-year survival is less than 10%.[138] Once glioblastomas recur, median OS is estimated to be 24–44 weeks.[139–141] Standard-of-care therapies for patients with newly diagnosed glioblastoma are summarized in Table 2, Fig. 6 and recurrent glioblastoma in Table 3, Fig. 7. Because none of these treatments are curative, the National Comprehensive Cancer Network (NCCN) recommends clinical trials as the preferred option for eligible patients.[142] Treatment must also be tailored to the individual based on age, functional status, goals of care, etc. Integration of palliative care early in the course of the illness is important, and best supportive care may be the most appropriate course in some patients.[66]

Surgical Management

Surgical procedures should be tailored to individual patients, taking into consideration indications, risk-benefit ratio, and prognostic impact for each patient. In the past, tumor extent has been mostly defined on MRI by T_1-weighted sequences with contrast enhancement; however, non-contrast enhancing tumor volume has to be incorporated as well into the target volume for resection.[151] Whenever microsurgical resection is deemed to be high risk based on the patient's medical condition and/or the functional topography or eloquence of the affected brain region, a stereotactic or open biopsy should be performed to obtain at least a histological and molecular diagnosis.[66] In order to obtain sufficient material for histological diagnosis and grading, the surgeon aims to target and biopsy areas of solid tumor mass that contain viable tumor cells, preferably avoiding necrotic areas or adjacent nonneoplastic brain. The most frequently requested genetic markers (*IDH1/2* mutation and *MGMT* promoter methylation) appear to be present homogeneously throughout the tumor, so the risk of a sampling error by obtaining a "false-negative" result or misclassification of the molecular profile is relatively low.[152] However, since additional molecular markers may gain clinical relevance in the future, multiple (larger) samples should be considered for more advanced genomic analyses. Whenever possible, areas of enhancement must be included in the target for the biopsy to ensure accurate WHO grade classification of the tumor. Extent of resection should be verified by an early postoperative contrast enhanced MRI, preferably within 48 hours after surgery.[151]

Radical microsurgical resection of a glioblastoma is limited by the highly invasive nature of the tumor with infiltrating tumor cells typically extending significant distances from the main tumor mass.[153] Nevertheless, the goal for glioblastoma surgery should be gross total resection of the enhancing solid tumor mass whenever feasible. While some studies report gradually improved outcome with increasing extent of resection above 78%, only gross total resection is likely to be associated with improved outcome in both newly diagnosed[69,154–158] and recurrent glioblastoma.[159,160] The goal is to leave the smallest amount of residual postoperative enhancing volume possible as this correlates with survival.[161] Current standard surgical adjuncts include stereotactic navigation systems using anatomical and functional MRI datasets, intraoperative MRI, ultrasound, intraoperative functional monitoring, and the fluorescent dye 5-aminolevulinic acid (5-ALA) to visualize vital tumor tissue, all of which are increasingly used to improve and maximize the extent of resection while reducing the risk of new neurologic deficits (Fig. 8).[155,162,163] As a general principle, preventing new permanent neurologic deficits is more important than maximizing the extent of resection, because glioblastomas are not cured by surgery alone, while recognizing and taking into consideration the benefits of maximal safe resection. Postoperative deficits due to emerging complications are a negative prognostic factor.[164,165] This emphasizes the relevance of a risk-adapted concept which embeds surgery into a thorough prognostic evaluation. Given the complexities of surgery for glioblastoma, consideration should be given to referring patients to high-volume centers specializing in the care of brain tumor patients.

Biodegradable polifeprosan 20 with carmustine wafers inserted at the time of surgery is approved by the US FDA and the European Medicines Agency for the treatment of both newly diagnosed high-grade glioma and recurrent glioblastoma.[166,167] They were shown to produce a modest survival advantage of approximately 2 months but are used only sporadically, in part because the efficacy data stem from the pre-temozolomide era, carmustine from the wafers has limited brain penetration, safety and tolerability are an issue in low-volume centers, and this treatment may preclude patients from enrolling into clinical trials.

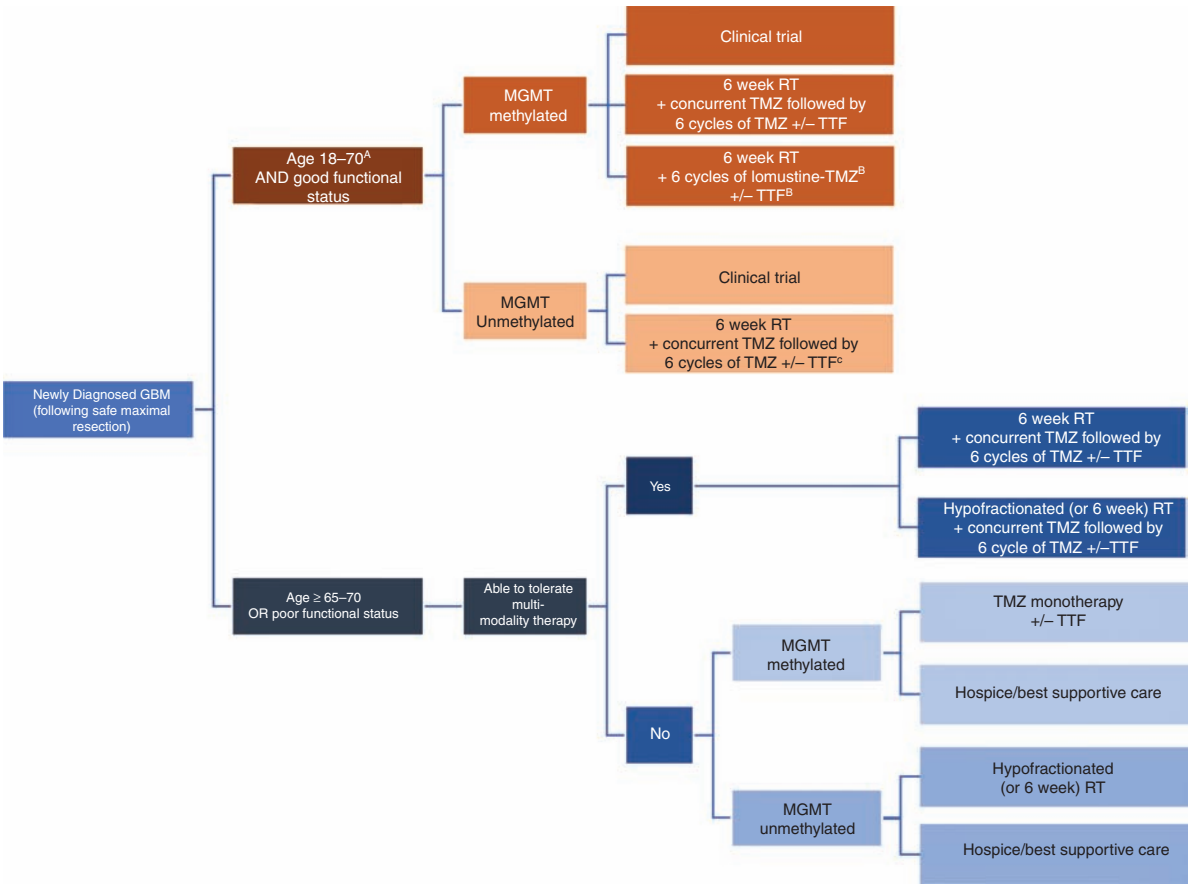
Postsurgical Management of Newly Diagnosed Glioblastoma

Following maximal safe resection, the generally accepted treatment for glioblastoma is radiotherapy (RT) with concurrent TMZ (75 mg/m^2/day × 6 wk) and maintenance TMZ (150–200 mg/m^2/day × 5 days for six 28-day cycles) (Figure 6).[58,138] Because *MGMT* promoter methylation status is predictive of the efficacy of TMZ,[49] TMZ can be withheld in select patients with *MGMT* unmethylated tumors where the benefit of TMZ is minimal, especially in the context of clinical trials,[61] or when the risks of TMZ outweigh the benefit (ie, toxicity limits TMZ use). During adjuvant TMZ, the addition of tumor treating fields (TTF), which provide low intensity, intermediate frequency (200 kHZ), alternating electric fields to produce antimitotic effects selective for dividing tumor cells with limited toxicity, extended survival by a median of 4.9 months in one study.[143] Neither dose-dense TMZ regimens,[59] extending the length of adjuvant TMZ treatment beyond 6 cycles,[168–170] nor the addition of bevacizumab[137,171] yield additional survival benefit.

Table 2 Selected phase III clinical trials in patients with newly diagnosed glioblastoma

Study Design	Study Population and Key Eligibility Criteria	Extent of Resection	Radiation Scheme	Systemic/Experimental Agent	Median OS, months	Median PFS/EFS, mo
Randomized phase III trial of RT ±TMZ ($N = 573$)[58]	Newly diagnosed GBM Age 18–70 years WHO PS ≤ 2	Biopsy: 16–17% Partial resection: 44–45% Complete resection: 39–40%	Fractionated focal irradiation in daily fractions of 2 Gy given 5 days per week for 6 weeks, for total of 60 Gy	TMZ 75mg/m^2/day during radiation from the first to the last day of RT (up to 49 days) followed by 6 cycles of adjuvant TMZ 150–200 mg/m^2 for 5 days during each 28-day cycle)	RT alone: 12.1 (95% CI, 11.2–13.0) RT +TMZ: 14.6 (95% CI, 13.2–16.8). Unadjusted HR for death 0.63; 95 % CI, 0.52–0.75; $P < 0.001$	RT alone: 5.0 (95% CI, 4.2–5.5) RT +TMZ: 6.9 (95% CI, 5.8–8.2)
Randomized, open-label trial of adjuvant TMZ ± TTF ($N = 695$)[143]	Newly diagnosed GBM who had completed concomitant RT +TMZ Age ≥ 18 years KPS ≥ 70 Supratentorial tumor	Biopsy: 13% Partial resection: 33–34% Gross total resection 53–54%	N/A	Adjuvant TMZ as per Stupp regimen above TTF initiated 4–7 weeks from last day of RT until second progression or for a maximum of 24 months	TMZ alone: 15.6 TMZ +TTF 20.5 HR 0.64; 99.4% CI, 0.42–0.98; $P = 0.004$	TMZ alone: 4.0 TMZ +TTFields: 6.7 HR 0.63; 95% CI, 0.52–0.76; $P < 0.001$
Studies in MGMT methylated GBM						
Randomized, open-label, phase III trial of standard TMZ versus lomustine-TMZ [144]	Newly diagnosed GBM Age ≥ 18 years KPS ≥ 70 Centrally confirmed methylated MGMT promotor	Biopsy: 2–5% Partial resection: 35–36% Complete resection: 59–63%	Standard involved-field RT to total dose of 59–60 Gy in 30–33 single day fractions	Standard concurrent + adjuvant TMZ as per Stupp above Lomustine-TMZ: 6-week cycles of lomustine 100 mg/m^2 on Day 1 and TMZ 100–200 mg/m^2 on days 2–6 for up to 6 cycles, starting in the first week of RT	In modified intention to treat population. Standard TMZ: 31·4 (95% CI, 27·7–47·1) Lomustine-TMZ: 48·1 (95% CI, 32·6–not assessable) HR 0·60; 95% CI 0·35–1·03; $P = 0.0492$	In modified intention to treat population. Standard TMZ: 16·7 (95% CI, 11·4–24·2) Lomustine-TMZ: 16·7 (95% CI, 12·0–32·0) HR 0·91; 95% CI 0·57–1·44; $P = 0.4113$
Studies in elderly patients (age ≥65 years)						
Randomized phase III trial of hypofractionated RT ±TMZ ($N = 562$) [145]	Newly diagnosed GBM Age ≥65 years ECOG PS ≤2 Deemed by their physicians not to be suitable to receive conventional RT	Biopsy: 31.7% Partial or complete resection: 68.3%	Fractionated focal irradiation administered in 15 daily fractions over a period of 3 weeks, for total of 40.05 Gy	TMZ 75 mg/m^2/day during radiation from the first to the last day of RT (21 consecutive days) followed by adjuvant TMZ 150–200 mg/m^2 for 5 days during each 28 day cycle) for up to 12 cycles	RT alone: 7.6 RT +TMZ: 9.3 HR 0.67 for death; 95% CI, 0.56 to 0.80; $P < 0.001$	RT alone: 3.9 RT +TMZ: 5.3 HR 0.50 for disease progression or death; 95% CI, 0.41 to 0.60; $P < 0.001$
NOA-08: Noninferiority, randomized phase III trial of TMZ vs RT ($N = 373$)[146]	Newly diagnosed GBM or AA Age ≥ 65 years KPS ≥ 70	Biopsy: 37–41% Partial resection: 31–35% Complete resection; 20–27%	Fractionated focal irradiation administered in 30 daily fractions over 6–7 weeks, total 60.0 Gy	TMZ 100 mg/m2 for 1 week on, 1 week off	TMZ: 8·6 (95% CI, 7·3–10·2) RT: 9·6 (95% CI, 8·2–10·8) HR 1·09, 95% CI 0·84–1·42, $p_{non\text{-}inferiority} = 0·033$	TMZ: 3·3 (95% CI, 3·2–4·1) RT: 4·7 (p5% CI, 4·2–5·2) HR 1·15, 95% CI 0·92–1·43, $p_{non\text{-}inferiority} = 0·043$
Nordic: Randomized, phase III trial of TMZ vs 6-week RT vs hypofractionated RT ($N = 291$)[147]	Newly diagnosed GBM Age ≥60 y WHO PS ≤ 2	Biopsy: 26–27% Partial or complete resection: 73–74%	Hypofractionated RT: 34·0 Gy administered in 3·4 Gy fractions over 2 weeks Standard RT: 60·0 Gy administered in 2·0 Gy fractions over 6 weeks	TMZ 200 mg/m^2 for 5 days during each 28 day cycle for up to 6 cycles	In comparison with standard RT: 6·0 months (95% CI, 5·1–6·8) TMZ: 8·3; HR 0·70; 95% CI 0·52–0·93, $P = 0.01$ Hypofractionated RT: 7·5 (95% CI, 6·5–8·6), HR 0·85; 95% CI 0·64–1·12, $P = 0.24$	Deliberately not collected

Abbreviations: CI, confidence interval; ECOG, Eastern Cooperative Oncology Group; EFS, event-free survival; HR, hazard ratio; KPS, Karnofsky performance status; OS, overall survival; PFS, progression-free survival; PS, performance status; RR, radiographic response rate; TTF, tumor-treating fields.



A In elderly patients with good performance status, standard 6-week radiation + TMZ can be considered
B It is unclear whether lomustine-TMZ is preferred over TMZ given the limitation of the study (see text.)
C Because MGMT methylation status is predictive of the efficacy TMZ, TMZ can be withheld in select patients with MGMT unmethylated tumors, especially in the context of cinical trials or when the risks of TMZ outweigh the benefit.

Fig. 6 Standard of care treatment paradigm for newly diagnosed glioblastoma.

A recent small randomized phase III trial examined the benefit of an intensified lomustine-TMZ regimen for newly diagnosed *MGMT* promoter methylated glioblastoma. When combined with radiotherapy, median OS increased from 31.4 months with standard TMZ to 48.1 months with lomustine-TMZ.[144] Since the sample size was small (~70 patients in each arm), the survival curves separated late (after 2–3 y), and in univariate analysis the effect was small, the role of this regimen remains unclear.[172] Hematologic toxicity was greater in the lomustine-TMZ arm, and fewer patients were able to complete all 6 cycles of adjuvant treatment.[144]

Radiotherapy Considerations

Most standard approaches recommend delivering RT in the range of 60 Gy in 30 fractions of 2 Gy, based on targets selected using the immediate postsurgical MRI. The recommendation of the European Organisation for Research and Treatment of Cancer (EORTC) is to perform RT in a single phase (60 Gy, 2 Gy per fraction) while the Radiation Therapy Oncology Group (RTOG) approach uses an initial larger volume defined by the fluid attenuated inversion recovery (FLAIR) abnormality plus a 2-cm margin, which receives 46 Gy, in 23 fractions of 2 Gy each, plus additional 14 Gy given to the resection cavity and residual enhancing tumor.[173] Great attention is paid to limit exposure of structures that are at risk of radiotherapy-induced damage, including ophthalmic and optic structures, brainstem, cervical cord, cochlea, and, where feasible, temporal lobes and/or hippocampi.[174] A number of institutions have published modifications of this approach, in an attempt to decrease the volume of normal brain irradiated.[175] There remains considerable disagreement regarding the optimum RT volume and margin expansions, and advanced imaging has not yet helped resolve this issue.[175,176] Several ongoing research efforts are focusing on better defining the volume that truly needs to be boosted to a higher dose by incorporating advanced imaging such as perfusion/diffusion MR, MRS, and amino-acid PET, but these remain

investigational. Prior dose-escalation efforts have largely failed, but these were conducted in the pre-temozolomide era, and current trials are investigating whether RT dose-escalation might be beneficial, at least in some patients, when combined with TMZ (eg, NCT02179086). It is also unclear whether modern RT techniques will yield superior outcomes (Fig. 9). For example, emerging data suggest that the reduction in the low dose volume to normal brain decreases therapy-associated lymphopenia,[177] and this has been suggested to be indirectly associated with improved survival.[178]

Pseudoprogression

Radiochemotherapy can produce transient worsening of contrast enhancement on MRI for several months in approximately 10–30% of patients, sometimes associated with symptoms of intracranial mass effect.[179,180] A similar problem may occur with immunotherapies. The diagnosis of pseudoprogression can be problematic; DSC-MRI[78,79] and amino acid PET imaging, as described above, may be helpful.[86] Because of the difficulty in differentiating pseudoprogression from progression, the RANO working group has recommended avoiding enrolling patients within 3 months of completion of radiochemotherapy into clinical trials for recurrent disease, unless the recurrence is mainly outside the RT field or there is tissue confirmation of progression.[89] However, histopathological distinction of "residual tumor" (apparently dormant and damaged) versus truly "recurrent tumor" (healthier and actively proliferating) can be challenging. [181]

Elderly Patients

Since the median age of glioblastoma is 65 years, a significant number of patients are considered "elderly."[1] Their treatment represents a particular challenge, as they generally have a worse prognosis and are less tolerant of toxicities.[182] There is evidence that hypofractionated RT (40 Gy/15 fractions of 2.67 Gy over 3 weeks) is as effective as the standard 60 Gy over 6 weeks.[183] An international phase III trial of newly diagnosed glioblastoma patients age 65 and older demonstrated an OS advantage with hypofractionated RT (40 Gy/15 fractions of 2.67 Gy) with TMZ compared with RT alone (9.3 vs 7.6 mo), with clinical benefit predominantly in patients with methylated *MGMT* promoter.[145] However, there has never been a direct comparison of hypofractionated RT with TMZ compared with the standard 6 weeks of RT with TMZ. For patients with poor functional status, single modality therapy may be better tolerated, but the recommendation varies depending on the *MGMT* promoter methylation status. In both the NOA-08[146] and the Nordic Clinical Brain Tumor Study Group trials[147] which compared RT versus TMZ, RT was more effective than TMZ for *MGMT* promoter-unmethylated tumors, whereas TMZ was more effective than RT for *MGMT* promoter-methylated tumors. Radiotherapy schedules used in the elderly population include 40 Gy delivered in 15 fractions,[183] 34 Gy in 10 fractions,[147] or 25 Gy in 5 fractions,[184] although the role of the latter regimen is more controversial.

Recurrent Glioblastoma

Glioblastoma patients invariably recur after a median interval of less than 7 months,[58] and there is no clear standard-of-care salvage therapy (Fig. 7). NCCN guidelines list clinical trials as the preferred option for eligible patients.[142] Surgery may have a role for symptomatic and/or large lesions. However, only patients who undergo complete resections have any survival benefit.[160] Other options include systemic therapy such as TMZ rechallenge, nitrosoureas, bevacizumab, re-irradiation, and TTF (in the US),[185] none of which have been shown to prolong survival in randomized trials in this setting, or palliative care for patients with poor performance status.

Bevacizumab

Multiple studies of the humanized vascular endothelial growth factor (VEGF) antibody bevacizumab for glioblastoma have failed to demonstrate a survival benefit.[148] However, bevacizumab is often effective in reducing peritumoral edema and related clinical symptoms and signs.[186] It is approved in the United States and some other countries, but not in the European Union, for use in recurrent glioblastoma due to improvement in progression-free survival (PFS) and reduction in corticosteroid use.[148] Continuation of bevacizumab post progression did not improve outcome in a small study.[187] Patients with recurrent glioblastoma should ideally be considered for clinical trials before receiving bevacizumab, as most trials exclude prior use of bevacizumab. Bevacizumab has also been proven to be effective in radiation-induced necrosis, although the doses used are lower than standard dosing for recurrent glioblastoma (typically 7.5 mg/kg every 3 wk for a maximum of 4 treatments).[188]

Temozolomide Rechallenge

Rechallenge with TMZ may be reasonable, especially in patients with *MGMT* promoter methylated glioblastoma that relapses more than a few months after completion of maintenance TMZ in the first-line setting.[149,150] The uncontrolled RESCUE study observed that patients who lived longest with dose-dense TMZ were those who progressed after a treatment-free interval.[149] While *MGMT* status was not predictive of outcome in the RESCUE study, the DIRECTOR trial did demonstrate increased time to treatment failure with TMZ rechallenge in patients with *MGMT* promoter methylated versus unmethylated tumors.[150] However, there is no evidence to suggest that TMZ rechallenge is superior to nitrosoureas in any patient population.

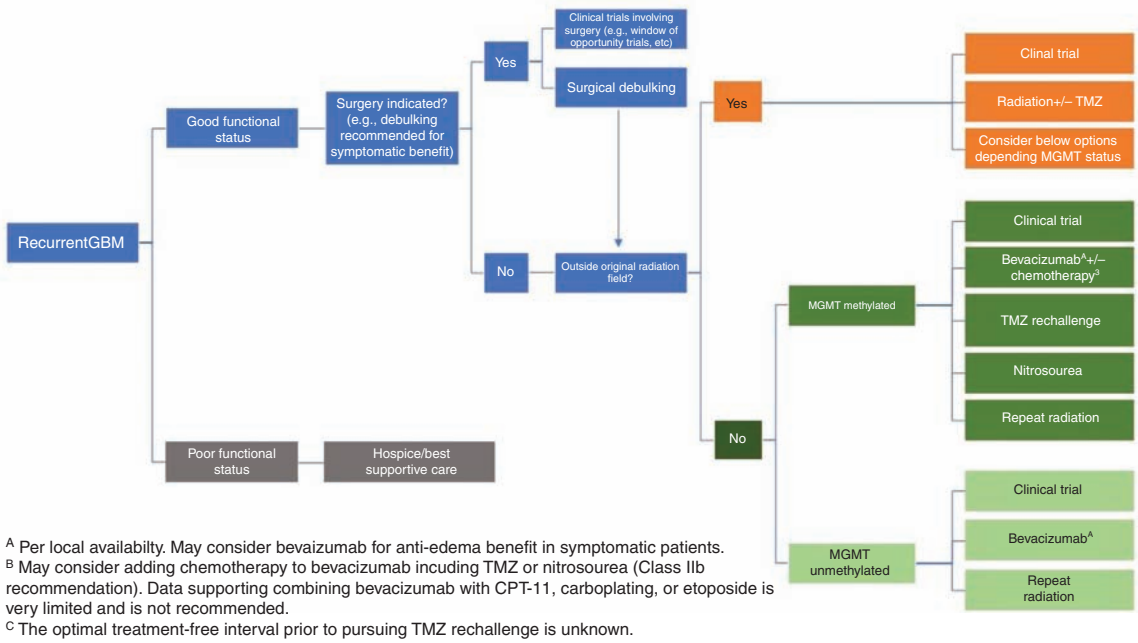


Fig. 7 Standard of care treatment paradigm for recurrent glioblastoma.

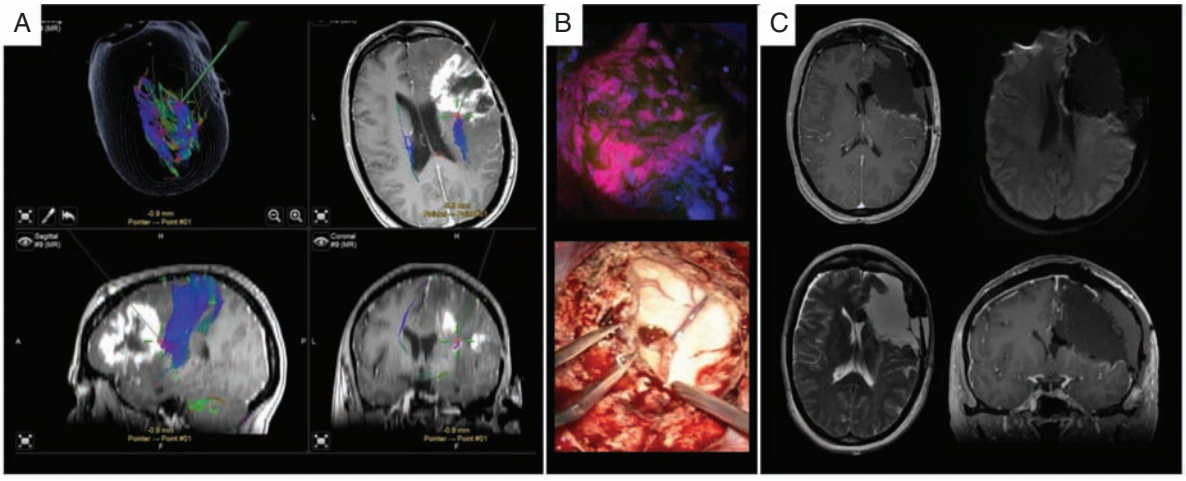


Fig. 8 Microsurgical resection of a right-sided recurrent IDHwt glioblastoma WHO grade IV using intraoperative neuronavigation, neuromonitoring and 5-ALA fluorescence techniques. (A) T1 contrast enhanced axial, sagittal and coronal planes including DTI fiber tracking (blue fibers). The green trajectories/red points represent the pointer for intraoperative neuronavigation. (B) Upper image: corresponding intraoperative 5-ALA fluorescence image taken from the area as depicted by neuronavigation. Lower image: opening of the right ventricle due to critical involvement by tumor formation. (C) Postoperative MRI confirms gross total resection without residual contrast enhancement, no perilesional ischemia (diffusion-weighted image upper right).

Nitrosoureas

Nitrosoureas, including lomustine, carmustine, and fotemustine, have good blood–brain barrier (BBB) penetration.[189] Fotemustine is available in some European countries, but has not been approved for use in the United States. Lomustine is generally preferred over carmustine given its oral formulation, schedule of administration, and better safety profile. In several phase III randomized trials, the lomustine monotherapy arm (dosed as 6 wk cycles of 100–130 mg/m^2 for up to 6 cycles) was associated with median OS of 7.1–8.6 months and PFS of 1.5–3 months.[148,190] Data from these trials also

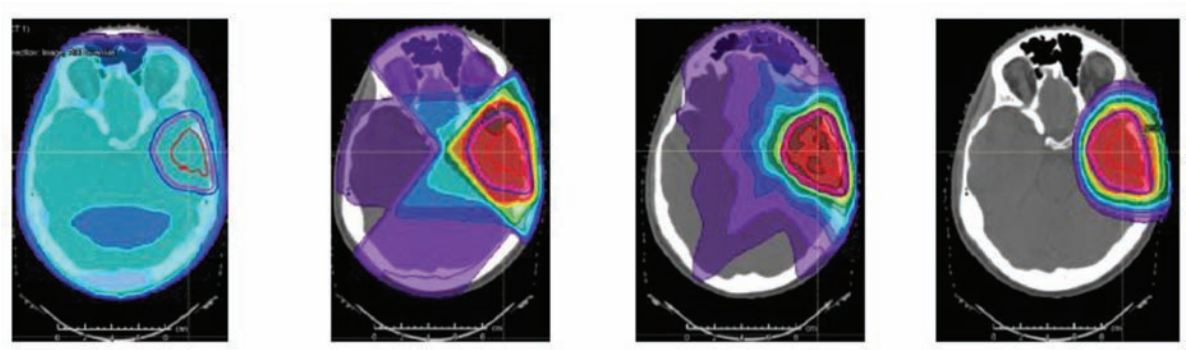


Fig. 9 This figure shows, from left to right, how the transition from 2D RT to 3D RT to intensity modulated radiotherapy to intensity modulated proton therapy harnesses the potential for sparing normal, uninvolved brain substructures from unnecessary RT dose; whether this produces meaningful patient clinical benefit is a subject of current clinical trial testing.

Table 3 Selected clinical trials of systemic agents in patients with recurrent glioblastoma

Systemic Agent(s)	Study Design	Study Population	Median OS, mo	Median PFS/ TTF, mo	6M-PFS	RR
EORTC 26101: Lomustine (nitrosurea) ± bevacizumab (VEGF inhibitor)[148]	Randomized phase III trial of lomustine +/- bevacizumab in recurrent GBM	437 with recurrent GBM at first progression	Combination: 9.1 Lomustine: 8.6 HR 0.95 [95% CI 0.74–1.21; $P = 0.65$)	Combination: 4.2 Lomustine: 1.5 HR 0.49 [95% CI, 0.39–0.61; $P < 0.001$).	Combination: 30.2% Lomustine: 16.9%	Combination: 41.5% Lomustine: 13.9%
RESCUE Study: TMZ rechallenge[149]	Nonrandomized, phase II trial of continuous TMZ 50 mg/m^2 daily for recurrent GBM	Recurrent GBM at first progression Group B1: 33 with early progression during the first 6 cycles of adjuvant TMZ Group B2: 27 with progression on adjuvant TMZ beyond standard 6 cycles but before completing of adjuvant TMZ Group B3: 28 who progressed after completing of upfront adjuvant TMZ (treatment free interval > 2 months)	NR	Group B1: 3.6 Group B2: 1.8 Group B3: 3.7	Group B1: 27.3% Group B2 7.4% Group B3: 35.7%	Group B1:3% Group B2: 0% Group B3: 11.1%
Director Trial: Temozolomide rechallenge[150]	Randomized, phase II trial of two different dose-intense TMZ regimens (note trial prematurely closed due to withdrawal of support)	Recurrent GBM at first progression randomized to Arm A: TMZ 120 mg/m2 one week on, one week off Arm B: TMZ 80 mg/m^3 three weeks on, one week off	Arm A: 9.8 Arm B: 10.6	Arm A: 1.8 Arm B: 2.0	Arm A: 17.1% Arm B: 25.0%	Arm A: 8% Arm B: 16%

Abbreviations: NR, not reported; PFS, progression-free survival; RR, radiographic response rate; VEGF, vascular endothelial growth factor.

suggest that patients with *MGMT*-methylated tumors are more likely to benefit from nitrosoureas than those with unmethylated *MGMT*.[148,191,192]

Other Therapies

Although other chemotherapeutic agents such as irinotecan, carboplatin, procarbazine, and etoposide are sometimes used for patients with recurrent glioblastomas, there are no data suggesting that they are beneficial.[142] A recent randomized phase II trial suggested that regorafenib, a VEGF receptor 2 and multikinase inhibitor, increased survival in patients with recurrent glioblastoma compared with lomustine.[193]

Re-Irradiation

Repeat RT in the form of radiosurgery or hypofractionated radiotherapy (30–35 Gy in 5–15 fractions) is increasingly used for recurrent glioblastoma, although there is currently no definitive data regarding benefit.[194,195] A secondary analysis of the NRG Oncology/RTOG 0525 trial showed no significant survival benefit of re-irradiation over systemic therapy after tumor progression.[196] Preliminary results of the NRG phase II trial comparing bevacizumab alone versus bevacizumab with re-irradiation in patients with recurrent glioblastomas showed that the addition of re-irradiation improved PFS (7.1 mo with the combination vs 3.8 mo with bevacizumab alone; $P = 0.05$) but not OS.[197]

Novel Therapies

Given the poor outcomes with current therapies, there is great interest in various experimental approaches under investigation.[198] These will be discussed in the following sections.

Targeted Molecular (Precision) Therapies

Despite advances in understanding the molecular pathogenesis of glioblastoma, there has been only modest progress in developing effective targeted molecular therapies.[199] Challenges include the paucity of agents that effectively cross the BBB,[22] the relative lack of "easy" targets such as *BRAFV600E* mutations, redundant signaling pathways,[28] and tumor heterogeneity.[19,36,42]

The 2016 update of the WHO classification incorporated molecular parameters into the definition of certain brain tumors.[50] Several of these markers are easily assessed by immunohistochemistry, including *IDH1-R132H* and histone *H3 K27M*, while other point mutations can be determined by sequencing. *BRAFV600E* mutation status, while challenging by immunohistochemistry is easily assessed by sequencing and has therapeutic implications for a subset of glioblastoma patients. For more comprehensive profiling, targeted NGS panels have proven to be useful, while some centers also have the capacity to perform whole exome sequencing or whole genome sequencing. Microsatellite instability can be readily assessed by either genome-wide or medium-sized panel approaches, and is relevant given the tumor-agnostic approval by the FDA for pembrolizumab for cancers with high microsatellite instability. Copy number variations—for example, the aforementioned chromosomal +7/–10 pattern—are relevant for glioma diagnosis and possibly treatment. Fusion detection, to identify a potentially relevant and druggable group of alterations (for example, fusions of neurotrophic-tropomyosin RTK [*NTRK* fusions]), requires specific coverage by either DNA-based approaches or alternatively mRNA-based analyses. Routine examination of these (and potentially additional) alterations will be critical if we are to make substantial steps forward for precision glioblastoma therapies.[200]

Examples of putative treatment-predictive biomarkers exist. The most often investigated biomarkers, high level *EGFR* amplification and EGFRvIII mutation, have been targeted with and without tumor pretesting, with the aim of suppressing pathway activation with EGFR inhibitors such as erlotinib,[201] targeting the heterogeneously expressed EGFRvIII neoantigen by vaccination with a peptide vaccine, rindopepimut,[202] or using the conformational change for specific binding of an antibody-drug conjugate, depatuxizumab mafodotin (ABT414)[203–207] without clinical activity.[207] Targeting *BRAFV600E* mutations showed responses to monotherapy with Raf inhibitors such as vemurafenib,[208] or dual therapy with combined BRAF/MEK inhibition with trametinib and dabrafenib,[209] but these mutations are rare in glioblastoma except for epithelioid glioblastoma,[210] a somewhat controversial entity likely to be often confused with pleomorphic xanthoastrocytoma. Other potentially targetable mutations, such as *NTRK* fusions,[211] *H3K27M* mutations,[212,213] and *FGFR* mutations and *FGFR3-TACC3* fusions,[214] are all uncommon in glioblastoma. Of note, mutations in the telomerase reverse transcriptase (*TERT*) promoter are found in up to 85% of glioblastomas,[215] although to date this mutation has been challenging to target.

The lack of success in targeted therapy trials in glioblastoma is likely due to tumor heterogeneity, lack of knowledge of the contribution of genetic alterations to tumor maintenance, targeting subclonal or unstable genetic alterations instead of stable and clonal oncogenic drivers, redundant signaling pathways, use of archival instead of freshly obtained recurrent tumor tissue for biomarker testing, insufficient assessment of drug brain tumor concentrations, failure of target inhibition, and development of rapid secondary resistance and clonal selection.

Currently, most therapeutic strategies and biomarkers are focused on single or multiple biological features that are differentially detected in patient groups responding to a given therapy. In several studies post-hoc exploratory analyses suggested subsets of patients that may have benefited from experimental treatments, but in the absence of validation, these remain only hypothesis generating. For example, the proneural subtype

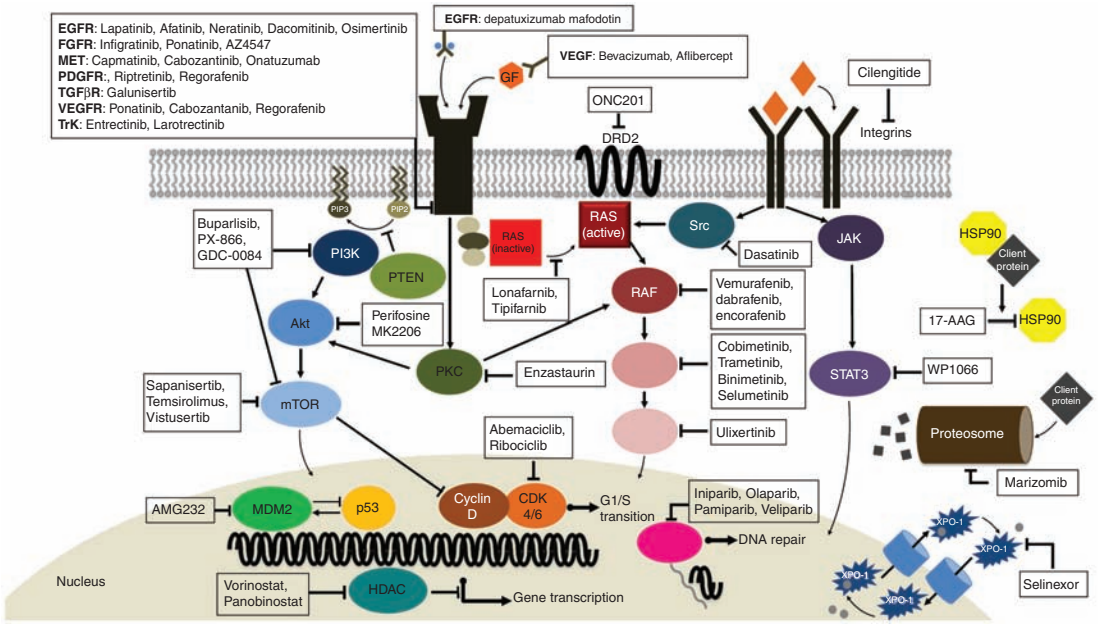


Fig. 10 Selected recently completed or ongoing trials with targeted molecular therapies. CDK = cyclin-dependent kinase; EGF = epidermal growth factor; EGFR = epidermal growth factor receptor; FGFR = fibroblast growth factor receptor; GF = growth factor; HDAC = histone deacetylase; HSP = heat shock protein; MDM2 = murine double minute 2; mTOR = mammalian target of rapamycin; PARP = poly(ADP-ribose) polymerase; PDGFR = platelet derived growth factor receptor; PKC = protein kinase C; RTK = receptor tyrosine kinase; TGF-β = transforming growth factor beta; TGFβR = transforming growth factor beta receptor; TrK = tropomyosin receptor kinase; VEGF = vascular endothelial growth factor; VEGFR = vascular endothelial growth factor receptor; XPO1 = exportin 1.

of glioblastoma defined by expression analyses[216,217] or MRI features[218] may derive benefit from the addition of bevacizumab to standard treatment. Lower levels of carboxypeptidase G2 promoter methylation of cluster of differentiation (CD)95 ligand (CD95L) were correlated with improved Overall survival with the CD95 inhibitory treatment asunercept (APG101) in combination with re-irradiation compared with re-irradiation alone.[219] Also, based on a retrospective analysis, mammalian target of rapamycin (mTOR) Ser2448 phosphorylation may be a putative predictive biomarker of response to the mTOR inhibitor temsirolimus plus radiation in patients with newly diagnosed glioblastoma lacking *MGMT* promoter methylation.[220] Others have suggested *PTEN* loss predicts benefit from mTOR inhibitors.[221] Without preselection, mTOR inhibition is not only ineffective but may even confer a survival disadvantage compared with the standard of care. For example, the addition of a different mTOR inhibitor, everolimus, resulted in worse outcome in an unselected group of patients with newly diagnosed glioblastoma irrespective of *MGMT* status (Table 4).[222]

Several clinical trials are based on well-defined molecular characteristics of the tumor, confirmation of adequate drug penetration and biological efficacy (eg, target engagement and modulation in neoadjuvant, "window-of-opportunity" surgery-based trials),[221,224] as well as necessary retrospective validation of potential biomarkers (Table 5). Several large clinical trials are underway where prospectively assigned biomarkers will enrich predefined patient cohorts for potentially benefiting patients. The National Center for Tumor Diseases–Heidelberg Neuro Master Match (N^2M^2) (NCT03158389), a trial of molecularly matched targeted therapies plus RT in patients with newly diagnosed glioblastoma without *MGMT* promoter methylation is currently ongoing.[227] Similarly, the National Cancer Institute MATCH trial, while designed mainly for extracranial solid tumors, does allow patients with glioblastoma if they meet the eligibility criteria. The Individualized Screening Trial of Innovative Glioblastoma Therapy (INSIGhT) trial evaluating EGFR, mTOR/DNA-PK, and CDK4/6 inhibitors,[228] and the GBM Adaptive, Global, Innovative Learning Environment (AGILE) consortium[229] are taking a different approach by enrolling patients into unselected cohorts with given therapies first, assessing potential biomarkers as the trial accrues and integrating this information via adaptive randomization processes to enrich specific arms that may be showing benefit with particular biomarkers (Table 5).[229]

The extensive tumor heterogeneity in glioblastoma suggests that combination therapy may be more effective than treatment with single agents. However, combination studies to date have been associated with little activity and often significant toxicity, and increase the need for assessment of the targets in the tumor.[199,230] Potentially, combinations of more potent selective agents with less off-target effects may be better tolerated. To address the issues of heterogeneity and redundant signaling pathways, there is significant interest in exploiting synthetic lethality (targeting tumor stem cells[231]) or common downstream pathways with agents such as marizomib,

Table 4 Selected completed trials with targeted molecular therapies

Molecular Target	Signaling Pathway	Therapy	Trial	Trial Concept (examples)	Trial Result
BRAFV600 mutation		Vemurafenib[208]	NCT01524978	Basket trial with recurrent glioma arm	ORR 25% overall 3/6 GBM had SD as best response
BRAFV600E mutation		Dabrafenib + Trematenib[210]	NCT02034110	Phase II basket trial using novel Bayesian hierarchical statistical design	ORR for GBM 29%; 62% for low grade gliomas
EGFR amplification		Depatuxizumab mafodotin (DM) (ABT414)[205]	NCT02573324 (Intellance 1)	Randomized phase III trial in newly diagnosed GBM with EGFR amplification comparing RT + TMZ ± DM	639 patients randomized Ocular toxicity common DM MS 18.9 (17.4, 20.8) Placebo: 18.7 (17.0, 20.3) HR 1.02 (0.82, 1.26); $P = 0.63$
EGFR amplification		Depatuxizumab mafodotin (DM) (ABT414)[206]	NCT02343406 (Intellance 2)	Randomized phase II in recurrent GBM comparing DM, DM + TMZ, or TMZ alone	260 patients 25–30% grade 3 or 4 ocular toxicity Hazard ratio (HR) for the combination arm DM+TMZ compared with the TMZ was 0.71, 95% CI [0.50, 1.02]; $P = 0.062$ at initial analysis. On long-term follow-up, HR for the comparison of the DM+TMZ compared with control was 0.66 (95% CI = 0.48, 0.93), $P = 0.017$. Efficacy of DM monotherapy was comparable to that of TMZ (HR = 1.04, 95% CI [0.73, 1.48]; $P = 0.83$)
Exportin 1	Important for transport of tumor suppressor proteins and oncoprotein mRNA from nucleus to cytoplasm	Selinexor	NCT01986348	Multi-arm phase II trial in recurrent GBM	ORR 10% PFS6 19% 6 cycle PFS (24 weeks) 30%
FGFR mutations and FGFR-TACC gene fusions	Highly oncogenic FGFR mutations and FGFR-TACC gene fusion that confers sensitivity to FGFR inhibitors	AZD4547	NCT02824133	Phase I/II study in patients recurrent glioma positive for FGFR fusion	Not available
FGFR mutations and FGFR-TACC gene fusions	Highly oncogenic FGFR mutations and FGFR-TACC gene fusion that confers sensitivity to FGFR inhibitors	Infigratinib (BGJ398)[223]	NCT01975701	Phase II study in recurrent GBM with FGFR1-TACC1, FGFR3-TACC3 fusion and/or activating mutation in FGFR1, 2 or 3	26 patients ORR 7.7% 4 patients disease control > 1 year (2 FGFR1 mutations, 1 FGFR3 mutation, 1 FGFR3-TACC3 fusion) PFS6 16%
mTOR		Everolimus[222]	NCT01062399	Randomized phase II trial of RT+TMZ ± everolimus in newly diagnosed GBM	171 patients No difference in PFS (median PFS 8.2 m for everolimus vs 10.2 m for control; $P = 0.79$) OS for everolimus was inferior to that for control patients (median OS: 16.5 vs 21.2 m, respectively; $P = 0.008$)

Table 4 Continued

Molecular Target	Signaling Pathway	Therapy	Trial	Trial Concept (examples)	Trial Result
mTOR		Temsirolimus	NCT01019434	Randomized phase II of RT+TMZ versus RT + temsirolimus in newly diagnosed unmethylated GBM	111 patients randomized Not difference in 1year survival (72.2% in TMZ arm; 69.6% in the temsirolimus arm. (HR 1.16; $P = 0.47$]. Phosphorylation of mTORSer2448 in tumor (HR 0.13; $P = 0.002$), detected in 37.6%, associated with benefit from temsirolimus
Phosphatidylinositol 3-kinase (PI3K)	*PIK3CA* or *PIK3R1* mutation, loss of PTEN activity through *PTEN* mutation, homozygous deletion or negative PTEN expression (<10% of tumor cells that stained positive), or positive phosphorylated AKT^{S473} ($pAKT^{S473}$)	Buparlisib[224]	NCT01339052	Multicenter, open-label, multi-arm, phase II trial in patients with PI3K pathway-activated glioblastoma at first or second recurrence	ORR = 0 PFS6 8% Median PFS 1.7 m
VEGF		Bevacizumab[171]	NCT0094382 (AVAGlio)	Phase III placebo-controlled trial comparing RT +TMZ ± bevacizumab	921 patients randomized Median PFS longer in the bevacizumab group than in the placebo group (10.6 months vs 6.2 months;HR 0.64; $P < 0.001$). OS did not differ between groups (HR, 0.88; $P = 0.10$).
VEGF		Bevacizumab[137]	NCT00884741 (RTOG 0825)	Phase III placebo-controlled trial comparing RT +TMZ ± bevacizumab	637 patients randomized No difference in OS (bevacizumab median, 15.7 m, control 16.1 m (HR 1.13) PFS was longer in the bevacizumab group (10.7 months vs 7.3 months;HR, 0.79)
VEGF		Bevacizumab[148]	NCT01290939 (EORTC 26101)	Phase III trial comparing lomustine to lomustine + bevacizumab in recurrent GBM	437 patients randomized No survival advantage with addition of bevacizumab Median OS 9.1 m with lomustine compared with 8.6 m in combination group (HR 0.95) PFS 4.2 m with bevacizumab + lomustine compared with 1.5 m with lomustine alone (HR 0.49; $P < 0.001$)

Table 4 Continued

Molecular Target	Signaling Pathway	Therapy	Trial	Trial Concept (examples)	Trial Result
VEGF receptors 1, 2, and 3 and PDGF receptors	No test yet required	Regorafenib[193]	NCT02926222	Randomized phase II comparing regorafenib with lomustine in patients with relapsed glioblastoma (REGOMA):	7·4 months (95% CI 5·8–12·0) in the regorafenib group and 5·6 months (4·7-7·3) in the lomustine group (hazard ratio 0·50, 95% CI 0·33-0·75; log-rank $P = 0.0009$)
VEGFR2, cMET, AXL, RET	No testing required	Cabozantinib[225,226]	NCT00704288	Single arm phase II in recurrent GBM	220 patients Bevacizumab naïve 14.5–17.6% ORR; PFS6 22.3 to 27.6% Bevacizumab failure 4.3% ORR.
CD95/CD95ligand	Lower levels of methylation of the CpG2 in the promoter of the CD95 ligand	Asunercept[219]	NCT01071837 NCT03152708	Re-irradiation ± asunercept in progressive GBM CAN008 biomarker CD95 Ligand and CpG2 methylation in Chinese patients with GBM	PFS6 rates were 3.8% [95% CI, 0.1–19.6] for rRT and 20.7% (95% CI, 11.2–33.4) for rRT+APG101 ($P = 0.048$). Ongoing

Abbreviations: CI, Confidence intervals; GBM, glioblastoma; HR, hazard ratio; mTOR; mammalian target of rapamycin; m, months; MS, Median survival; ORR, objective response rate; PFS, progression-free survival; PFS6, Progression-free survival at 6 months; rRT, reirradiation; SD, stable disease; VEGF, vascular endothelial growth factor.

a proteasome inhibitor (NCT03345095), and selinexor, an exportin 1 inhibitor.[232]

Fig. 10 shows selected targeted molecular therapies evaluated in recently completed or ongoing trials.

Targeting DNA Damage Response Pathways

The most effective nonsurgical treatments for glioma are DNA-damaging agents, including RT and cytotoxic chemotherapy.[58] Enhancing their effect in tumor while sparing normal tissue is an appealing strategy that is particularly relevant in tumors such as glioblastoma. One emerging approach is to target tumor-specific DNA repair vulnerabilities in glioblastoma, which appears to have a significant stem cell compartment in which DNA repair is upregulated and contributes to treatment resistance.[233,234]

The complex signaling and effector events following DNA damage, often referred to as the DNA damage response (DDR), are summarized in Fig. 11 and have been reviewed recently.[236–238] DNA double-strand breaks (DSBs) are the main toxic lesion induced by DNA damaging agents, but single strand breaks (SSBs) are also now recognized as important lesions for lethality. Unrepaired SSBs are thought to stall replication forks, which may indirectly contribute to the DSB load, particularly in the context of replication stress. Combining DNA damaging agents with DDR inhibitors will increase the levels of unrepaired DSBs and SSBs in cells, and thus has the potential for significant chemo- and radiosensitization. However, specific DDR inhibitors, such as poly(ADP-ribose) polymerase (PARP) inhibitors, induce myelosuppression when given with DNA damaging agents, potentially limiting their use in combination with TMZ. As such, it will be important to identify glioma-associated molecular biomarkers (eg, tumor mutations not found in normal tissue), which could allow the administration of active but safe drug combinations.

Multiple DDR inhibitors are now being tested in clinical trials for glioblastoma (summarized in Table 6). Recent studies have elucidated important links between intrinsic DNA repair defects and sensitivity to specific DDR inhibitors in glioblastoma, which likely will serve as key molecular biomarkers for patient selection in these trials. Loss of MGMT protein expression is a possible predictor for TMZ sensitivity, and emerging data suggest that it may also be an important biomarker for TMZ-based combinations with inhibitors of PARP, ataxia telangiectasia, and Rad3-related protein.[239–242]

Targeting Tumor Metabolism

In the past decade there have been converging data to support tumor metabolism as a key determinant of glioma progression. Oncogenic mutations modulate glioblastoma metabolism to promote survival, proliferation, and evasion of therapy, in addition to tumor microenvironmental factors influencing glioblastoma metabolism.[20,242] Data suggest that regulators of glioblastoma metabolism can be used as prognostic, diagnostic, and therapeutic tools that

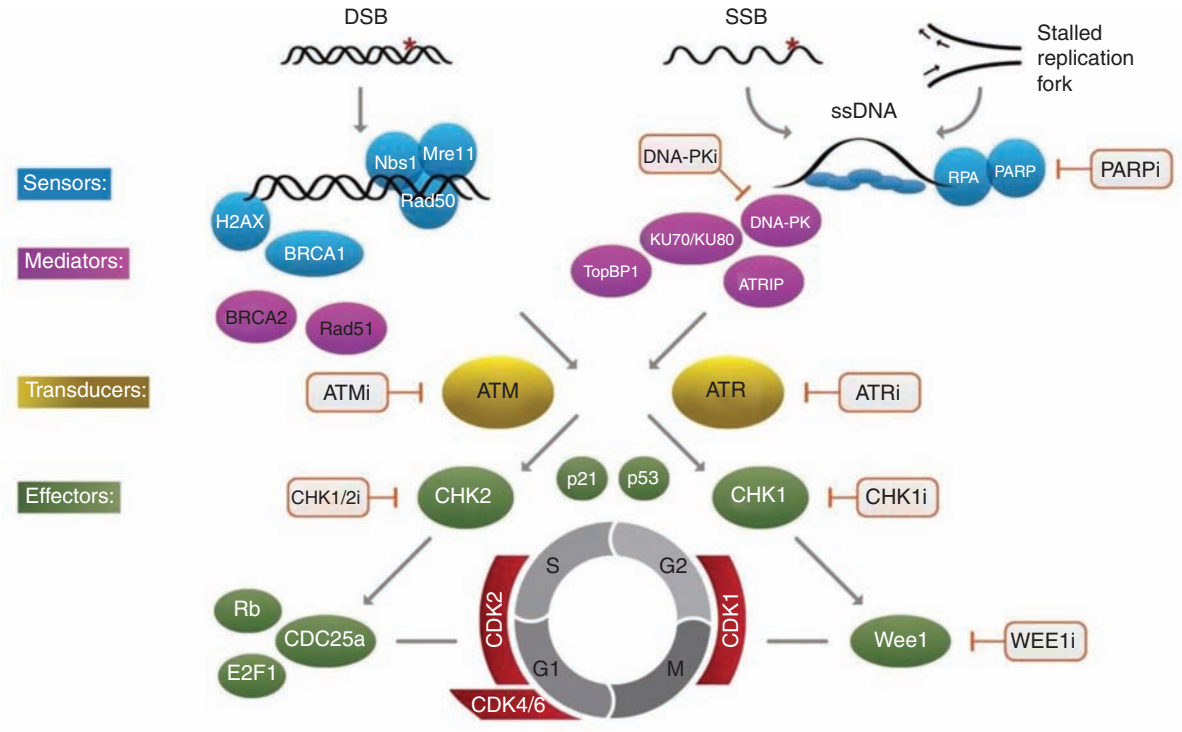


Fig. 11 A simplified overview of signaling from common types of DNA damage to the DDR and cell cycle checkpoint pathways. Initial damage is sensed by proteins including the histone γ -H2AX, which is rapidly phosphorylated by ATM at a specific serine residue in response to chromatin structure alteration at DBS sites, activating recruitment of repair proteins including BRCA1 and the MRN complex (MRE11, Rad51, NBS1). DSB repair is undertaken by the end-joining pathway involving the kinase DNA-PK and Ku protein binding partners and the homologous recombination pathway involving Rad51 and associated proteins. Single strand breaks (SSB) and replication stress leading to stalled replication forks activate PARP which in turn recruits repair factors including XRCC1 and promotes chromatin remodeling at the break site and base excision repair. ATR and ATM function both in the initial signaling cascade and as transducers to downstream activation of the cell cycle checkpoints inhibitors, Chk1 and Chk2 producing cell cycle delay to facilitate repair. Points in the pathway at which specific inhibitors are available are indicated. As predicted from their roles in the DDR pathway, ATM and ATR inhibitors sensitize to a broad range of DNA damaging agents causing single or double strand breaks. PARPi and cell cycle checkpoint inhibitors including Wee1 inhibitors are specifically effective in cells undergoing rapid replication. DSB = Double Strand Break; SSB = Single Strand Break.

can advance management of glioblastoma.[20] There is also growing evidence that tumor genotype and the brain's biochemical and cellular microenvironment shape the metabolic reprogramming of glioblastoma cells, generating vulnerabilities that could be exploited therapeutically (Fig. 12).[20]

A classic and recognized biochemical adaptation in glioblastomas, as with other solid cancers, is the metabolic shift to aerobic glycolysis rather than mitochondrial oxidative phosphorylation, regardless of oxygen availability, a phenomenon referred to as the Warburg effect.[20] Targeting genes that regulate tumor metabolism can be an ideal candidate for rational drug design. Some of the regulators involved in glioblastoma have been shown to be *PTEN* induced kinase 1 (PINK1)[243] and hexokinase 2 (HK2),[244] where inhibition of *HK2* and activation of *PINK1* in preclinical models have shown therapeutic benefit in glioblastoma. Similarly, cholesterol metabolism may be a therapeutic target in certain glioblastomas. In *EGFR* driven tumors, there is high dependency on cholesterol uptake, rendering the glioblastoma cells vulnerable to liver X receptor agonists, which reduce cholesterol uptake.[20,245]

Immunotherapies

Unlike several other solid tumors, no breakthrough has been achieved with current immunotherapy strategies for glioblastoma.[21,246] Although the concept that relieving glioma-associated immunosuppression to allow immune-mediated antitumor responses is attractive and has received preclinical experimental support,[247–252] clinical trials testing this hypothesis using targeted therapies such as transforming growth factor beta (TGF-β)[253] or colony-stimulating factor receptor inhibitors,[254] vaccines,[202] or more recently, immune checkpoint blockade with the anti–programmed cell death protein 1 (PD1) antibody nivolumab in recurrent and newly diagnosed *MGMT* unmethylated glioblastoma, as well as other agents were unsuccessful (Table 7).[21,246,255] However, that does not

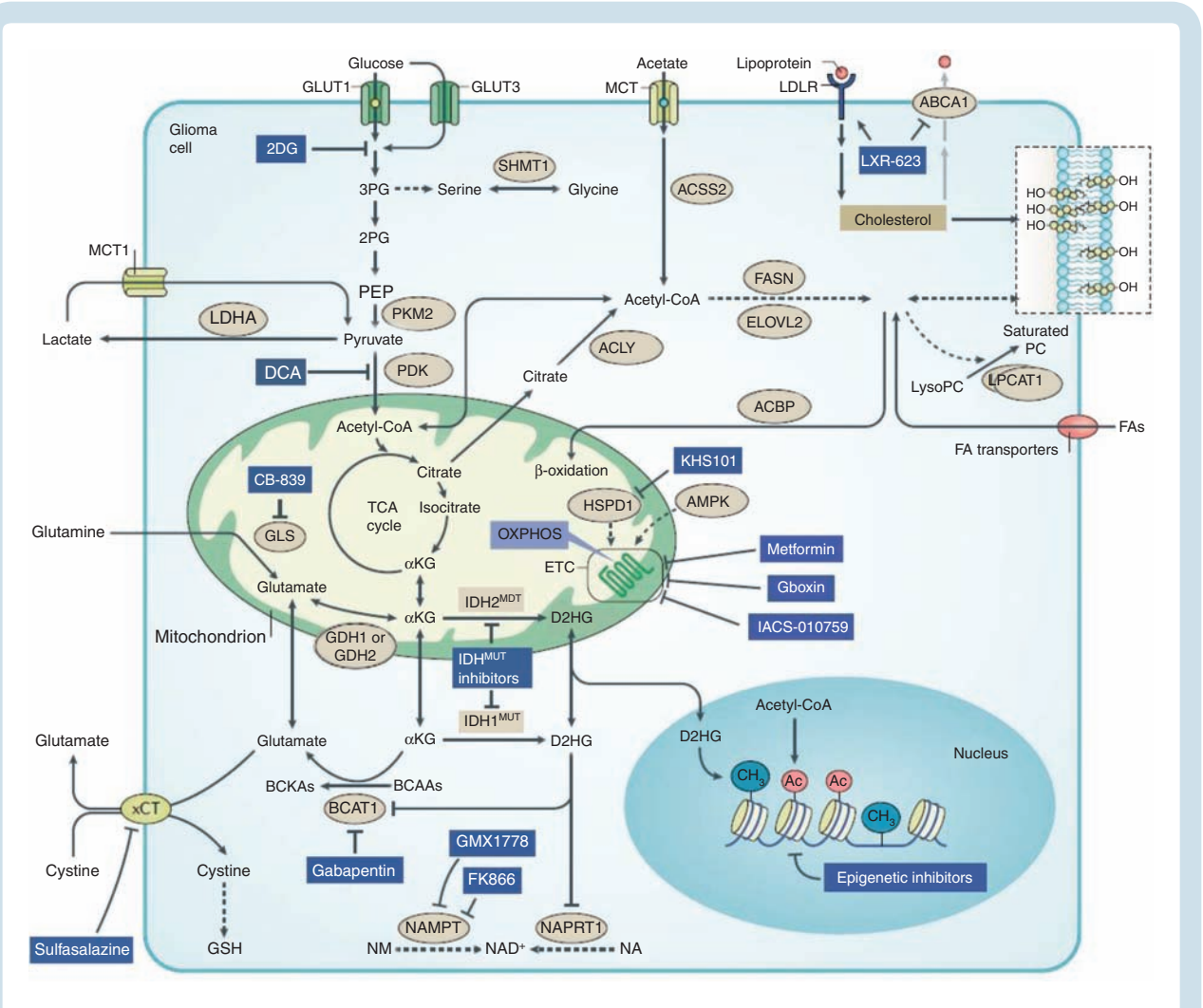


Fig. 12 An expanded pharmacopoeia of metabolic drug targets in glioblastoma (Adapted with permission from Bi et al. Nature Rev Cancer 2020;20:57–70.) The extensive focus on altered glioma metabolism has led to a considerable expansion in the list of potential drug targets. Receptor tyrosine kinase (RTK)-driven metabolic dependencies have also been identified. For example, epidermal growth factor receptor (EGFR) amplification produces major changes in metabolic enzyme dependencies, including in glucose uptake, glycolysis, fatty acid (FA) synthesis, membrane lipid remodeling, cholesterol uptake, NAD+ production and epigenetic remodeling. Targeting lysophosphatidylcholine (LysoPC) acyltransferase 1 (LPCAT1) decreases the level of saturated phosphatidylcholines (PCs) and disrupts plasma membrane localization of EGFR variant III (EGFRvIII), which blocks EGFRvIII- driven oncogenic signaling and suppresses glioblastoma (GBM) tumor growth. LXR-623, a brain- penetrant liver X receptor (LXR) agonist, targets the cholesterol homeostasis of GBM cells by promoting ATP- binding cassette subfamily A member 1 (ABCA1)-mediated cholesterol efflux and inhibiting low- density lipoprotein receptor (LDLR)-mediated cholesterol uptake. Isocitrate dehydrogenase (IDH) mutants in glioma cells generate the oncometabolite d-2-hydroxyglutarate (D2HG), which defines the dependencies of NAD+ and glutathione (GSH) production and impacts epigenetic events in glioma cells. The oxidative phosphorylation (OXPHOS) inhibitors, including metformin, Gboxin and IACS-010759, target glioma cells by inhibiting transmembrane protein complexes in the mitochondrial inner membrane, known as the electron transport chain (ETC). 2DG, 2-deoxy-d-glucose; 2PG, 2-phosphoglyceric acid; αKG, α-ketoglutarate; ACBP, acyl-CoA-binding protein; ACLY, ATP citrate lyase; ACSS2, acetyl-CoA synthetase; AMPK, AMP-activated protein kinase; BCAA, branched-chain amino acid; BCAT1, branched-chain amino acid transaminase 1; BCKA, branched-chain keto acid; BRD4, bromodomain containing 4; DCA, dichloroacetate; ELOVL2, ELOVL FA elongase 2; FASN, FA synthase; GDH1, glutamate dehydrogenase 1; GLS, glutaminase; GLUT1, glucose transporter 1; HSPD1, heat shock protein family D (Hsp60) member 1; IDH1, isocitrate dehydrogenase 1; LDHA, lactate dehydrogenase A; MCT1, monocarboxylate transporter 1; NA, nicotinic acid; NAMPT, nicotinamide phosphoribosyl-transferase; NAPRT1, nicotinate phosphoribosyltransferase domain containing 1; NM, nicotinamide; PDK, pyruvate dehydrogenase kinase; PEP, 2-phosphoenolpyruvate; PKM2, pyruvate kinase muscle isozyme M2; SHMT1, serine hydroxymethyltransferase 1; TCA, tricarboxylic acid; xCT, cystine/glutamate transporter. Reproduced with permission from Bi J, et al.[20]

necessarily imply that attempts to improve outcome with immunotherapy approaches may not be effective, as appropriate target inhibition in the glioma microenvironment or even immunogenicity assessments were largely lacking, and read-out was mainly limited to classical efficacy endpoints. As more is learned about the role of the tumor microenvironment in immunotherapy responses, it may be possible to enrich for select glioblastoma

Table 5 Selected ongoing trials with molecularly targeted treatments

Molecular Target	Therapy	Phase	Design	Tumor Type	Trial
MDM2	AMG-232	Phase 0/I	• P53 wildtype status • Phase 0/I to measure concentrations in tumor in patients with recurrent GBM and of AMG 232 in combination with RT in patients with newly diagnosed GBM and unmethylated MGMT promoter	Recurrent and newly diagnosed GBM	NCT03107780
mTORC1/2	Sapanisertib (MLN0128)	Phase 0	• No selection • Phase 0 to evaluate tumor PK and PD effects	Recurrent GBM	NCT02133183
CDK4/6	Abemaciclib	0/II	• Patients with activation of CDK4/6 pathway and intact RB	Recurrent GBM	NCT02981940
CDKs 1, 2, 7, and 9, JAK2 and FLT3	Zotiraciclib (TG02) with metronomic TMZ	I/randomized phase II	• Phase I with metronomic TMZ followed by randomized phase II comparing zoltiraciclib = TMZ versus TMZ	Recurrent grade III glioma and GBM	NCT02942264
CDKs 1, 2, 7 and 9, JAK2 and FLT3	Zotiraciclib (TG02) with metronomic TMZ	I	• Zotiraciclib + RT for unmethylated MGMT patients • Zotiraciclib with TMZ for methylated MGMT patients • Zotiraciclib alone for recurrent patients	Newly diagnosed and recurrent grade III glioma and GBM in elderly population	NCT03224104
H3K27M mutation	ONC201 (dopamine receptor D2 inhibitor and ClpP agonist)[212,213]	II	• *H3K27M* mutated gliomas • Non *H3K27M* mutated midline GBM	Recurrent *H3K27M* mutated gliomas and other GBM	NCT02525692 NCT03295396
Interleukin-4 (IL-4) receptor	MDNA55	II	• Convection enhanced delivery of genetically engineered IL-4 linked to a modified version of the Pseudomonas aeruginosa exotoxin A	Recurrent GBM	NCT02858895
HIF2α	PTC2977	II	• No selection	Recurrent GBM	NCT02974738
Proteasome	Marizomib	III	• No selection	Newly diagnosed GBM	NCT03345095
			Platform Trials		
Alk MDM2 SHH CDK4/6 mTOR	Alectinib Idasanutlin Vismodegib Palbociclib Temsirolimus	Phase II	• Umbrella trial N2M2/NOA-20 • Alk expression • P53wild-type/MDM2 high • SHH activation • CDK4/6 high or codeletion of CDKN2A/B • Phospho mTOR Ser 24448	Newly diagnosed GBM without MGMT hypermethylation, targeted treatment according to molecular profile	NCT03158389
EGFR mTOR/DNA PK CDK4/6	Neratinib CC115 Abemaciclib	Bayesian adaptive randomized phase II platform trial	INSIGhT Agnostic (assessment post hoc)	Newly diagnosed unmethylated GBM	NCT02977780
Agnostic (assessment post hoc)	Multiple regimens (regorafenib)	Bayesian adaptive randomized phase II/III platform trial	GBM AGILE Multiple	Newly diagnosed and recurrent GBM	NCT03970447

Abbreviations: GBM, glioblastoma; HIF2α, hypoxia-inducible factor alpha; MDM2, mouse double minute 2; m, months; ORR, objective response rate; PD, pharmacodynamics; PK, pharmacokinetics; RB, retinoblastoma; SD, stable disease; SHH, sonic hedgehog.

patient subsets that respond to specific immunotherapy regimens.

It has become evident that glioblastoma is an immunologically "cold" tumor characterized by a paucity of tumor infiltrating effector lymphocytes.[18,21] In understanding mechanisms of immune resistance, we have evolved from the 3 "E" hypothesis of elimination, equilibrium, and escape.[262] Hence to reconcile this concept of "hot" and "cold" tumors with the 3 "E" hypothesis, we must also consider the magnitude of a tumor's adaptive and intrinsic resistance.[18] Factors that drive intrinsic resistance for glioblastoma include a paucity of neoantigens (most glioblastomas

have low mutational burden relative to other cancers) and active inhibition including the release of soluble immunosuppressive mediators such as TGF-β, interleukin (IL)-10, and prostaglandin E2, and production of tryptophan and indolamine 2,3 dioxygenases and arginase, which deplete tryptophan and arginine and result in the accumulation of metabolites such as kynurenine, leading to suppression of T-cell activity.[18,21,263] Furthermore, there are data to suggest that location (ie, having a tumor in the brain) negatively influences the immune system globally by actively deleting antigen specific T cells[264] and potentially sequestering them in the bone marrow.[265] Glioblastoma induces adaptive resistance by promoting exhaustion of infiltrating T cells[266] and recruiting suppressive myeloid cells and regulatory T cells.[18,246] In addition, the corticosteroids frequently used in these patients also contribute to immunosuppression and impair the efficacy of immunotherapies.[259,267]

The immunologically "cold" microenvironment of glioblastoma tumors likely contributed to the negative phase III studies of the PD1 antibody nivolumab in patients with recurrent (CheckMate-143)[21,255] and *MGMT* unmethylated, newly diagnosed (CheckMate-498) glioblastoma. Hence current strategies are focusing on overcoming both intrinsic and/or adaptive resistance. Efforts to enhance effector immune infiltrate into the microenvironment such as cellular therapies including chimeric antigen receptor (CAR) T cells,[269,270] oncolytic viruses (OVs),[259,271,272] and vaccines[267,273,274] are being developed to meet this challenge (Table 8).

Sporadic partial and complete responses with immune checkpoint blockade among patients with hypermutated tumors due to germline DNA repair deficits suggest that these tumors likely exhibit low innate resistance and possess immunologically relevant mutations, including tumor-specific neoantigens or tumor-associated antigens that the immune system can recognize and attack.[275,276] However, the numbers of mutations alone may not be sufficient to generate an immune response. Roughly 10% of patients may develop hypermutated tumors at recurrence after TMZ chemoradiotherapy,[36,277] and an 8% response rate was seen in the CheckMate-143 study with nivolumab in recurrent glioblastoma.[255] Yet, importantly, tumor mutational burden at recurrence was not captured in this study, precluding firm assumptions that hypermutation was indeed associated with response; in fact, the immunogenicity and clonality of mutations, not just their quantity, may determine responsiveness to immunotherapy.[278] Furthermore, the negative phase III study of rindopepimut,[202] an EGFRvIII peptide vaccine, argues that targets must be present and stably expressed in all tumor cells or that targeting multiple tumor antigens may be important. Current approaches to overcome intrinsic resistance have revolved around novel antigen identification strategies by targeting multiple overexpressed and private mutations derived from NGS[267,274,279] and mass spectrometry analysis of the human leukocyte antigen (HLA) ligandome. Whereas peptide-based approaches targeting these antigens have been successful in eliciting systemic as well as local antigen-specific CD8 responses, the limited magnitude of the response may benefit from other potentially augmentative strategies such as transgenic T-cell receptors, combinations with appropriate checkpoint inhibitors, or other measures targeting the suppressive myeloid compartment.[21,246]

Approaches to overcome adaptive resistance for glioblastoma initially focused on checkpoint molecules.[21,246] This approach has not been successful for at least two key reasons: first, intratumoral T cells are severely exhausted with loss of effector function and hence these cells appear to not be rescuable with immune checkpoint inhibitor therapy; and second, myeloid cells including macrophages and/or microglia are programmed by glioblastomas to be highly suppressive in the tumor microenvironment.[18,251] Therapies such as OVs that can activate macrophages from an M2 to an M1 phenotype, induce antigen presentation, and promote migration of antigen presenting cells to regional lymph nodes may overcome some of these obstacles.[272] However, it should be noted that since macrophages exist in complex activation continuums the situation is likely to be more complicated.[280] Combination approaches with local therapies such as stereotactic radiosurgery,[248,249] laser ablation (NCT03277638), and local chemotherapy[281] are also potential means to overcome the adaptive resistance of glioblastomas. Another interesting approach is the concept of neoadjuvant anti-PD1 treatment administered prior to planned debulking surgery. Two recent studies demonstrated favorable modulation of local immune reactivity in recurrent glioblastoma patients using such an approach.[282,283] An improved outcome in one of these studies,[282] as well as encouraging benefit in other solid tumors, including significant rates of pathologic response,[284,285] suggest that further evaluation of neoadjuvant checkpoint administration in glioblastoma is warranted.

There is also growing interest in cellular therapies, especially CAR T cells, and more recently, CAR-transduced natural killer cells. CAR T cells have been engineered to express CAR molecules on their surface, which allow them to recognize and bind to specific antigens on tumor cells, leading to target cell killing in an HLA-independent manner.[286] Although one patient with leptomeningeal spread of glioblastoma responded to treatment with CAR T cells against IL-13 receptor subunit alpha-2,[269] the experience with CAR T cells to date for glioblastoma has been generally disappointing.[270,286] Current efforts are focused on developing next generation CAR T cells directed against multiple antigens, designing them to induce epitope spreading, combining them with checkpoint inhibitors to help overcome immunosuppression or with conventional therapies such as radiotherapy, and delivering them directly into the tumor.[21,287,288]

Viral Therapies

There has been resurgent interest in OVs and gene therapy (GT) in clinical trials for glioblastoma.[272] Oncolytic viruses are either natural viral strains or genetically engineered viruses designed to infect and/or replicate selectively in tumor cells.[289,290] Gene therapy instead utilizes viruses that have been rendered replication incompetent but deliver anticancer cDNAs. With either therapy there is an initial phase of direct cytotoxic

Table 6 Current Clinical Trials Testing DDR Inhibitors in Glioma

Target	Agent	Trial Name	Phase	Regimen	Tumor Type(s)/ Patient Populations	Status	PI/Co-PI	Trial ID(s)
PARP	Veliparib	A071102 (Alliance)	2/3	TMZ-/+Veliparib	Newly diagnosed GBM, Adults	Active, not recruiting	Sarkaria	NCT02152982
	Olaparib	OPARATIC	1	Olaparib and TMZ	Recurrent GBM, adults	Completed	Chalmers	-
		PARADIGM	1/2	Olaparib and RT	Newly diagnosed GBM, 65+ y	Recruiting (Phase II)	Chalmers	-
		PARADIGM-2	1	Olaparib and RT	Newly diagnosed GBM, Adults	Recruiting (MGMT- cohort)	Chalmers	-
		ETCTN 10129	2	Monotherapy	Recurrent IDH1/2-mutant glioma, adults	Recruiting	LoRusso/ Bindra	NCT03212274
	BGB290	Study 104	1/2	BGB290 with RT and/or TMZ	Recurrent GBM, adults	Recruiting	Brachman	NCT03150862
		ABTC-1801	1/2	BGB290 with TMZ	Recurrent IDH1/2-mutant glioma, adults	Recruiting	Bindra/ Schiff	NCT03914742
		PNOC017	1	BGB290 with TMZ	Recurrent IDH1/2-mutant glioma, ages 13–25 y	Recruiting	Marks/ Bindra	NCT03749187
ATM	AZD1390	AstraZeneca	1	AZD1390 and RT	Newly diagnosed and recurrent GBM, adults	Recruiting	Wen	NCT03423628
DNA-PK	CC115	INSIGhT	GBM	CC115 and GBM	Newly diagnosed GBM, adults	Completed	Wen/ Alexander	NCT02977780
Wee1	AZD1775	ABTC-1202	GBM	AZD1775, TMZ and RT	Newly diagnosed and recurrent GBM, adults	Completed	Lee	NCT01849146
	AZD1775	-	0	Monotherapy	Recurrent GBM, adults	Completed	Sanai	NCT02207010

Abbreviations: RT, Radiotherapy; TMZ, TMZ; GBM, Glioblastoma.

activity caused by OV replication or the GT-delivered anticancer cDNA. This cytotoxicity may then induce a second phase of innate and adaptive antitumor immunity caused by released tumor antigens.[291] There is one OV (talimogene laherparepvec) that has been FDA approved for melanoma,[292] and several GTs have been approved since 2017, such as voretigene neparvovec (Luxturna) for blindness and onasemnogene abeparvovec (Zolgensma) for spinal muscular atrophy.

For glioblastoma, several phase I clinical trials of both OVs and GTs are in progress or have been completed, usually in the recurrent setting.[293,294] In most, the treatment is delivered by intratumoral injection at the time of surgery. Currently there are several open GT trials (see Clinicaltrials.gov) that include: (i) injection in the resected recurrent glioblastoma cavity of an adenoviral GT vector that delivers an IL-12 cDNA whose transcription is activated by an oral agent, veledimex (NCT03636477)[259]; and (ii) injection into the resected newly diagnosed glioblastoma cavity of an adenoviral vector that delivers a thymidine kinase cDNA that leads to cytotoxicity when subjects take the oral drug, valacyclovir, combined with chemoradiation (NCT03576612).[260] Both trials also entail neoadjuvant or adjuvant immune checkpoint inhibition to counteract T-cell dysfunction. The latter trial is also being tested in pediatric brain tumors. Currently open OV trials in patients with recurrent glioblastoma include: (i) stereotactic injection of an oncolytic herpes simplex virus type 1 (oHSV) that delivers an IL-12 cDNA (NCT02062827); (ii) stereotactic injection of an oHSV that has been engineered to replicate better in glioblastoma cells that express the stem cell marker, nestin (NCT03152318); and (iii) monthly injections of oHSV G47Δ.[295] There are also trials delivering OV with stem cells: (i) intra-arterial delivery of allogeneic bone marrow–derived human mesenchymal stem cells loaded with the oncolytic adenovirus DNX-2401 (BM-hMSCs-DNX2401) (NCT03896568); and (ii) injection of neural stem cells that deliver an oncolytic adenovirus into newly diagnosed glioblastoma (NCT03072134). A general conclusion is that both OV and GT treatments have been well tolerated. When post-tissue treatment is available, there has been evidence of increased infiltration of immune cells, including cytotoxic T cells that also may have upregulated inhibitory immune checkpoint signaling.[296]

More advanced trials (phase II and beyond) are also ongoing mostly for OVs in the recurrent glioblastoma setting. These include: (i) convection-enhanced delivery of an engineered poliovirus (PVSRIPO; NCT02986178);[258] (ii)

Table 7 Selected completed trials with immunotherapies (including viral therapies)

Vaccines	Type	Phase	Trial	Trial Result
ICT107 (dendritic cell vaccine against MAGE-1, HER-2, AIM-2, TRP-2, gp100, and IL13Rα2)[273]	Newly diagnosed GBM	Randomized placebo controlled phase II	NCT01280552	• 124 patients randomized • PFS increased by 2.2 months ($P = 0.011$) • OS increased by 2.0 months (NS) • HLA-A2 subgroup showed increased clinical benefit and immune response
Rindopepimut (EGFRvIII peptide vaccine) ACT IV[202]	Newly diagnosed GBM with EGFRvIII mutation	Double blind phase III	NCT01480479	745 patients randomized • No difference in outcome with addition of rindopepipimut • Median overall survival was 20·1 months (95% CI 18·5–22·1) in the rindopepimut group versus 20·0 months (18·1–21·9) in the control group (HR 1·01, 95% CI 0·79-1·30; $P = 0.93$)
DC Vax (dendritic cell vaccine)[256]	Newly diagnosed GBM	Phase III	NCT00045968	• 331 patients treated • Primary endpoint of PFS not reported • 90% crossover at progression • Median OS was 23.1 months from surgery
Checkpoint Inhibitors	**Type**	**Phase**	**Trial**	**Trial result**
Nivolumab versus bevacizumab (CheckMate 143)[255]	Recurrent GBM	III	NCT02017717	• 369 patients randomized • No difference in outcome between the nivolumab or bevacizumab arm • Median OS was 9.8 months with nivolumab and 10.0 months with bevacizumab (NS), and the 12-mo OS rate was 42% in both arms. • Median PFS was 1.5 months for nivuolumab and 3.5 months for bevacizumab ORRs were 8% for nivolumab and 23% for bevacizumab • No steroid use and MGMT promoter methylation were associated with longer OS in the nivolumab arm versus the bevacizumab arm
Viral Therapies	**Type**	**Phase**	**Trial**	**Trial Result**
DNX-2401 (Delta-24-RGD) Oncolytic adenovirus[257]	Recurrent GBM	I	NCT02197169	• 37 patients • Fairly well-tolerated • 20% of patients survived > 3 years • 12% response • Evidence of virus replication in tumor • Cases of pseudoprogression
Polio virus (PVSRIPO)[258]	Recurrent GBM	1 (convection enhanced delivery)	NCT01491893	• 61 patients enrolled • Dose level –1 (5.0×10^{7} $TCID_{50}$) was identified as the phase 2 dose • 19% of the patients had a PVSRIPO-related adverse event of grade 3 or higher • OS reached a plateau of 21% (95% confidence interval, 11 to 33) at 24 months that was sustained at 36 months
Ad-RTS-hIL12 (adenovirus producing IL-12) + velidimex[259]	Recurrent GBM	1	NCT03679754	• 31 patients • Fairly well tolerated but cytokine syndrome observed in some • Median OS = 12.7 months • Inflammatory responses seen in recurrent tumors • Concurrent corticosteroids negatively affected survival: Patients cumulatively receiving >20 mg versus ≤20 mg of dexamethasone (days 0 to 14), median OS was 6.4 and 16.7 months, respectively
Gene mediated cytotoxic immunotherapy (GMCI; AdV-Tk) + valacyclovir + RT and TMZ[260]	Newly diagnosed GBM	II	NCT00589875	• 48 patients • No dose-limiting toxicities • Median OS was 17.1 months for GMCI + SOC versus 13.5 months for SOC alone ($P = 0.0417$) • Greatest benefit was observed in gross total resection patients: median OS of 25 versus 16.9 months ($P = 0.0492$)
TOCA 511 (replication competent retrovirus which transduces tumor cells with the cytosine deaminase gene) in combination with TOCA FC (5-flucytosine) versus SOC (TOCA 5 Study)[261]	Recurrent GBM	II/IIII	NCT02414165	• 403 patients treated • Fairly well tolerated • No difference in primary endpoint of OS between TOC 511 and lomustine (HR = 1.06 (95% CI: 0.83, 1.35; P-value = 0.6154) • Median OS: Toca 511: 11.07 months • SOC 12.22 months • Durable response rate 2.5% with TOCA 511; 4.5% with SOC (NS)

GBM; glioblastoma; NS, not significant; SOC, standard of care; Tk, thymidine kinase.

Table 8 Examples of ongoing trials with immunotherapies

Vaccine	Tumor Type	Phase	Trial
Personalized neoantigen cancer vaccine with RT and pembrolizumab	Newly diagnosed unmethylated GBM	I	NCT02287428
Personalized neoantigen DNA vaccine in combination with immune checkpoint blockade therapy	Newly diagnosed unmethylated GBM	I	NCT03068832
Personalized neoantigen- based vaccine in combination with nivolumab and ipilimumab	Newly diagnosed unmethylated GBM	I	NCT03422094
Personalized peptide vaccine in combination with standard therapy and TTFields	Newly diagnosed GBM	I	NCT03223103
pp65 CMV RNA-Pulsed Dendritic Cells With Tetanus-Diphtheria Toxoid Vaccine	Newly diagnosed	II	NCT02465268
SurVaxM (peptide vaccine against survivin) with TMZ following RT and TMZ	Newly diagnosed GBM	II	NCT02455557
INO-5401 (DNA plasmids targeting Wilms tumor gene-1 (WT1) antigen, prostate-specific membrane antigen (PSMA) and human telomerase reverse transcriptase (hTERT) genes) and INO-9012 (DNA plasmid expressing IL-12) in combination with cemiplimab (REGN2810), with radiation and chemotherapy	Newly diagnosed GBM	I/II	NCT03491683
VXMO1 (Attenuated Salmonella typhi Ty21a carrying a plasmid encoding for vascular endothelial growth factor receptor (VEGFR)-2) + avelumab	Recurrent GBM	I	NCT03750071
CMV vaccine VBI-1901	Recurrent GBM	I	NCT03382977
CMV pp65 peptide DC vaccine in combination with nivolumab	Recurrent GBM	I	NCT02529072
Pembrolizumab and ATL-DC (dendritic cell tumor lysate) vaccine	Recurrent GBM	I	NCT04201873
EO2401, Multipeptide Vaccine, With and Without Check Point Inhibitor	Recurrent GBM	I/II	NCT04116658
IMA950/Poly-ICLC + pembrolizumab	Recurrent GBM	I/II	NCT03665545
CMV RNA- loaded DC vaccine +/– anti- CD27 therapy varlilumab (to deplete Treg cells)	Recurrent GBM	II	NCT03688178
WT1 peptide vaccine (DSP-7888) in combination with bevacizumab	Recurrent GBM	II	NCT03149003
SurVaxM + pembrolizumab	Recurrent GBM	II	NCT04013672
Checkpoint Inhibitors and combinations	**Tumor Type**	**Phase**	**Trial**
Nivolumab + Gene Mediated Cytotoxic Immunotherapy (GMCI; Ad-Tk) + valacyclovir + RT + TMZ	Newly diagnosed GBM	I	NCT03576612
Nivolumab + ipilimumab + short course RT	Newly diagnosed unmethylated GBM	I	NCT03367715
Nivolumab, IDO inhibitor (BMS-986205), and RT With or Without TMZ	Newly diagnosed GBM	I	NCT04047706
Pembrolizumab + vorinostat (HDAC inhibitor) with RT and TMZ	Newly diagnosed GBM	I	NCT03426891
Atezolizumab + RT and TMZ	Newly diagnosed GBM	I/II	NCT03174197
Nivolumab + TMZ versus TMZ (NUTMEG)	Newly diagnosed elderly GBM	II	NCT03367715
Nivolumab + Gliadel wafers	Newly diagnosed GBM	II	
RT +/- Nivolumab (CheckMate 498) *	Newly diagnosed unmethylated GBM	III	NCT02617589
RT + TMZ +/- Nivolumab (CheckMate 548)#	Newly diagnosed methylated GBM	III	NCT02667587
Nivolumab +anti-LAG3 or anti-CD137	Recurrent GBM	I	NCT02658981
Avelumab + laser interstitial therapy	Recurrent GBM	I	NCT03341806
Nivolumab + Ad-RTS-hIL12 (adenovirus producing IL-12) + velidimex	Recurrent GBM	I	NCT03636477
Cemiplimab + Ad-RTS-hIL12 + velidimex	Recurrent GBM	I	NCT04006119
Biomarker driven therapy using immune activators with nivolumab (Nivolumab + anti-GITR (MK4166) or Nivolumab + IDO1 inhibitor (INCB024360) or Nivolumab + Ipilimumab	Recurrent GBM	I	NCT03707457
Anti-TIM3 monoclonal (TSR-022) +/– nivolumab	Advanced solid tumors	I	NCT02817633

Table 8 Continued

Vaccine	Tumor Type	Phase	Trial
Indoximod (IDO inhibitor) and TMZ	Recurrent GBM	I	NCT02052648
Neoadjuvant pembrolizumab	Recurrent GBM undergoing surgery	II	NCT02852655
Pembrolizumab	Hypermutated recurrent GBM	II	NCT02658279
Nivolumab +ipilimumab	Hypermutated recurrent GBM	II	
Nivolumab	Recurrent IDH mutated glioma	II	NCT03718767
Pembrolizumab and re-irradiation	Recurrent GBM (bevacizumab naïve or refractory)	II	NCT03661723
Nivolumab + standard or low dose bevacizumab	Recurrent GBM	II	NCT03452579
Nivolumab + ipilimumab + TTF	Recurrent GBM	II	NCT03430791
Pembrolizumab + DNX-2401 (CAPTIVE)	Recurrent GBM	II	NCT02798406
Pembrolizumab + abemaciclib (CDK4/6 inhibitor)	Recurrent GBM	II	NCT04118036
Pembrolizumab + levantinib (VEGFR and multikinase inhibitor)	Recurrent GBM	II	NCT03797326
Intratumor INT230-6 (amphiphilic cell penetration enhancer molecule combined with cisplatin and vinblastine) + nivolumab and ipilimumab	Recurrent GBM + other cancers	I/II	NCT03058289
Targeted Therapies and Other Agents	**Tumor Type**	**Phase**	**Trial**
WP1066 (STAT 3 inhibitor)	Recurrent GBM and melanoma	I	NCT01904123
Cellular Therapies Including CAR T cells	**Tumor Type**	**Phase**	**Trial**
EGFRvIII CAR T cells + pembrolizumab	Newly diagnosed EGFRvIII mutated unmethylated GBM	I	NCT03726515
Intracerebral EGFRvIII CAR T cells (INTERCEPT)	Recurrent GBM	I	NCT03283631
IL13Ralpha2-Targeted CAR T cells with or without nivolumab and ipilimumab	Recurrent GBM	I	NCT04003649
Memory-Enriched T Cells Transduced to Express a HER2-Specific, Hinge-Optimized, 41BB-Costimulatory Chimeric Receptor and a Truncated CD19	Recurrent GBM	I	NCT03389230

GBM, glioblastoma; HDAC, histone deacetylase; VEGFR2, RT, radiotherapy; TMZ, termozolomide; vascular endothelial growth factor receptor 2; TTF, tumor treating fields.
*Reported to be negative.
PFS reported to be negative; OS results pending.

stereotactic injection of an oncolytic adenovirus with selectivity for glioblastoma cells driven by the p16/retinoblastoma (RB) pathway and integrin expression (tasadenoturev; DNX-2401) in combination with pembrolizumab (NCT02798406);[257] and (iii) intracavitary injection after glioblastoma resection of a retrovirus that delivers a cytosine deaminase cDNA that provides chemosensitivity to 5-fluorocytosine (Toca 511; NCT02414165).[271,297] However, the phase III trial of Toca 511 was recently reported to show no survival benefit compared with standard of care in patients with recurrent glioblastoma.[261] A phase III trial of another viral therapy, ofranergene obadenovec (VB-111), which targets tumor endothelium, also failed to show a survival advantage in combination with bevacizumab compared with bevacizumab alone,[298] although it is possible that the simultaneous administration of bevacizumab may have impeded the effects of the virus.[298,299] Therefore, while there is currently optimism in the pursuit of novel concepts, this optimism must also be coupled with ongoing efforts to find molecular and immunologic variables and targets that may be associated with benefit.

Other Therapies

Overall, almost 100 therapies are under evaluation for glioblastomas. In addition to the ones listed above, other treatments include cytotoxic agents such as Val 083 (NCT02717962), BAL101553 (NCT03250299), and agents that may augment the activity of TMZ, such as ibudilast (NCT03782415).

Improving Clinical Trial Design

An important factor limiting the development of more effective therapies for glioblastoma is the slow and inefficient

clinical trial process. Frequently glioblastoma patients are excluded from phase I oncology trials evaluating novel agents without sound rationale.[300] As glioblastoma patients are generally healthy,[301] greater inclusion of these patients in phase I oncology trials will facilitate the identification of novel agents for further testing at an earlier stage.

Since the ability of many agents to cross the BBB to achieve therapeutic tumor concentrations and inhibit the appropriate molecular pathways adequately is either unknown or inadequate, there is a need for more "window-of-opportunity" "phase 0" surgical trials early during drug development. In these studies patients receive a therapeutic agent for 1–2 weeks prior to surgery, and tumor from both enhancing and non-enhancing areas obtained at surgery are analyzed for drug concentrations and pharmacodynamic effects. There is a need to develop more efficient clinical trial networks focused on these studies to identify agents worthy of further development.

Most treatments in glioblastoma have been initially assessed in uncontrolled single-arm studies using PFS or OS compared with contemporary or historical controls as primary endpoints. Limitations of these approaches have been the inadequacy of historical controls compared with external control data from prior trials[302] and, commonly, the failure to develop a biomarker to enrich patient populations in parallel or to inform on likelihood of success or failure of a new treatment. These shortcomings led to several inadequate phase II to III transitions, including the development of cilengitide,[303] enzastaurin,[304] bevacizumab,[148,186] cediranib,[190] rindopepimut,[202] and nivolumab.[255] Moreover, the frequent failure to understand why these trials were unsuccessful prevented lessons that could be learned to inform the design of future trials. No single therapeutic biomarker, not even *MGMT* promoter methylation, has been uniformly applied despite evidence that even TMZ only benefited approximately a third of patients with glioblastoma.[49] Beyond that, it seems unlikely today that there are new treatment options that would be active in an all comer trial, reinforcing the need for more elaborate research efforts prior to embarking on large clinical trials.

Steps to increase the likelihood of a drug to be successful in glioblastoma include preclinical modeling and window-of-opportunity (phase 0) surgical assessment, the parallel (and mandatory) assessment of tissue, CSF or blood for biomarkers and molecular imaging that may aid in enriching for benefiting versus failing patients, and the use of active, randomized control groups in earlier stages.[302] Innovative clinical trial concepts are based on the idea that phase II clinical evaluation must have a control arm, but could add several experimental arms. The endpoints of such trials might be pharmacodynamic-biomarker based or mainly imaging based—relying on more advanced MRI (or PET) techniques, including artificial intelligence algorithms[94,95]—and allow termination or expansion of cohorts in a dynamic fashion based on their likelihood of success. If biomarker based, adaptations may take place on the basis of quick, prospectively assessed biomarkers that are correlated to patients' performance with a given treatment and allow enrichment for subsequent biomarker-positive patients with the same therapy. Examples of this approach are GBM AGILE (NCT03970447)[229] and INSIGhT (NCT02977780).[228] Another opportunity is the assignment of patients to a specific therapy based on real-time assessment of a panel of biomarkers to be tested or even on high-throughput molecular tumor characterization, to allow (theoretically) treatment in the group of greatest likelihood of success, as done in the N^2M^2 trial.[227] These trials are most efficiently performed with multiple experimental groups and one standard arm. The basic requirements are a recent, non-historical tissue sample, adequate tests and assignment algorithms, and a broader tumor board, including biomarker/bioinformatics specialists.

The only randomized effort so far to evaluate the value of treatment allocation based on molecular testing over standard of care, the French SHIVA trial,[305] comes from the non–neuro-oncology area and failed to demonstrate overall benefit using historical tissue information guiding treatment decisions at progression. Nonetheless, there are many options to improve on this important first effort. One example is the WINTHER trial, which tested the role of the tumor transcriptome in identifying tumor vulnerabilities that may be treated with targeted therapies, an approach that may expand data-driven therapeutic options for patients.[306] While such modern clinical trial concepts are innovative and promising, the risk is that most glioblastomas are not a single pathway-driven disease and therefore will not be amenable to single agent targeted therapy selected based on molecular profiling.

As the design of clinical trials improves, it will also be important to consider incorporation of patient-reported outcomes and the input of patient advocates.

Challenges and Future Directions

Despite decades of research into the biology and treatment of glioblastoma, many challenges remain to treat this universally lethal cancer (Fig. 13). Glioblastomas are particularly aggressive and treatment refractory, resulting in disproportionate mortality, as reflected in the fact that they account for only 1.4% of cancers but 2.9% of cancer-related deaths.[307]

A major impediment to improving outcome is the fact that currently only approximately 11% of newly diagnosed glioblastoma patients enroll in clinical trials.[308] Reasons for this deficiency were recently reviewed and include many factors, including lack of knowledge regarding availability of trials[309] and the fact that physical or cognitive symptoms may reduce ability or willingness to travel for patients in the community who are seeking clinical trials at academic centers. Indeed, a survey of 57 patients demonstrated that travel time below 1 hour was significantly (4x) associated with increased willingness to consider clinical trial participation.[310] Developing strategies to improve clinical trial accrual will be critical.[309] Overly strict eligibility criteria are another barrier to accrual, and efforts are under way to address this.[311]

There are many other challenges that need to be addressed to improve therapy for patients with glioblastoma. A key consideration is the CNS location of these tumors and the need to consider treatment-related neurologic toxicities (eg, RT-induced neurocognitive injury, accelerated

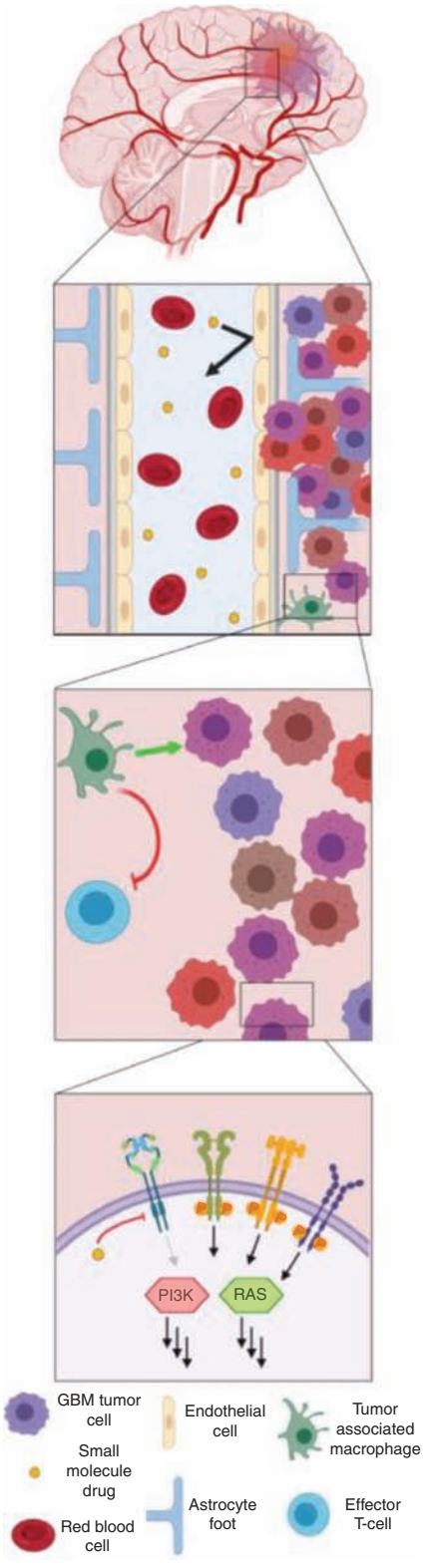


Figure 13. Challenges to effectively treat GBM include (top) the presence of the blood–brain barrier that precludes the delivery of many drugs into the brain coupled to (middle) an immunosuppressive microenvironment and (bottom) compensatory signaling networks that can render GBM therapies ineffective.

atherosclerotic disease),[312] which may profoundly impact quality of life. Another critical consideration is the BBB. Glioblastomas reside in and intertwine with the brain, where these tumors exploit the brain's natural defense mechanism against toxins via the BBB.[22,313]The BBB is composed of endothelial cells linked by tight junctions against a basement membrane that are surrounded by pericytes and astrocyte foot processes.[22] This barrier limits the diffusion of compounds to small, uncharged, lipid-soluble molecules. The vast majority of drugs do not possess these properties and therefore do not cross the BBB to a significant degree.[314] In addition to the physical barrier, the BBB is also reinforced with ATP-binding cassette transporter family proteins—drug efflux transporters on the luminal side of the BBB that remove toxic metabolites, xenobiotics, and drugs from the brain.[22,314]Together, these components prevent 98% of all small molecules from crossing the BBB.[314] Although it is well recognized that portions of glioblastoma tumors can have a leaky, compromised BBB, significant regions of the tumor (often the infiltrative tumor edge left behind in the patients after resection) still have an intact BBB and impede effective drug delivery.[22,313] With many recent major clinical trials failing to improve survival due to the compounds not achieving therapeutic concentrations at the target site,[315] the issue of brain penetration remains a major challenge to the treatment of glioblastoma. Strategies to overcome this issue include the development of significantly more agents with good BBB penetration,[316] hijacking endogenous influx transporters such as low-density lipoprotein receptor-related protein 1,[317] inhibiting efflux pumps, cell mediated drug delivery, convection-enhanced delivery, and focused ultrasound and microbubbles to transiently disrupt the BBB.[22,318]

Another critical therapeutic challenge for glioblastoma is the high degree of inter- and intratumoral heterogeneity. As the first cancer to be characterized by The Cancer Genome Atlas, glioblastoma has been shown to have multiple different genetic drivers.[28] The differences among glioblastomas are further complicated by the existence of intratumoral heterogeneity at both molecular and functional levels. For example, different regions within the same tumor may contain cells having distinct genetic compositions,[44,45] transcriptional subtypes,[19,43] and/or proliferation kinetics.[319,320] While the impact of this intratumor heterogeneity on therapeutic outcome remains poorly characterized, preclinical evidence suggests that functionally distinct glioma cells (eg, putative glioma stemlike cells compared with more differentiated counterparts) within a tumor can have differential responses to TMZ[319,320] or ionizing radiation,[234] which may underlie resistance to these conventional treatments. Additional work is necessary to examine the impact of glioblastoma heterogeneity on more contemporary therapies, including molecularly targeted therapies and immunotherapies. For example, comparisons of tumor specimens obtained at diagnosis and at recurrence suggest that temporal heterogeneity may occur with certain genetic alterations, such as EGFRvIII mutations, which are lost in 30–60% of recurrent tumors.[36,42,202] This raises the possibility that re-biopsy and genotyping, and/or improvements in minimally invasive liquid biopsy technology, may be necessary for therapies directed at targets that change over time.

In addition to the differential intrinsic drug sensitivity across distinct glioblastoma cell subpopulations, glioblastoma cells also display remarkable plasticity as a means to circumvent the toxic effects of cancer therapy. In response to targeted tyrosine kinase inhibitors, glioblastoma has been shown to adapt and survive through a wide variety of mechanisms, including the dynamic regulation of extrachromosomal DNA, chromatin remodeling to a slow-cycling/drug-tolerant persistent state, suppression of PTEN tumor suppressor, and reactivation in oncogenic signaling pathways (eg, phosphatidylinositol-3 kinase, Ras–mitogen-activated protein kinase signaling).[221,321,322] This redundancy in restoring oncogenic signaling flux can manifest via RTK switching[323] or the coactivation of multiple RTKs,[325] both of which can maintain persistent oncogenic signaling to promote tumor viability. Although there have been some examples of benefit with targeted molecular therapies (dabrafenib and trametinib for glioma with BRAFV600E mutations,[209] and entrectinib and larotrectinib for NTRK fusions,[211] and possibly ONC201 for H3K27M mutations),[212,213] most targeted therapies have failed because of low BBB penetration of the drugs employed, redundant signaling pathways, molecular heterogeneity, as well as the enhanced toxicity of the drug combinations, thus requiring suboptimal dosing. Alternative combination approaches, such as those that target orthogonal signaling/functional networks to induce synthetic lethality in glioblastoma,[322,324] are potential options to augment drug responses to therapies against the primary genetic driver. A likely corollary to these advanced approaches is that an approach based on a single mutation matched with a putative targeted therapy is unlikely to work in most glioblastomas, and efforts to integrate multiplatform molecular analyses (gene expression, copy number changes, immune cell/pathway profiling) are going to be required in future clinical trial designs to utilize advanced enriching strategies and maximize what we can learn even when specific therapeutic agents are not efficacious in a glioblastoma patient population

Although immunotherapy holds great promise as a new treatment option for glioblastoma, the negative results in large randomized studies to date[21,202,255] indicate the increased complexity and difficulty in achieving a clinically meaningful immune therapy effect in glioblastoma. In fact, it appears that glioblastoma provides challenges in almost every area of the cancer immunity cycle, including limited antigenicity, impaired antigen presentation, intrinsic and therapy-induced systemic immune suppression, and a unique immune suppressive microenvironment.[18] A functional and mechanistic understanding of these immune deficits will be required in order to construct effective immune therapies for glioblastoma.

Summary

Although there has been important progress in understanding the molecular pathogenesis and biology of glioblastoma, this has not translated into significantly improved outcomes for patients. While much remains to be learned, important therapeutic strategies have been identified that are being translated clinically. In addition to developing novel therapies based on strong scientific rationale, there is a need to increase the efficiency with which they are evaluated in clinical trials. This includes greater inclusion of glioblastoma patients in phase I oncology trials, an expanded network for conducting "window-of-opportunity" "phase 0" surgical studies to assess BBB penetration and pharmacodynamic effects, greater incorporation of molecular imaging and blood and CSF biomarkers, integration of a broad range of molecular biomarkers into clinical trial schema, more efficient design of clinical trials, and significantly increased trial accrual. These changes will hopefully lead to the identification of more effective therapies for patients with glioblastoma.

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